



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 179398

TO: Patricia Duffy
Location: REM/3B05/3C18
Art Unit: 1645
Thursday, February 16, 2006
Case Serial Number: 09/900766

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Duffy,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact*:

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☒ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.



STIC-Biotech/ChemLib

179308

From: Duffy, Patricia
Sent: Thursday, February 09, 2006 4:42 PM
To: STIC-Biotech/ChemLib
Subject: SEQ search

In re: 09/900,766

Please search SEQ ID NO:1 and 7.
Please print out top 75 hits for each.
Please include both a commercial and interference search

Thank you,

Pat Duffy
REMSSEN 3B05; mailbox 3C18
571-272-0855

RECEIVED
FEB 13 2006
STIC

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:08:10 ; Search time 201.229 Seconds
(without alignments)
1467.298 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522

Sequence: 1 EVLOQSGDPLVKPGASVKI.....EATHKTSPIVKSPFNRNES 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : A Geneseq_21.*

- 1: Geneseqp1990s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3522	100.0	672	6	ABP58454
2	1832.5	52.0	478	8	ADN97499
3	1832.5	52.0	509	8	ADN97517
4	1653	46.9	552	8	ADN97513
5	1644	46.7	573	4	AG64459
6	1321.5	37.5	669	9	ADY97271
7	1218	34.6	233	6	ABP58455
8	1130	32.1	233	6	ABP58457
9	1113	31.6	245	2	AAW35375
10	1107	31.4	233	6	ABP58456
11	1107	31.4	257	4	AAU14103
12	1107	31.4	257	6	ABO10268
13	1107	31.4	257	8	ADF9830
14	1096.5	31.1	720	4	AG65572
15	1095.5	31.1	603	9	ADM44587
16	1093.5	31.0	621	9	ADM44588
17	1093	31.0	230	4	ABP67339
18	1091	31.0	245	2	AAW35374
19	1072	30.4	248	6	ABU79072
20	1072	30.4	248	7	ADP43296
21	1072	30.4	248	9	AEA02990
22	1069	30.4	592	4	AB83838
23	1069	30.4	595	2	AAW86003
24	1064	30.2	469	8	ADR59118

25	1059.5	30.1	464	2	AA76088
26	1055.5	30.0	445	2	AA76085
27	1048	29.8	230	2	AA45012
28	1048	29.8	460	9	ADW97108
29	1044	29.6	230	5	ABP76235
30	1044	29.6	459	9	ADW97104
31	1044	29.6	460	9	ADW97139
32	1042	29.6	467	8	ADQ14477
33	1035	29.4	230	2	AA13204
34	1028	29.2	597	5	AAE18377
35	1028	29.2	597	5	ABG76352
36	1025.5	29.1	464	2	AAW83041
37	1025.5	29.1	464	3	AA14747
38	1025.5	29.1	464	3	AAW90897
39	1025.5	29.1	464	5	ABW74912
40	1025.5	29.1	464	5	ABW74866
41	1025.5	29.1	466	9	ADX39100
42	1025.5	29.1	466	9	ADX39137
43	1024.5	29.1	613	5	AAE18380
44	1024.5	29.1	613	5	ABG76355
45	1023.5	29.1	441	9	AEC20771
46	1023.5	29.1	456	5	AAE18370
47	1023.5	29.1	456	5	ABG76345
48	1023.5	29.1	456	9	ABW96754
49	1023.5	29.1	493	5	AAE18379
50	1023.5	29.1	493	5	ABG76354
51	1023.5	29.1	510	5	AAE18378
52	1023.5	29.1	510	5	ABG76353
53	1022.5	29.0	438	5	AAE18372
54	1022.5	29.0	438	5	ABG76347
55	1020	29.0	697	8	ADQ07403
56	1020	29.0	697	8	ADQ12180
57	1018	28.9	206	2	AAV39452
58	1018	28.9	465	2	AAW66758
59	1013.5	28.8	462	9	ADW44429
60	1006	28.6	701	8	ADQ07409
61	1006	28.6	701	8	ADQ12186
62	1000	28.4	464	9	ADW97112
63	1000	28.4	700	8	ADN97521
64	980.5	27.8	711	2	AAW85692
65	979.5	27.8	223	7	ADE06766
66	977.5	27.8	626	3	AAV55081
67	972.5	27.6	243	2	AAW86002
68	972.5	27.6	243	2	AAW42294
69	972.5	27.6	243	2	AAV27407
70	972.5	27.6	243	4	AAW83835
71	970	27.5	214	2	AAV44176
72	967.5	27.5	488	2	AAW86004
73	967.5	27.5	488	4	AAW83836
74	967.5	27.5	488	6	ABU07262
75	967.5	27.5	488	6	ABU07253
76	966.5	27.4	209	6	ABP96772
77	966.5	27.4	209	6	ABP96771
78	966	27.4	468	2	AA131061
79	966	27.4	468	2	ADQ91057
80	965.5	27.4	510	8	ADN97519
81	965.5	27.4	510	8	ADN97501
82	961.5	27.3	225	2	AAW40385
83	960	27.3	212	2	AAW15932
84	960	27.3	212	2	AAW13203
85	960	27.3	369	9	ABE13483
86	959	27.2	301	9	ABE13483
87	958	27.2	214	8	ADN97511
88	956	27.1	461	8	ADT08443
89	955.5	27.1	244	8	ADG28554
90	955	27.1	243	8	ADT77692
91	954	27.1	239	9	AEA27483
92	954	27.1	546	9	ABE92076
93	953.5	27.1	223	2	AAW75456
94	953	27.1	220	2	AAW53802
95	952	27.0	222	8	ADN97509
96	952	27.0	243	8	ADT77693
97	951.5	27.0	469	2	AAW40384

AA76088	MAB 55.1
AA76085	MAB 55.1
AA45012	Staphyloc
ADW97108	Murine MA
ABP76235	Staphyloc
ADW97104	Murine MA
ADW97139	Murine MA
ADQ14477	Mouse ant
AA13204	Staphyloc
AAE18377	Human N-t
ABG76352	Mouse DAV
AAW83041	Anti-Pas
AA14747	Mouse ant
AAW90897	Murine an
ABW74912	Humanised
ABW74866	Humanised
ADX39100	Mouse mon
ADX39137	Mouse mon
AAE18380	Human N-t
ABG76355	Mouse DAV
AEC20771	M-CSF spe
AAE18370	Human pen
ABG76345	Mouse DAV
ABW96754	DAV-1 ant
AAE18379	Human N-t
ABG76354	Mouse DAV
AAE18378	Human N-t
ABG76353	Mouse DAV
AAE18372	Human pen
ABG76347	Portion o
ADQ07403	hCBE11/hB
ADQ12180	Heavy cha
AAV39452	Antibody
AAW66758	Anti-toba
ADW44429	Mouse ant
ADQ07409	hCBE11 mo
ADQ12186	Heavy cha
ADW97112	Murine MA
ADN97521	Artificia
AAW85692	MoTabII f
ADE06766	D18 heavy
AAV55081	Single ch
AAW86002	Murine an
AAW42294	Anti-5r4
AAV27407	5T4 scFv
AAW83835	Amino aci
AAV44176	MAB Fab13
AAW86004	Human B7-
AAW83836	Amino aci
ABU07262	Human exp
ABU07253	Human exp
ABP96772	TSH recep
ABP96771	TSH recep
AA131061	Monoclon
ADQ91057	Murine OK
ADN97519	Artificia
ADN97501	Artificia
AAW40385	Monoclon
AAW15932	Antibody
AAW13203	Staphyloc
ABE13483	VEGF-SEA f
ABE13483	EGF-SEA f
ADN97511	Artificia
ADT08443	Novel ant
ADG28554	Paramyxov
ADT77692	Monoclon
AEA27483	Monoclon
ABE92076	Undefined
AAW75456	Mouse ant
AAW53802	FAB light
ADN97509	Artificia
ADT77693	Monoclon
AAW40384	Monoclon

98	950.5	27.0	621	9	ADM44596	Adw44596	PRIMATIZE	171	912	25.9	238	5	AAE18371	Human pen
99	949.5	27.0	467	9	ADV26107	Adv26107	Mouse OKT	172	912	25.9	238	5	ABG76346	Mouse DAV
100	948.5	27.0	467	9	ADW71833	Adw71833	Murine OK	173	912	25.9	238	9	AE96755	DAV-1 ant
101	948.5	26.9	244	9	ADR59117	Adr59117	Anti-K88/	174	912	25.9	448	2	ADX31673	Mouse ant
102	948	26.9	214	3	AAU78253	Aau78253	Mouse agg	175	911	25.9	234	9	ADX39101	Mouse mon
103	948	26.9	233	6	ABP58458	Abp58458	Staphyloc	176	911	25.9	234	9	ADX39138	Mouse mon
104	948	26.9	257	4	AAU14104	Aau14104	Peptide s	177	910	25.8	214	6	ABP96756	TSH recep
105	948	26.9	257	6	ABO10269	Abu10269	S. aureus	178	910	25.8	214	6	ABP96755	TSH recep
106	948	26.9	257	7	ADW10299	Adw10299	Staphyloc	179	910	25.8	214	9	AEC20774	M-CSF spe
107	948	26.9	257	8	ADH10956	Adh10956	Enterotox	180	910	25.8	218	6	ABP96773	TSH recep
108	948	26.9	257	8	ADH11662	Adh11662	Staphyloc	181	910	25.8	218	6	ABP96774	TSH recep
109	947	26.9	214	9	AEC20772	Aec20772	M-CSF spe	182	909.5	25.8	254	2	AAV30117	Murine an
110	945	26.8	234	6	AAO29870	Aao29870	Mouse ant	183	909.5	25.8	254	2	AAV30119	Murine an
111	945	26.8	234	7	ADJ79788	Adj79788	TRA-8 ant	184	909.5	25.8	254	9	ADW10850	Polypepti
112	944.5	26.8	209	6	ABP96752	Abp96752	TSH recep	185	909	25.8	272	9	AEA29814	Mouse ZMC
113	944.5	26.8	209	6	ABP96751	Abp96751	TSH recep	186	909	25.8	448	2	AAR06476	Heavy cha
114	944.5	26.8	239	2	AAR76087	Aar76087	Mab 55.1	187	908.5	25.8	219	3	AAV95258	WOM-1 Fab
115	944	26.8	233	2	AAW06738	Aaw06738	Staphyloc	188	908.5	25.8	219	8	ADP84966	Murine an
116	944	26.8	233	8	ADI95318	Adi95318	OSPF-rela	189	908	25.8	257	3	AAV70102	Staphyloc
117	942	26.7	233	2	AAR45011	Aar45011	Staphyloc	190	907.5	25.8	216	8	ADU86562	Immunoglo
118	941.5	26.7	219	2	AAR76086	Aar76086	Mab 55.1	191	907	25.8	222	2	AAW01751	MH1 monoc
119	941	26.7	233	2	AAW35373	Aaw35373	Staphyloc	192	906	25.7	214	8	ADW41870	Amino aci
120	941	26.7	233	4	AAW67338	Aaw67338	Staphyloc	193	904.5	25.7	219	3	AAV68994	Amino aci
121	940	26.7	243	8	ADT77694	Adt77694	Monoclon	194	904.5	25.7	238	2	AAV17416	Mouse imm
122	938	26.6	234	5	AAU72802	Aau72802	TRA-8 lig	195	904	25.7	214	6	ABP96763	TSH recep
123	935	26.5	257	6	ABU79068	Abu79068	S. aureus	196	904	25.7	214	6	ABP96764	TSH recep
124	935	26.5	257	7	ADF43288	Adf43288	Staphyloc	197	904	25.7	448	2	AAR99643	Anti-bGH
125	935	26.5	257	9	AEA02982	Aea02982	Staphyloc	198	903.5	25.7	219	8	ADJ15725	Murine an
126	933	26.5	222	2	AAW15934	Aaw15934	Antibody	199	903	25.6	233	3	AAV70103	Mutant Sc
127	933	26.5	233	5	ABB76234	Abb76234	Staphyloc	200	902.5	25.6	219	8	ADR19323	Murine Ig
128	932.5	26.5	218	7	ADD05274	Add05274	Female mo	201	901.5	25.6	219	8	ADN41874	Amino aci
129	932.5	26.4	218	8	ADM80365	Adm80365	Murine ho	202	901	25.6	218	2	AAR75459	Mouse ant
130	931	26.4	223	1	AAP40031	Aap40031	Kappa ant	203	901	25.6	218	2	AAR75457	Mouse ant
131	926	26.3	451	8	ADN97545	Adn97545	Artificia	204	900.5	25.6	215	8	ADO19050	Murine an
132	925	26.3	257	5	ABB79501	Abb79501	Staphyloc	205	900.5	25.6	462	6	AAO29869	Mouse ant
133	925	26.3	257	6	ABU10081	Abu10081	Staphyloc	206	900.5	25.6	462	5	ADJ79787	TRA-8 ant
134	925	26.3	257	7	ABU62334	Abu62334	S. aureus	207	900.5	25.6	464	5	AAU72801	Anti-K88/
135	925	26.3	257	7	AAE37676	Aae37676	Protein #	208	898.5	25.5	240	8	ADR59121	Anti-K88/
136	923.5	26.2	219	9	ADZ00217	Adz00217	Mouse OKT	209	897.5	25.5	215	8	ADO19052	Murine an
137	923.5	26.2	219	9	ADZ00217	Adz00217	Mouse OKT	210	897.5	25.5	223	2	AAR75458	Mouse ant
138	921	26.1	233	5	AAV54463	Aav54463	Amino aci	211	897.5	25.5	474	9	ADV86668	FLJ32028
139	921	26.1	233	5	ABW79502	Abw79502	Staphyloc	212	896	25.4	214	9	AEC20765	M-CSF spe
140	921	26.1	233	6	ABU10082	Abu10082	Staphyloc	213	895	25.4	214	6	ABP96759	TSH recep
141	921	26.1	233	7	ABU62335	Abu62335	S. aureus	214	895	25.4	214	6	ABP96760	TSH recep
142	921	26.1	233	7	AAE37677	Aae37677	Protein #	215	895	25.4	216	2	AAW15935	Antibody
143	921	26.1	233	9	ADY93173	Ady93173	Bacterial	216	895	25.4	216	6	ABP96776	TSH recep
144	919.5	26.1	219	2	AAR44495	Aar44495	Sequence	217	895	25.4	216	6	ABP96775	TSH recep
145	918.5	26.1	465	8	ADT77691	Adt77691	Monoclon	218	894	25.4	218	8	ADN97507	Artificia
146	917.5	26.1	219	6	ABP96777	Abp96777	TSH recep	219	894	25.4	712	8	ADN97543	Artificia
147	917.5	26.1	219	6	ABP96778	Abp96778	TSH recep	220	893.5	25.4	219	2	AAW53597	Amino aci
148	917	26.0	238	6	ABU10099	Abu10099	Staphyloc	221	893.5	25.4	233	9	ADW97106	Murine MA
149	916.5	26.0	238	2	AAW31752	Aaw31752	L chain s	222	893.5	25.4	233	9	ADW97102	Murine MA
150	916.5	26.0	238	2	AAW71889	Aaw71889	Anti-huma	223	893.5	25.4	470	8	AEA27481	Monoclon
151	916.5	26.0	238	3	AAW12909	Aaw12909	Anti-huma	224	892.5	25.3	463	9	AEA27481	Monoclon
152	916	26.0	454	5	ABB76124	Abb76124	Recombina	225	892.5	25.3	599	2	AAR90837	3B1 singl
153	916	26.0	462	5	ABB76126	Abb76126	Recombina	226	892	25.3	232	9	ADW97131	Murine MA
154	915.5	26.0	234	2	AAV30123	Aav30123	Murine an	227	891	25.3	214	9	AEC20776	M-CSF spe
155	915.5	26.0	254	2	AAV30121	Aav30121	Murine an	228	891	25.3	215	3	AAR78254	Mouse agg
156	915.5	26.0	254	9	ADW10852	Adw10852	BotFab5 h	229	891	25.3	218	6	ABP96770	TSH recep
157	915.5	26.0	254	9	ADW10854	Adw10854	BotFab20	230	891	25.3	218	6	ABP96769	TSH recep
158	915	26.0	231	8	ADR98924	Adr98924	Staphyloc	231	890.5	25.3	215	8	ADN97547	Artificia
159	915	26.0	238	2	AAW83042	Aaw83042	Anti-Fas	232	890.5	25.3	483	8	ADN97549	Artificia
160	915	26.0	238	3	AAW14748	Aaw14748	Mouse ant	233	890	25.3	214	6	ABP96766	TSH recep
161	915	26.0	238	3	AAW90898	Aaw90898	Murine an	234	890	25.3	214	6	ABP96765	TSH recep
162	915	26.0	238	5	ABB74913	Abb74913	Humanised	235	889.5	25.3	235	2	AAW06178	Murine A5
163	915	26.0	238	5	ABB74867	Abb74867	Humanised	236	889.5	25.3	235	2	AAW06178	Murine A5
164	914.5	26.0	219	2	AAR59416	Aar59416	6D9 antib	237	889	25.2	467	6	AAE38408	Mouse vir
165	914.5	26.0	219	8	ADP84965	Adp84965	Murine Ig	238	888	25.2	214	6	ABP96762	TSH recep
166	914.5	26.0	220	9	AE808093	Ae808093	Murine Ig	239	888	25.2	214	6	ABP96761	TSH recep
167	913	25.9	448	2	AAR97376	Aar97376	Murine an	240	888	25.2	214	8	ADJ15723	Murine an
168	912.5	25.9	235	2	AAR47449	Aar47449	T84.12 l1	241	888	25.2	438	8	ADJ15726	Murine an
169	912.5	25.9	235	2	AAR47451	Aar47451	T84.12 L4	242	886	25.2	237	7	ADE57549	Human Pro
170	912	25.9	233	6	ABU10098	Abu10098	Staphyloc	243	886	25.2	237	7	ADD47098	Human Pro

QY 301 ATSEYEGSSVDLYGAYYQACGTPNKTACMYGGVTLHDNNRLTEEEKVPINLWIDGKQ 360
Db 245 HRDDPPPTASDI----- 256
QY 361 TTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQORGLIVFHSSEGSTVS 420
Db 257 -----GKRGKRGD----- 265
QY 421 YDLFDAQQGYPTDLLRIYRDNWTTISSTLSLSLYLTTSIVMTQTPSSLVLSAGDRVIT 480
Db 266 -----IVMTQSHKFMSTSVGDRVSIT 286
QY 481 CKASQSVNDVAMYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTLTSSVQAE 540
Db 287 CKASQDVNTAVAMYQKPGHSPKLLIYSASFRYTGVPDRFTGNRSRGTDFTLTSSVQAE 346
QY 541 AAVYFCQDYNSTPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFLNNFPK 600
Db 347 LAVYCOQHYTTPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFLNNFPK 406
QY 601 DINVKWKIDGSEQRQGVLSNWTDDSKDSTYSMSSTLTLTCKDEYERHNSVTCBATHKTS 660
Db 407 DINVKWKIDGSEQRQGVLSNWTDDSKDSTYSMSSTLTLTCKDEYERHNSVTCBATHKTS 466
QY 661 SPIVKSFRNE 671
Db 467 SPIVKSFRNE 477

RESULT 3
ADN97517
ID ADN97517 standard; protein; 509 AA.
AC ADN97517;
XX
DT 01-JUL-2004 (first entry)
XX
DE Artificial protein construction protein #17.
XX
KW artificial proprotein; propeptide; protein engineering; antibody.
XX
OS Unidentified.
XX
PN WO2004031362-A2.
XX
PD 15-APR-2004.
XX
PF 03-OCT-2003; 2003WO-US031420.
XX
PR 03-OCT-2002; 2002US-0415940P.
XX
PA (LARG-) LARGE SCALE BIOLOGY CORP.
XX
PI Reini SJ, Edwards P;
XX
DR WPI; 2004-330170/30.
XX
DR N-PSDB; ADN97516.
XX
PT New artificial proprotein comprises three peptide sequences, useful for
XX
PT artificial multimeric protein engineering in eukaryotes.
XX
PS Example 12; SEQ ID NO 90; 244pp; English.
XX
CC The invention relates to an artificial proprotein comprising three
XX
CC peptide sequences: a first peptide sequence of interest, a propeptide
XX
CC sequence attached to the C-terminus of the first peptide sequence of
XX
CC interest, and a second peptide of interest attached to the C-terminus of
XX
CC the propeptide sequence. The artificial proprotein and polynucleotides
XX
CC are useful for artificial multimeric protein engineering, e.g. antibodies
XX
CC and antibody fragments in eukaryotes. This sequence corresponds to a
XX
CC protein used in the generation of the protein of the invention.
XX

SQ Sequence 509 AA;
Query Match 52.0%; Score 1832.5; DB 8; Length 509;
Best Local Similarity 56.5%; Pred. No. 1.1e-100;
Matches 379; Conservative 32; Mismatches 65; Indels 195; Gaps 5;
QY 1 EVLQSQGPDLPKASVKISCKASGYSFTGYMHWKQSPGKGLWIGRINPNNGVTLY 60
Db 33 QVQLQQSGPELVKPGASLKLCTASGFNIDKTIHWYKQRPQGLWIGRIYPTNGVTRY 92
QY 61 NQPKDKATLTVDKSSSTAYMELRSITSEDSAVYVCARSTMIINYMDYWGQGTSTVVS 120
Db 93 DPKFQKATITADTSSNTAYLQSRITSEDTAVYCSRWGGDGFANDYWGQGSASVVS 152
QY 121 AKTTPSVVPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVTTPFAVLQSD 180
Db 153 AKTTPSVVPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVTTPFAVLQSD 212
QY 181 LYTLSSSVTPSSTWSPSETVTCNVAHPASSTKDKIIVPRDSGGPSEKSEINEKDLKK 240
Db 213 LYTLSSSVTPSSTWSPSETVTCNVAHPASSTKDKIIVPRDCG-----GK 258
QY 241 SELOQTALGNLKOIYYNNSKAITSSSEKSAQDLTNTLLFKGPTFGHPWYNDLLVDLSTA 300
Db 259 RTIQDSA-----TDT-----VDLGAE 275
QY 301 ATSEYEGSSVDLYGAYYQACGTPNKTACMYGGVTLHDNNRLTEEEKVPINLWIDGKQ 360
Db 276 HRDDPPPTASDI----- 287
QY 361 TTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQORGLIVFHSSEGSTVS 420
Db 288 -----GKRGKRGD----- 296
QY 421 YDLFDAQQGYPTDLLRIYRDNWTTISSTLSLSLYLTTSIVMTQTPSSLVLSAGDRVIT 480
Db 297 -----IVMTQSHKFMSTSVGDRVSIT 317
QY 481 CKASQSVNDVAMYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTLTSSVQAE 540
Db 318 CKASQDVNTAVAMYQKPGHSPKLLIYSASFRYTGVPDRFTGNRSRGTDFTLTSSVQAE 377
QY 541 AAVYFCQDYNSTPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFLNNFPK 600
Db 378 LAVYCOQHYTTPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFLNNFPK 437
QY 601 DINVKWKIDGSEQRQGVLSNWTDDSKDSTYSMSSTLTLTCKDEYERHNSVTCBATHKTS 660
Db 438 DINVKWKIDGSEQRQGVLSNWTDDSKDSTYSMSSTLTLTCKDEYERHNSVTCBATHKTS 497
QY 661 SPIVKSFRNE 671
Db 498 SPIVKSFRNE 508

RESULT 4
ADN97513
ID ADN97513 standard; protein; 552 AA.
XX
AC ADN97513;
XX
DT 01-JUL-2004 (first entry)
XX
DE Artificial protein construction protein #15.
XX
KW artificial proprotein; propeptide; protein engineering; antibody.
XX
OS Unidentified.
XX
PN WO2004031362-A2.
XX
PD 15-APR-2004.
XX


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Db 187 SVTVSSAKTTPSPYPLAPGSAQTNSMVTLCGLVKGYPPEPVTVTWNSGSLSSGVHTFP 246
Qy 175 AVLOSGLYTLSSSVTPSPSTWPCNVAHPASSTKVDKIVPRDSGGPSEKSEBINE 234
Db 247 AVLOSGLYTLSSSVTPSPSTWPCNVAHPASSTKVDKIVPRD----- 293
Qy 235 KDLRKSELOGTALGNLKQIYYNSKAITSEKSDAQFLTNTLLFKGFTTGHWPYNDLLV 294
Db 294 -----CTSDAEST----- 301
Qy 295 DLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINL 354
Db 302 -----TVSKTENLSGGSSVIEFRAGY-----LFF 326
Qy 355 WIDG-KOTTVPIDKVTSKKEVTVQELDLQARHVLHGKFGLYNSDSFGKVGQRLIVFHS 413
Db 327 WMEAMKOSTI----- 336
Qy 414 SEGSTVSYDLFDAGQGYPTDLLRIYRDNNTISSTLSISLYLT-----TSIVMTQPT 467
Db 337 -----LALLLLLLLTPVTKAMAEVMTQPTL 362
Qy 468 SLIVSAGDRVTITCKASQSV--SND-----VAVYQKPGQSPKLLISYTSRYAGVDPDRFSG 522
Db 363 SLFVSLGDQASISCRSQTIVHSGDYLDFWFLQKPGQSPKLLIYKVSNRFSGVDPDRFSG 422
Qy 523 SGVGTDTLTISSVQAEADAVYFCQDYNPPTFGGTTKLEIKRADAAPTIVSIFPPSSEQ 582
Db 423 SSGGTDTLTKISRVEADLGVYICFGSHVPTFGGTTKLEIKRADAAPTIVSIFPPSSEQ 482
Qy 583 LTSGASVVCFLNNFYFKDINVWKIDGSRQNGVLSNWDQSDKSTYSMSSTLTITKD 642
Db 483 LTSGASVVCFLNNFYFKDINVWKIDGSRQNGVLSNWDQSDKSTYSMSSTLTITKD 542
Qy 643 EYERHNSYTCEATHTKSTSPIVKSFNRNE 671
Db 543 EYERHNSYTCEATHTKSTSPIVKSFNRNE 571

RESULT 6
ADY97271
ID ADY97271 standard; protein; 669 AA.
AC ADY97271;
XX
XX
DT 16-JUN-2005 (first entry)
XX
DE Exemplary antibody fusion protein SEQ ID NO:3.
XX
XX antibody engineering; fusion protein; cytostatic; antimicrobial;
XX virucide; antibacterial; cancer; infection.
XX
OS Synthetic.
XX
XX US2005069552-A1.
XX
XX 31-MAR-2005.
XX
XX 28-JUL-2004; 2004US-00900928.
XX
XX 28-JUL-2003; 2003US-0490569P.
XX
XX (BLEC/) BLECK G T.
XX (YORK/) YORK D.
XX (COLL/) COLLINS I.
XX
XX Bleck GT, York D, Collins I;
XX
XX WPI; 2005-261600/27.
XX N-PSDB; ADY97269.
XX
XX Composition useful as cancer vaccine, comprises polypeptide having
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```
PT antibody heavy chain fused to antibody light chain, or multivalent
PT antibody having two polypeptides with antibody heavy chain fused to
PT antibody light chain.
XX
XX Disclosure; SEQ ID NO 3; 101pp; English.
XX
CC The invention describes a composition (I) comprising: (a) a polypeptide
CC comprising at least one antibody heavy chain fused to at least one
CC antibody light chain; or (b) a multivalent antibody comprising at least
CC two polypeptides, where each of the polypeptides comprises at least one
CC antibody heavy chain fused to at least one antibody light chain. Also
CC described: (1) a composition (II) comprising a nucleic acid comprising at
CC least one antibody heavy chain gene and at least one antibody light chain
CC gene, where the nucleic acid encodes a polypeptide comprising at least
CC one antibody heavy chain fused to at least one antibody light chain; (2)
CC a method (M1) of binding an antigen, involves providing a polypeptide
CC comprising at least one antibody heavy chain fused to at least one
CC antibody light chain, and contacting the polypeptide with a sample having
CC an antigen under conditions such that the polypeptide binds to the
CC antigen; (3) a method (M2), which involves providing a vector comprising
CC a bicistronic expression construct comprising genes encoding an antibody
CC heavy chain gene and an antibody light chain gene, and altering the
CC nucleic acid sequence of a splice acceptor sequence or a splice donor
CC sequence in the antibody light chain gene or the antibody heavy chain
CC gene under conditions such that splicing is prevented at the splice
CC acceptor sequence or donor sequence; (4) a nucleic acid sequence produced
CC by (M2); (5) a vector (III) comprising a modified antibody heavy or light
CC gene, where modification eliminates a splice donor or acceptor sequence
CC in antibody heavy or light chain gene; and (6) a host cell comprising
CC in a mixture or determining the presence or absence of expression of a
CC particular protein. (I) is also useful as vaccine for treating cancer and
CC infections caused by pathogens e.g. virus or bacteria. The present
CC sequence represents an exemplary antibody fusion protein from the present
CC invention.
XX
SQ Sequence 669 AA;
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Query Match 37.5%; Score 1321.5; DB 9; Length 669;
Best Local Similarity 40.8%; Pred. No. 3.9e-70;
Matches 303; Conservative 94; Mismatches 199; Indels 147; Gaps 17;

Qy 1 EVOLQSGDPLVKPGASVKISCKASGYFTGYMHWVKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVOLVESGGGVQPGRRSLRSCSGSDFDTTYNWSVVRQAPGKLEWIGRIHPDSSTNY 60
Qy 61 NQKFKDKATLTVDKSSSTTAYMELSLTSEDSAVYCYCARSTMIYNYMDYNGQSTVTVSS 120
Db 61 APSLKDRFTISRDNAXNTLFLQMDSLRPEDTGYVFCA-SLYFGFPWFAYWGQGPVTVSS 119
Qy 121 AKTTTPSVYPLAPGSAQAQTNSMVTLCGLVKGYPPEPVTVTWNSGSLSSGVHTFPVLQSD 180
Db 120 ASTKGFSVFLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
Qy 181 -LYLTSSSVTPSPSTWPCNVAHPASSTKVDKIVPRDS-----GG 224
Db 180 GLYSLSSVTPSPSSSLGTQYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELGG 239
Qy 225 PSEKSEINEKD---LRKSELOGTALGNLKQIYYNSKAITSEKSDAQFLTNTLLFKG 281
Db 240 PSVFLFPKPKDTLMISRTPEVTCVVVD-----VSHEDPEVK----- 277
Qy 282 FFTGHPWYND-LLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHD 340
Db 278 -----NWYVDGVEVHNKTKPREEQYNSTYRVVSVL-----TVLHQ 313
Qy 341 NNRLTEKKVPINLWIDGKQ-----TTVPIDK-----VKTSKEV 375
Db 314 D-----WLNKKEYCKVSNKALPAPIETKTISKAKGQPRPQVYVTLPPSREEM 360
Qy 376 TVQELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHSSEGS-----TVSVDLFDAGQY 430
Db 361 TKNQVSLTCL-----VKGFYPSD-----IAVEWESNGQPENNYKTTTPPVLDSDGSF 406
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QY 431 -----PDLLRIYRDNNTTSSLSLSLYLT--SIWMTQTPS 468
DB 407 FLYSKLTVDKSRWQGNVFCSSVHEALHNHYTKLSLSLPGILFHATQADIQLTQSPSS 466
QY 469 LLVSGDRVTITCKASQSVNDVAVYQOKPGQSPKLLISYTSRYAGVDPDRFSGSGYGT 528
DB 467 LNSVGDRTVITCKASQDVCTSVAVYQOKPGKPKLLIYWTSTRHGTGVSFRFSGSGT 526
QY 529 FTLTSSVQADAAVYFCQDYNSPPTFGGTTKLEIKRADAAPTVAIFPPSSQLTSGGA 588
DB 527 FTFITSSLOPEDIATVYCOQ-YSLYRSFGQTKVEIKRTVAAPSVFIPPSDQLKSGTA 585
QY 589 SVVCFLLNFPKDVNKWIDGSEKQVNLNSWTDQSDKSTYSMSSTLTLTQDEYERHN 648
DB 586 SVVCLLNFPYPRKQVWKVDNALQSGNSQSVTEQDQSDKSTYSLSSTLTLSKADYERKH 645
QY 649 SYTCEATHKTSTSPVIVKSFNRNE 671
DB 646 VVACEVTHQGLSSPVTKSFNRGE 668
RESULT 7
ID ABP58455 standard; protein; 233 AA.
XX ABP58455;
XX 14-APR-2003 (first entry)
DT Engineered superantigen SEA/E-120 for human cancer therapy.
DE Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
KW cytostatic; vaccine; SEA/E-120; mutant; mutein.
XX Staphylococcus sp.
OS Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 20 /note= "wild-type Arg substituted by Gly"
FT Misc-difference 21 /note= "wild-type Asn substituted by Thr"
FT Misc-difference 24 /note= "wild-type Ser substituted by Gly"
FT Misc-difference 27 /note= "wild-type Arg substituted by Lys"
FT Misc-difference 79 /note= "wild-type Lys substituted by Glu"
FT Misc-difference 81 /note= "wild-type Lys substituted by Glu"
FT Misc-difference 83 /note= "wild-type Lys substituted by Ser"
FT Misc-difference 84 /note= "wild-type Lys substituted by Ser"
FT Misc-difference 227 /note= "wild-type Asp substituted by Ser"
XX WO2003002143-A1.
PN 09-JAN-2003.
XX 19-JUN-2002; 2002WO-SE001188.
XX 28-JUN-2001; 2001SE-00002327.
XX (ACTI-) ACTIVE BIOTECH AB.
XX Forsberg G, Erlandsson E, Antonsson P, Walsee B;
XX WPI; 2003-201467/19.
XX Conjugate for therapy, has bacterial superantigen with a region in T-cell

PT receptor and four regions to determine binding to class II major
PT histocompatibility complex, antibody to cancer associated cell surface
XX structure.
PS Claim 8; Fig 2; 102pp; English.
XX The present sequence is the protein sequence of engineered staphylococcal
CC superantigen SEA/E-120. The superantigen is derived from staphylococcal
CC enterotoxin E (SEE) by the incorporation of the following amino acid
CC substitutions to reduce seroreactivity whilst maintaining production
CC levels and biological activity: R20G, N21R, S24G, K27K, K79E, K81E, K83S
CC and D227S. SEA/E-120 has been genetically fused to the Fab moiety of the
CC tumour reactive antibody 5T4 to form a claimed conjugate (see ABP58454)
CC designed to target and destroy cancer cells, including cancer of the
CC lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and
CC prostate (claimed)
XX SQ Sequence 233 AA;
Query Match 34.6%; Score 1218; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.6e-64;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELGQTALGNLQIYYNSKAITSEKSADQFLNTLLFKGFFTG 285
DB 1 SEKSEINEKDLRKSELGQTALGNLQIYYNSKAITSEKSADQFLNTLLFKGFFTG 60
QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
DB 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
QY 346 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 405
DB 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
QY 406 RGLIVFHSSEGSTSVSYDLFDAQQYPTDLLRIYRDNNTTSSLSLSLYLT 458
DB 181 RGLIVFHSSEGSTSVSYDLFDAQQYPTDLLRIYRDNNTTSSLSLSLYLT 233
RESULT 8
ABP58457
ID ABP58457 standard; protein; 233 AA.
XX ABP58457;
AC ABP58457;
DT 14-APR-2003 (first entry)
XX Engineered superantigen SEA/E-18 for human cancer therapy.
DE Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
KW cytostatic; vaccine; SEA/E-18; mutant; mutein.
XX Staphylococcus sp.
OS Synthetic.
XX WO2003002143-A1.
PN 09-JAN-2003.
XX 19-JUN-2002; 2002WO-SE001188.
XX 28-JUN-2001; 2001SE-00002327.
XX (ACTI-) ACTIVE BIOTECH AB.
XX Forsberg G, Erlandsson E, Antonsson P, Walsee B;
XX WPI; 2003-201467/19.
XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
PT receptor and four regions to determine binding to class II major
PT histocompatibility complex, antibody to cancer associated cell surface

```

PT structure.
PS Example 3; Fig 3; 102pp; English.
XX
XX
CC The present sequence is the protein sequence of engineered staphylococcal
CC superantigen SEA/E-18. The superantigen is based on staphylococcal
CC enterotoxin E (SEE, see ABP58456) except for 4 amino acid residues close
CC to the N-terminal that were from enterotoxin A and one substitution in
CC the C-terminal part, D227A. Models of new superantigen variants were
CC constructed using the SEA/E-18 model as the template. These include the
CC new engineered superantigen SEA/E-120 (see ABP58455), which has been
CC genetically fused to the Fab moiety of the tumour reactive antibody 574
CC to form a conjugate (see ABP58454) polypeptide. The conjugate is a
CC claimed example of novel conjugates and an antibody comprising an
CC engineered bacterial superantigen and an antibody moiety. The conjugates
CC are designed to target and destroy cancer cells, including cancer of the
CC lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and
CC prostate (claimed)
XX
XX Sequence 233 AA;
XX
XX Query Match 32.1%; Score 1130; DB 6; Length 233;
XX Best Local Similarity 91.4%; Pred. No. 2.7e-59;
XX Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
XX
QY 226 SEKSEINEKDLRKKSELOQTALGNLKKQIYYNKAITSSEKSGADQFLTNTLLFKGFFTG 285
DB 1 SEKSEINEKDLRKKSELOQTALGNLKKQIYYNKAITENKESDDQFLENTLLFKGFFTG 60
QY 286 HPWYNLLVDLGSTATSEYEGSSVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 346 EEKKVPINLWIDGKQTTVPIDKVTSKKVTQVELDLQARHYLHGKFGVNSDFGKQV 405
DB 121 EEKKVPINLWIDGKQTTVPIDKVTSKKVTQVELDLQARHYLHGKFGVNSDFGKQV 180
QY 406 RGLIVFHSSEGSTSVSYDLFDAQGGYPTDTLRIYRDNTTISSTLSISLYTT 458
DB 181 RGLIVFHSSEGSTSVSYDLFDAQGGYPTDTLRIYRDNTINSENHLALYLYTT 233
RESULT 9
AAW35375
ID AAW35375 standard; peptide; 245 AA.
XX
XX AC AAW35375;
XX
XX DT 20-APR-1998 (first entry)
XX
XX DE Staphylococcus enterotoxin SEE modified superantigen.
XX
XX KW SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
XX cancer; infection; autoimmune disease; antibody; modified.
XX
XX OS Staphylococcus sp.
XX
XX PH Key Location/Qualifiers
XX FT Misc-difference 20 /label= R20G
XX FT /note= "wild-type Arg is replaced by Gly"
XX FT Misc-difference 21 /label= N21T
XX FT /note= "wild-type Asn is replaced by Thr"
XX FT Misc-difference 24 /label= S24G
XX FT /note= "wild-type Ser is replaced by Gly"
XX FT Misc-difference 27 /label= R27K
XX FT /note= "wild-type Arg is replaced by Lys"
XX
XX PN W09736932-A1.
XX

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PD 09-OCT-1997.
XX
XX PF 26-MAR-1997; 97WO-SR000537.
XX
XX PR 29-MAR-1996; 96SE-00001245.
XX 12-AUG-1996; 96US-00695692.
XX (PHAA ) PHARMACIA & UPJOHN AB.
XX
XX PI Antonsson P, Hansson J, Bjoerk P, Dohlsten M, Kalland T;
XX PI Abrahmsen L, Forsberg G;
XX DR WPI; 1997-503052/46.
XX
XX PT Conjugate of target seeking moiety and modified superantigen - useful for
XX PT activating the immune system to treat cancer, viral infections, parasitic
XX PT infestations and autoimmune diseases.
XX
XX PS Claim 5; Page; 58pp; English.
XX
XX CC This is a modified Staphylococcus enterotoxin SEE superantigen. The wild-
XX CC type SEE superantigen is modified to be used in a novel conjugate. The
XX CC novel conjugate comprises a target seeking moiety and a modified wild
XX CC type superantigen. This modified superantigen retains its ability to
XX CC activate a subset of T cells, even though 1 or more wild-type amino acid
XX CC residues in at least 1 region which functions in determining binding to T
XX CC cell receptor (TCR) and activation of a subset of T cells has/have been
XX CC replaced. Such a modified superantigen can optionally be used as part of
XX CC a conjugate with a target seeking moiety, for activating the immune
XX CC system to treat a mammalian disease. A pharmaceutical composition can be
XX CC prepared comprising a modified antibody (preferably a Fab fragment fused
XX CC to a peptide moiety providing activation of T cells in Vbeta specific
XX CC manner) in which cysteines providing for interchain cysteine linkages in
XX CC the native antibody have been replaced (preferably by serine residues) to
XX CC prohibit cysteine formation. The modified wild-type superantigen is used
XX CC for treating cancer, viral infections, parasitic infestations and
XX CC autoimmune disease. The modified wild type superantigen has a lower
XX CC immunogenicity and reactivity with neutralising antibodies and has fewer
XX CC side-effects when used as a drug, compared to wild type superantigen.
XX CC Note: This sequence is not provided in the specification. It has been
XX CC created by modifying the wild-type SEE superantigen sequence in Pages 38-
XX CC 39 of the specification
XX
XX SQ Sequence 245 AA;
XX
XX Query Match 31.6%; Score 1113; DB 2; Length 245;
XX Best Local Similarity 86.9%; Pred. No. 2.9e-58;
XX Matches 213; Conservative 8; Mismatches 12; Indels 12; Gaps 1;
XX
QY 226 SEKSEINEKDLRKKSELOQTALGNLKKQIYYNKAITSSEKSGADQFLTNTLLFKGFFTG 285
DB 1 SEKSEINEKDLRKKSELOQTALGNLKKQIYYNKAITENKESDDQFLENTLLFKGFFTG 60
QY 286 HPWYNLLVDLGSTATSEYEGSSVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 346 EEKKVPINLWIDGKQTTVPIDKVTSKKVTQVELDLQARHYLHGKFGVNSDFGKQV 405
DB 121 EEKKVPINLWIDGKQTTVPIDKVTSKKVTQVELDLQARHYLHGKFGVNSDFGKQV 180
QY 406 RGLIVFHSSEGSTSVSYDLFDAQGGYPTDTLRIYRDNTTISSTLSISLYTT 453
DB 181 RGLIVFHSSEGSTSVSYDLFDAQGGYPTDTLRIYRDNTINSENHLIDLYTINSENHLIDL 240
QY 454 YLYTT 458
DB 241 YLYTT 245

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RESULT 10
ABP58456
ID ABP58456 standard; protein; 233 AA.

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XX AC ABP58456;
XX DT 14-APR-2003 (first entry)
XX DE Staphylococcal enterotoxin E.
XX KW Superantigen; staphylococcal enterotoxin E; antibody; cancer; tumour;
XX OS cytostatic; vaccine.
XX PN Staphylococcus sp.
XX PD WO2003002143-A1.
XX XX 09-JAN-2003.
XX PF 19-JUN-2002; 2002WO-SE001188.
XX PR 28-JUN-2001; 2001SE-00002327.
XX XX (ACTI-) ACTIVE BIOTECH AB.
XX PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
XX DR WPI; 2003-201467/19.
XX XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
PT receptor and four regions to determine binding to class II major
PT histocompatibility complex, antibody to cancer associated cell surface
PT structure.
XX PS Example 3; Fig 4; 102pp; English.
XX CC The present sequence is the protein sequence of staphylococcal
CC enterotoxin SEE. The invention provides novel conjugates (see ABP58454)
CC for human cancer therapy. These comprise an engineered bacterial
CC superantigen, such as novel SEA/E-120 (see ABP58455), which is based on
CC SEE, and an antibody moiety, such as tumour reactive antibody 574. The
CC superantigen is engineered to reduce seroreactivity whilst maintaining
CC biological activity and production levels. The conjugates are designed to
CC target and destroy cancer cells, including cancer of the lung, breast,
CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX Sequence 233 AA;
XX SQ
Query Match 31.4%; Score 1107; DB 6; Length 233;
Best Local Similarity 89.7%; Pred. No. 6.3e-58;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSDAQLNTLLFKGFFTG 285
Db 1 SEKSEINEKDLRKSELOQTALGNLSNRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
QY 286 HPWYNDLLVDLGSSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCWYGGVTLHDNNRLT 345
Db 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCWYGGVTLHDNNRLT 120
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 405
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
QY 406 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYLYTT 458
Db 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTINSENHLDLYLYTT 233
RESULT 11
ID AAU14103
XX AC AAU14103;
XX DT 21-NOV-2001 (first entry)

XX DE Peptide sequence from Staphylococcus aureus enterotoxin type E.
XX KW Anti-retroviral; DP178-like; DP107-like; enterotoxin type E;
XX KW antifusogenic; antiviral; HIV transmission.
XX OS Staphylococcus aureus.
XX PN WO200151673-A2.
XX PD 19-JUL-2001.
XX PF 05-JUL-2000; 2000WO-US035727.
XX PR 09-JUL-1999; 99US-00350841.
XX PA (TRIM-) TRIMERIS INC.
XX PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX DR WPI; 2001-442157/47.
XX XX Identifying a compound that inhibits the formation of or disrupts a
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
PT or intracellular modulatory activity, by detecting the formation of a
PT DP107/DP178 complex.
XX PS Disclosure; Fig 41; 259pp; English.
XX CC The present invention relates to peptides which exhibit anti-retroviral
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
CC amino acids 639-673 of the transmembrane protein gp41 from human
CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
CC also relates to a method of identifying compounds that inhibit the
CC formation of or disrupts a DP107/DP178 complex. The method comprises
CC detecting the formation of a DP107/DP178 complex, both in the presence or
CC absence of a test compound, in a reaction mixture containing DP107 and
CC DP178 peptides. The method is useful for identifying compounds, including
CC small molecule compounds, which may themselves exhibit antifusogenic,
CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
CC peptides are useful to inhibit human and non-human retroviral,
CC particularly HIV, transmission to uninfected cells. The present sequence
CC represents a peptide sequence from Staphylococcus aureus enterotoxin type
XX E
XX SQ
Sequence 257 AA;
Query Match 31.4%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 7.1e-58;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSDAQLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLSNRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 286 HPWYNDLLVDLGSSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCWYGGVTLHDNNRLT 345
Db 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCWYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 405
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 406 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYLYTT 458
Db 205 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTINSENHLDLYLYTT 257
RESULT 12
ID ABO10268
XX ABO10268 standard; protein; 257 AA.


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QY 346 EEKVPINLWIDKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQV 405
Db 145 EEKVPINLWIDKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQV 204
QY 406 RGLIVFHSSEGSTSVSYDLFDAQSQYPTDLLRIYRDNTTISSTLSLSLYTT 458
Db 205 RGLIVFHSSEGSTSVSYDLFDAQSQYPTDLLRIYRDNTTINSENHIDLVLTYT 257

RESULT 14
AAG65572
ID AAG65572 standard; protein; 720 AA.
AC AAG65572;
DT 30-NOV-2001 (first entry)
DE Amino acid sequence of a plasmid pFCAH9-B8d.
KW Gene library; immunoglobulin; antibody library.
XX Synthetic.
XX WO200162907-A1.
PN 30-AUG-2001.
PD 22-FEB-2001; 2001WO-JP001298.
PF 22-FEB-2000; 2000JP-00050543.
PR (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
PA Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
PI Okuno Y, Shiraki K;
XX WPI; 2001-565420/63.
DR N-PSDB; AAH47738.
XX Producing gene libraries and antibody libraries, involves selecting a
PT light chain that binds to a heavy chain product to produce a functional
PT formation, and producing a gene library of the light chain variable
PT regions.
XX Example; Fig 3-6; 181pp; Japanese.
XX The invention relates to producing gene libraries, comprising
CC immunoglobulin light and heavy variable region. The method involves
CC selecting light chain that binds with the heavy chain product to produce
CC a functional conformation, producing a gene library comprising a
CC collection of these light chain variable genes, and combining with gene
CC library of heavy chain variable genes. The method is used for production
CC of gene and antibody libraries. The present sequence represents the amino
CC acid sequence of a plasmid pFCAH9-B8d
XX
SQ Sequence 720 AA;
Query Match 31.1%; Score 1096.5; DB 4; Length 720;
Best Local Similarity 37.9%; Pred. No. 1e-56;
Matches 256; Conservative 39; Mismatches 55; Indels 325; Gaps 9;
QY 1 EVOLQSGPDLVKPGASVKISCKASGYFTGYMHVWVKQSPGKLEWIGRINPNNVTLY 60
Db 23 QVQLQSGHAEVLPFGASVKLSCTASGFINIKDTTHHWVKQRPKG----- 66
QY 61 NQKFKDKATLTVDKSSTTAYMELRLSTSDSAVYICARSTMITNY---VMDYWGQSTSVT 117
Db 67 -----LTSEDATVYYCA-----GYDYGNFYWGQSTTVT 95
QY 118 VSSAKTTPSPVPLARGSAQAQTNMWTLCGLVKGYPPEPVTVTWNSGSLSSGVHTTFAVL 177
Db 96 VSSASTKSPVPLAPSPSSKSTSGTAALGCLVKDYPPEPVTVTWNSGALTSVHTTFAVL 155
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QY 178 QSD-LYTLSSSVTPSSSTWPESETVCNVAHPASSTKVKDKKIVPRDSGGPSEKSEINEKD 236
Db 156 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKSNYKVKDKVEPK----- 199
QY 237 LRKKSSELOCTALGNLKKQIYYNKAITSSEKSADQFLTNTLLFKGFTTGHFWNDLLVDL 296
Db 200 ----- 199
QY 297 GSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTEKKVPINLWI 356
Db 200 -----SCHH----- 203
QY 357 DGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGKGLIVFHSSEG 416
Db 204 -----HHHMKYLLPTAAA-----GLLL----- 221
QY 417 STVSVDLFDAGQYPTDLLRIYRDNTTISSTLSLSLYTTYSIVMTQPTSLLSVAGDR 476
Db 222 -----LAAQPAMATSDIELTQSPASLSASVGET 249
QY 477 VNTCKASQSVSNVDVAYVQKPGQSPKLLISYTSRYAGVPDRFSGSGYCTDFTLTISVV 536
Db 250 VTITCRASGNIIHNYLA----- 265
QY 537 QAEDAAVYFCQDYNSPPTFGGGTKLEIKRAADAAPTVISIFPPSSEQLTSGGASVVCFLNN 596
Db 266 -----KLEIKRAADAAPTVISIFPPSSEQLTSGGASVVCFLNS 301
QY 597 FYPKQINVKWKIDGSRQNGVLSNWTQDSKOSTYSMSSTLTLTQKDEYERHNSYTCEATH 656
Db 302 FYPKQINVKWKIDGSRQNGVLSNWTQDSKOSTYSMSSTLTLTQKDEYERHNSYTCEATH 361
QY 657 KTSTSPVKSENRNE 671
Db 362 KTSTSPVKSENRNE 376

RESULT 15
ADW44587
ID ADW44587 standard; protein; 603 AA.
AC AC
XX ADW44587;
DT 24-MAR-2005 (first entry)
XX Antibody huCC49 heavy chain (CH2 domain deleted).
DE XX
KW Antibody engineering; bispecific antibody; Cytostatic; Immunosuppressive;
KW Antinflammatory; Gastrointestinal-Gen.; Dermatological; Antiulcer;
KW Antiinflammatory; Antiarthritic; Nephrotropic; Antithyroid; Thyromimetic;
KW Muscular-Gen.; Neuroprotective; Antianemic; CNS-Gen.; Respiratory-Gen.;
KW Vulnerary; cancer; neoplasm; lymphoma; autoimmune disease; inflammation;
KW huCC49; Tag72; heavy chain variable region.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX WO2005000899-A2.
PN PN
XX 06-JAN-2005.
PD 28-JUN-2004; 2004WO-US020945.
PF 27-JUN-2003; 2003US-0483877P.
PR 03-OCT-2003; 2003US-0508810P.
PR 28-OCT-2003; 2003US-0515351P.
PR 30-OCT-2003; 2003US-0516030P.
XX (BIOG-) BIOGEN IDEC MA INC.
PA Glaser S, Reff M, Yang T, Wu X, Chinn P;
PI
```


XX	WPI; 2005-058133/06.	Db	176	GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVPEKSCDKTHTCTPCPGGGSS---	232
DR	N-PSDB; ADW44584.	Qy	230	EEINEKDLRKSELOQTALGNLKIQIYYNSKAITSSSEKSADQFLTN-----TLIFKGFFTG	285
XX		Db	233	-----GGSGGQPREPOVY-----TLPPSRDELTKQVSLTCLVKGFYV-	271
PT	New composition comprising polypeptide dimers comprising at least four	Qy	286	HPWYNLLVDLGTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLLHNNRLT	345
PT	binding sites and at least two polypeptide chains linked via at least one	Db	272	-----SDIAV-----EWE-----SNGQP-----ENN---	287
PT	interchain disulfide linkage, useful for treating e.g., cancer or				
PT	autoimmune diseases.				
XX	Example 8; SEQ ID NO 19; 172pp; English.	Qy	346	EEKVPINIWIDGK---QTTVPIDKVKTSKKEVTQVQLDQA---RHYLHGKFGLYNSDSF	400
XX	The invention relates to a composition comprising polypeptide dimers	Db	288	-YKTPPVLSDSGSFFLYSKLTVDKRWQGNVFCSSVMEALHNHHTQKSLSLSPKSG	346
CC	comprising at least four binding sites and at least two polypeptide	Qy	401	GKGVQVQGLIVFHSSSEGSTVSVDLFDAGQGVPTDLLRIYRDNNTTISSTLSLSLYLYTTSI	460
CC	chains, where the polypeptide chains comprise at least one heavy chain	Db	347	GGSGGG-----GSGGG-----GSDI	362
CC	portion and a synthetic connecting peptide, and where greater than about	Qy	461	VMQTPTSLLSVAGDRVTITCKASQSV-----SNDVAVTQKPGQSPKLLISVTSRYA	514
CC	50% of the dimers comprise polypeptide chains that are linked via at	Db	363	VMSQSPDSLAVSLGERVTLLNCKSSQSLLYSGNKNVLAWTYQKPGQSPKLLIYWASARES	422
CC	least one interchain disulfide linkage, or comprising minibody molecules	Qy	515	GVDPDRSGSGVGTDFTLTITSSVOAEAAVYFCODYNSPPTFGGTTKLEIKRADAAPTUS	574
CC	comprising two polypeptide chains, where the polypeptide chains comprise	Db	423	GVDPDRSGSGGDTFTLITSSVQAEADVAVYCYQYYSYPLTFGAGTKLELKGSGSGGGG	482
CC	a heavy chain portion and a synthetic connecting peptide, where the	Qy	575	IFPPSSSE-QLTSGGASV-----CFLNNFYPKDINVKW-KIDGSEKQ-----GVLNSW	621
CC	polypeptide chains lack all or part of a CH2 domain, and where greater	Db	483	SGGGGQVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHFWKQNPQGRLEWIGYFSPG	542
CC	than about 50% of the molecules are present in a form in which one of the	Qy	622	TDQSKDSTVMSSTLT	638
CC	polypeptide chains are linked via at least one interchain disulfide	Db	543	NDDFKYNERPKRATLT	559
CC	linkage. Also included are a nucleic acid molecule comprising a				
CC	nucleotide sequence encoding a polypeptide chain as defined above, a host				
CC	cell comprising a vector and a binding molecule comprising CH2 deleted				
CC	heavy and light chains of the antibodies huCC49 and PRIMATEZED p388. The				
CC	synthetic connecting peptide comprises a (Gly-Ser)n linker attached to a				
CC	portion of a hinge region from IgG1, IgG3 or IgG4. The molecules are				
CC	bispecific and comprise at least one binding site specific for a soluble				
CC	ligand or for a cell surface molecule. The molecules comprise two binding				
CC	sites specific for a tumor cell antigen and two binding sites specific				
CC	for a prodrug. The synthetic connecting peptide comprises a proline				
CC	residue at position 243, Kabat numbering system. The synthetic connecting				
CC	peptide further comprises an alanine residue at position 244 and a				
CC	proline residue at position 245, Kabat numbering system. The polypeptide				
CC	dimers are tetraivalent minibody molecules. The composition is useful for				
CC	treating a subject that would benefit from treatment with an antigen				
CC	binding molecule, where the subject is suffering from cancer, lymphoma,				
CC	an autoimmune disease or disorder, or an inflammatory disease or disorder				
CC	The composition is useful for treating autoimmune diseases such as				
CC	Crohn's disease, inflammatory bowel disease, systemic lupus				
CC	erythematosus, ulcerative colitis, rheumatoid arthritis, Goodpasture's				
CC	syndrome, Grave's disease, Hashimoto's thyroiditis, pemphigus vulgaris,				
CC	myasthenia gravis, scleroderma, autoimmune hemolytic anemia, pernicious				
CC	anemia, Sjogren's syndrome, neurological disorders such as multiple				
CC	sclerosis, and inflammatory diseases or disorders such as cystic				
CC	fibrosis, sinusitis, gastroenteritis, drug reactions and burns. The				
CC	polypeptide is useful for diagnostic or therapeutic purposes. The binding				
CC	molecules are also useful for pretargeting applications for				
CC	chemotherapeutic drug delivery. The present sequence represents a heavy				
CC	chain variable region (optionally CH2 domain deleted) from the anti-Tag72				
CC	antibody huCC49.				
XX					
SQ	Sequence 603 AA;				
	Query Match 31.1%; Score 1095.5; DB 9; Length 603;				
	Best Local Similarity 40.9%; Pred. No. 9.5e-57;				
	Matches 279; Conservative 72; Mismatches 171; Indels 157; Gaps 20;				
Qy	1 EVQLQQSGDPLVKPGASVKISCKASGYFTGYVHWYKQSPKGLWIGRINPNNGTLY 60				
Db	1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHFWKQNPQGRLEWIGYFSPGNDPDFY 60				
Qy	61 NQPKDKATLTVDKSSSTAYMEIRSLTSEDSAVTYCARSTMTITNYVMDYQGQTSVTSS 120				
Db	61 NERFKGATLTADTSASTAVVELSLRSEDATVFCRSLN-----MAYWGQGLTVTVSS 115				
Qy	121 AKTTPPSVYPLAPGAAQTNSMWTGLCLVKGYPPEPVTVNWSGLSSGVHTPPAVLQSD 180				
Db	116 ASTKGPSVFPPLAPSGKSTSGTAAALGCLVADYFPPEPVTVSNWSGALTSVHTPPAVLQSS 175				
Qy	181 -LYTLSSSVTVPSSTWSETVTCNVAHPASSTKVDKKIIVRD-----SGGSPSEKS 229				

Db	176	GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVPEKSCDKTHTCTPCPGGGSS----	233
Qy	230	EEINEKDLRKSELOQTALGNLKOIYYNSKAITSSSEKSADQFLTN-----TLFLKGFPTG	285
Db	233	-----GGSGGQPREPOVY-----TLPPSRDELTKNQVSLTCLVKGFYP-	271
Qy	286	HPWYNLLVDLGSSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLLHNNRLT	345
Db	272	-----SDIAV-----EWE-----SNGQP-----ENN----	287
Qy	346	EEKVPINILWIDGK---QTTVPIDKVKTSKKEVTVQELDLQA--RHYLHGKFGLYNSDSF	400
Db	288	-YKTPPVLDSGGSFFLYSKLTVDKSRWQGNVFCSSVMEALHNHHTQKSLSLSPKSG	346
Qy	401	GKGVQVQGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNNTTISSTLSLSLYLYTTSI	460
Db	347	GGSGGGG-----GSGGG-----GSDI	362
Qy	461	VMTQPTSLLSAGDRVTITCKASQSV-----SNDVAVTQKPGQSPKLLISVTSRYA	514
Db	363	VMSQSPDSLAVSLGERVTLLNCKSSQSLLYSGNQKNYLAWTYQKPGQSPKLLIYWASARES	422
Qy	515	GVDPDRSGSGYGTDFTLTITSSVQAEAAVYFCQDYNSPPTFGGTTKLEIKRADAAPTUS	574
Db	423	GVDPDRSGSGGDTFTLTITSSVQAEADVAVYCYQYYSYPLTFGAGTKLELKGSGSGGGG	482
Qy	575	IFPPSSSE-QLTSGGASV-----CFLNNFYPKDINVKW-KIDGSEKQN--GVLNSW	621
Db	483	SGGGGQVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHFWKQNPQGRLEWIGYFSPG	542
Qy	622	TDQDSKDYTSMSSTLT	638
Db	543	NDDPKYNERPKGKATLT	559
RESULT 16			
ADW44588			
XX	ID	ADW44588 standard; protein; 621 AA.	
XX	AC	ADW44588;	
XX	DT	24-MAR-2005 (first entry)	
XX	DE	Antibody huCC49 heavy chain (CH2 domain deleted/synthetic hinge).	
XX	KW	Antibody engineering; bispecific antibody; Cytostatic; Immunosuppressive;	
XX	KW	Antiinflammatory; Gastrointestinal-Gen.; Dermatological; Antiulcer;	
XX	KW	Antirheumatic; Antiarthritic; Nephrotoxic; Antithyroid; Thyromimetic;	
XX	KW	Muscular-Gen.; Neuroprotective; Antianemic; CNS-Gen.; Respiratory-Gen.;	
XX	KW	Vulnerary; cancer; neoplasm; lymphoma; autoimmune disease; inflammation;	
XX	KW	huCC49; Tag72; heavy chain variable region.	
OS	Mus sp.		
OS	Homo sapiens.		
OS	Synthetic.		
OS	Chimeric.		
XX	Key	Location/Qualifiers	
XX	Misc-difference	243, 245	
XX	FT	/note= "Encoded by CCAGGA"	
XX	PN	WO2005000899-A2.	
XX	PD	06-JAN-2005.	
XX	PF	28-JUN-2004; 2004WO-US020945.	
XX	PR	27-JUN-2003; 2003US-0483877P.	
XX	PR	03-OCT-2003; 2003US-0508810P.	
XX	PR	28-OCT-2003; 2003US-0515351P.	
XX	PR	30-OCT-2003; 2003US-0516030P.	
XX	PA	(BIOG-) BIOGEN IDEC MA INC.	

XX	Glaser S, Reff M, Yang T, Wu X, Chinn P;	
PI	WPI; 2005-058133/06.	
DR	N-PSDB; ADW44585.	
XX	New composition comprising polypeptide dimers comprising at least four	
PT	binding sites and at least two polypeptide chains linked via at least one	
PT	interchain disulfide linkage, useful for treating e.g., cancer or	
PT	autoimmune diseases.	
XX	Claim 34; SEQ ID NO 20; 172pp; English.	
XX	The invention relates to a composition comprising polypeptide dimers	
CC	comprising at least four binding sites and at least two polypeptide	
CC	chains, where the polypeptide chains comprise at least one heavy chain	
CC	portion and a synthetic connecting peptide, and where greater than about	
CC	50% of the dimers comprise polypeptide chains that are linked via at	
CC	least one interchain disulfide linkage, or comprising minibody molecules	
CC	comprising two polypeptide chains, where the polypeptide chains comprise	
CC	a heavy chain portion and a synthetic connecting peptide, where the	
CC	polypeptide chains lack all or part of a CH2 domain, and where greater	
CC	than about 50% of the molecules are present in a form in which one of the	
CC	polypeptide chains are linked via at least one interchain disulfide	
CC	linkage. Also included are a nucleic acid molecule comprising a	
CC	nucleotide sequence encoding a polypeptide chain as defined above, a host	
CC	cell comprising a vector and a binding molecule comprising CH2 deleted	
CC	heavy and light chains of the antibodies huCC49 and PRIMATIZED p388. The	
CC	synthetic connecting peptide comprises a (Gly-Ser) ⁿ linker attached to a	
CC	portion of a hinge region from IgG1, IgG3 or IgG4. The molecules are	
CC	bispecific and comprise at least one binding site specific for a soluble	
CC	ligand or for a cell surface molecule. The molecules comprise two binding	
CC	sites specific for a tumor cell antigen and two binding sites specific	
CC	for a prodrug. The synthetic connecting peptide comprises a proline	
CC	residue at position 243, Kabat numbering system. The synthetic connecting	
CC	peptide further comprises an alanine residue at position 244 and a	
CC	proline residue at position 245, Kabat numbering system. The polypeptide	
CC	dimers are tetraivalent minibody molecules. The composition is useful for	
CC	treating a subject that would benefit from treatment with an antigen	
CC	binding molecule, where the subject is suffering from cancer, lymphoma,	
CC	an autoimmune disease or disorder, or an inflammatory disease or disorder	
CC	The composition is useful for treating autoimmune diseases such as	
CC	Crohn's disease, inflammatory bowel disease, systemic lupus	
CC	erythematosus, ulcerative colitis, rheumatoid arthritis, Goodpasture's	
CC	syndrome, Grave's disease, Hashimoto's thyroiditis, pemphigus vulgaris,	
CC	myasthenia gravis, scleroderma, autoimmune hemolytic anemia, pernicious	
CC	anemia, Sjogren's syndrome, neurological disorders such as multiple	
CC	sclerosis, and inflammatory diseases or disorders such as cystic	
CC	fibrosis, sinusitis, gastroenteritis, drug reactions and burns. The	
CC	polypeptide is useful for diagnostic or therapeutic purposes. The binding	
CC	molecules are also useful for pretargeting applications for	
CC	chemotherapeutic drug delivery. The present sequence represents a heavy	
CC	chain variable region (optionally CH2 domain deleted) from the anti-Rag72	
CC	antibody huCC49.	
XX	Sequence 621 AA;	
SQ		
Query Match 31.0%; Score 1093.5; DB 9; Length 621;		
Best Local Similarity 41.0%; Pred. NO. 1.3e-56;		
Matches 279; Conservative 74; Mismatches 182; Indels 145; Gaps 20;		
Qy	1 EVQLQSGDPLVPGASVKISCKASGYSTGYVMHWKSPGKGLRWIGRIHPNNGVTLY 60	
Db	1 QVQLVQSGAEVPGASVKISCKASGYSTFDHAIHWKQNPGRLEWIGYFSPGNDDFKY 60	
Qy	61 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYCYCARSTMITNYMDYWGQGTSTVTS 120	
Db	61 NERFKKATLTATDSASTAYVELLSRSEDATYFCTRLN-----MAYWGQGLTVTS 115	
Qy	121 AKTTPSVPLAPGSAQNTNMYTLGCLVKGYPEPVVTWNSSGSLSSGVVHTPEAVLQSD 180	
Db	116 ASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYPEPVVTWNSSGALTSGVHTPEAVLQSS 175	
Qy	181 -LYTLSSSVTPSPSTVTCNVAHPASSTKVDKKIVPRDSGG-----PSEKSEEI 232	
Db	176 GLYSLSVVTPFSSSLGQTQTYICNVNHRPSNTKVKVEPKSCDKTHTCPPEPEKSCDT 235	
Qy	233 NEKDLRKKSLEQGTALGNL-----KQIYYNYSKAITSEKSGADQFLTN-----TLFLKGF 282	
Db	236 PPPCPRCPPAGGSGSGGGGQPREPQVY-----TLPPSRDELTKKQVSLTCLVKGF 287	
Qy	283 FTGHPWYNLLVDLGSTAATSIEYEGSSVDLYGAYGYQCAGGTPNKTAICYMGVTLHDNN 342	
Db	288 YP-----SDIAV-----EWG-----SNGQP-----ENN 305	
Qy	343 RLTEEKVPIINLWDGK---QTTVPIDKVKTSKEVTQVQELDLQA---RHYLHGKFGLYNS 397	
Db	306 ----YKTTFPVLDSGSPFLYSKLTVDKSRWQGNVFSVMHEALHNHYTKSLSPG 361	
Qy	398 DSFGGKQVQRLIVFHSSSEGSTVSVDLFDAGQGVYPTDFTLLRIYRDNTTISSTLSISLYLT 457	
Db	362 KSGGGGSGGG-----GSGGG-----SNDVAVYQOKPGOSPCLLIYSYTS 511	
Qy	458 TSIVMTQTPTSLVSGADRVTTITCKASQSV-----SNDVAVYQOKPGOSPCLLIYSYTS 511	
Db	378 SDIVMSQSPDSLAVSLGERVTLNCKSSQSLYSGNQKNLAWYQOKPGOSPCLLIYWSA 437	
Qy	512 RVAGVPDRFSGSGYGTDFLTITSSVQAEADAAVYFCQDYNSPPTFGGKLEIKRADAAP 571	
Db	438 RESGVDPDRFSGSGGTDFLTITSSVQAEADVAVYCYQYISYPLTFGAGTKLELKGSGG 497	
Qy	572 TVSIIPPSSE-QLTSGGASW-----CFLNNFYPKDINVKW-KIDGSRQN--GVL 618	
Db	498 GGGSGGGGSGVQLVQSGAEVWPKGASVKISCKASGYTFTDHA1HWKQNPGRLEWIGYF 557	
Qy	619 NSWTQDSDKSTYSMSLT 638	
Db	558 SPGNDDFKYNERFPKGKATLT 577	
RESULT 17		
AAB67339		
ID	AAB67339 standard; peptide; 230 AA.	
XX	AAB67339;	
XX	23-APR-2001 (first entry)	
DT	Staphylococcus aureus enterotoxin E protein.	
XX	Tumour; cancer; immune; enterotoxin.	
OS	Staphylococcus aureus.	
XX	US6180097-B1.	
XX	30-JAN-2001.	
XX	30-OCT-1998; 98US-00183437.	
XX	03-OCT-1989; 89US-00416530.	
PR	17-JAN-1990; 90US-00466577.	
PR	17-JAN-1991; 91WO-US000342.	
PR	01-JUN-1992; 92US-00891718.	
PR	02-MAR-1993; 93US-00025144.	
PR	31-JAN-1994; 94US-00189424.	
PR	19-JUN-1995; 95US-00491746.	
XX	(TERM/) TERMAN D S.	
PA	Terman DS;	
PI	WPI; 2001-158657/16.	
XX	Tumor cell capable of stimulating antitumor immune reactivity in vitro or	
PT	in vivo comprises exogenous nucleic acids encoding a superantigen and a	

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PT costimulatory molecule.
XX Disclosure; Fig 2; 16pp; English.
XX
XX The present invention relates to a tumour cell capable of stimulating
CC antitumor immune reactivity in vitro or in vivo contains and expresses an
CC exogenous nucleic acid molecule encoding a superantigen or its active
CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
CC molecule that activates T cells in conjunction with an antigenic
CC stimulus. The invention may be used for cancer therapy by stimulating an
CC anticancer immune response in vivo or ex vivo
XX
XX Sequence 230 AA;
SQ
Query Match 31.0%; Score 1093; DB 4; Length 230;
Best Local Similarity 89.6%; Pred. No. 4.2e-57;
Matches 206; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 229 SEINEKDLRKKSSELOQTALGNLKOIYYNYSKAITSEKSDAQFLNTLLFKGFFTGHPW 288
DB 1 SEINEKDLRKKSSELOQTALGNLKOIYYNYSKAITSEKSDAQFLNTLLFKGFFTGHPW 60
QY 289 YNDLLVDLGSSTAESEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 348
DB 61 YNDLLVDLGSSTAESEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 120
QY 349 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVQGL 408
DB 121 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVQGL 180
QY 409 IVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYTT 458
DB 181 IVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYTT 230
RESULT 18
AAW35374
ID AAW35374 standard; peptide; 245 AA.
XX
XX AAW35374;
XX
XX 20-APR-1998 (first entry)
XX
XX Staphylococcus enterotoxin SEE wild-type superantigen.
DE
XX SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
XX cancer; infection; autoimmune disease; antibody.
XX
XX Staphylococcus sp.
XX
XX Key Location/Qualifiers
FH Misc-difference 20 /note= "can be mutated at this position"
FT FT Misc-difference 21 /note= "can be mutated at this position"
FT FT Misc-difference 24 /note= "can be mutated at this position"
FT FT Misc-difference 27 /note= "can be mutated at this position"
XX
XX WO9736932-A1.
XX
XX 09-OCT-1997.
XX
XX 26-MAR-1997; 97WO-SE000537.
XX
XX 29-MAR-1996; 96SE-00001245.
XX 12-AUG-1996; 96US-00695692.
XX
XX (PHAA ) PHARMACIA & UPJOHN AB.
XX
XX Antonsson P, Hansson J, Bjoerk P, Dohlaten M, Kalland T;
PI Abrahmsen L, Forsberg G;
XX
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XX WPI; 1997-503052/46.
XX
XX Conjugate of target seeking moiety and modified superantigen - useful for
PT activating the immune system to treat cancer, viral infections, parasitic
PT infestations and autoimmune diseases.
XX
XX Claim 4; Page 38-39; 58pp; English.
XX
XX This is the wild-type Staphylococcus enterotoxin SEE superantigen. This
CC SEE superantigen can be modified to be used in a novel conjugate. The
CC novel conjugate comprises a target seeking moiety and a modified wild
CC type superantigen. The modified superantigen retains its ability to
CC activate a subset of T cells, even though 1 or more wild-type amino acid
CC residues in at least 1 region which functions in determining binding to T
CC cell receptor (TCR) and activation of a subset of T cells has/have been
CC replaced. Such a modified superantigen can optionally be used as part of
CC a conjugate with a target seeking moiety, for activating the immune
CC system to treat a mammalian disease. A pharmaceutical composition can be
CC prepared comprising a modified antibody (preferably a Fab fragment fused
CC to a peptide moiety providing activation of T cells in Vbeta specific
CC manner) in which cysteines providing for interchain cysteine linkages in
CC the native antibody have been replaced (preferably by serine residues) to
CC prohibit cysteine formation. The modified wild-type superantigen is used
CC for treating cancer, viral infections, parasitic infestations and
CC autoimmune disease. The modified wild type superantigen has a lower
CC immunogenicity and reactivity with neutralising antibodies and has fewer
CC side-effects when used as a drug, compared to wild type superantigen
XX
XX Sequence 245 AA;
SQ
Query Match 31.0%; Score 1091; DB 2; Length 245;
Best Local Similarity 85.3%; Pred. No. 6e-57;
Matches 209; Conservative 9; Mismatches 15; Indels 12; Gaps 1;
QY 226 SEKSEINEKDLRKKSSELOQTALGNLKOIYYNYSKAITSEKSDAQFLNTLLFKGFFTG 285
DB 1 SEKSEINEKDLRKKSSELOQTALGNLKOIYYNYSKAITSEKSDAQFLNTLLFKGFFTG 60
QY 286 HPWYNDLLVDLGSSTAESEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 61 HPWYNDLLVDLGSSTAESEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 346 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 405
DB 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
QY 406 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSL 453
DB 181 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSL 240
QY 454 YLYTT 458
DB 241 YLYTT 245
RESULT 19
ABU79072
ID ABU79072 standard; protein; 248 AA.
XX
XX AC ABU79072;
XX
XX 18-JUN-2003 (first entry)
XX
XX S. aureus SEE (staphylococcus enterotoxin E) protein.
XX
XX Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
KW gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
KW APC; antitumour.
XX
XX Staphylococcus aureus.
XX
```


Qy	226	SEKSEEINEKDLRKKESELOGTALGNLKOIYYNNSKAITSSSEKSAQDPLTNTLLPKGFPTG	289
Db	25	SEKSEEINEKDLRKKESELOQRNLSNLKQIYYNNEKAITENKESDDQFLNTLLPKGFPTG	84
Qy	286	HPWYNDLLVDLGSNTAATSEYEGSSVDLYGAYGYGOCAGGTPNKTCMVGCVTLHDNNRLT	345
Db	85	HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYGOCAGGTPNKTCMVGCVTLHDNNRLT	144
Qy	346	EEKVVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ	405
Db	145	EEKVVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ	204
Qy	406	RGLIVFHSSEGSTVSYDILFDAQGYPDPTLLRIYRDNFTTISSTSL	449
Db	205	RGLIVFHSSEGSTVSYDLFDQAQGYPDPTLLRIYRDNKTIENSENL	248
RESULT 21			
AEA02990			
ID	AEA02990 standard; protein; 248 AA.		
XX			
AC	AEA02990;		
XX			
DT	28-JUL-2005 (first entry)		
XX			
DE	Staphylococcal enterotoxin E (SEE) amino acid sequence SEQ ID NO:16.		
XX			
KW	tumor; neoplasm; gene therapy; immunotherapy; cytostatic;		
KW	Staphylococcal enterotoxin E.		
XX			
OS	Staphylococcus sp.		
XX			
FN	US2005112141-A1.		
XX			
PD	26-MAY-2005.		
XX			
PF	08-SEP-2004; 2004US-009377758.		
XX			
PR	30-AUG-2000; 2000US-00650884.		
XX			
PA	(TERM/) TERMAN D S.		
XX			
PI	Terman DS;		
XX			
DR	WPI; 2005-394926/40.		
DR	N-PSDB; AEA02989.		
XX			
FT	New composition for treating a tumor or neoplastic disease in a subject		
PT	comprises conjugates comprising superantigen polypeptides or nucleic		
PT	acids with other molecules that produce a tumoricidal response.		
XX			
PS	Example 3; SEQ ID NO 16; 125pp; English.		
XX			
CC	The invention relates to a composition for treating a tumor or neoplastic		
CC	disease in a subject. Also described: (1) a mammalian cell comprising an		
CC	exogenous nucleic acid encoding a superantigen expressed in the cell,		
CC	which cell also produces or expresses all alpha-anomers of		
CC	monoglycosylceramide or diglycosylceramide, where expression of the		
CC	superantigen and the mono- or diglycosylceramide is capable of eliciting		
CC	an antitumor immune response in a mammal into which the cell is		
CC	introduced; (2) treating a tumor or neoplastic disease in a subject; (3)		
CC	preparing a population of immunotherapeutic T or natural killer T (NKT)		
CC	cells useful to treat a tumor or neoplastic disease in a subject; (4) an		
CC	apoptotic cell preparation or lysate useful for treating a tumor or		
CC	neoplastic disease in a subject, comprising a cell population that has		
CC	been transfected with naked DNA encoding a superantigen, and treated to		
CC	undergo apoptosis or lysis; and (5) a cell that has ingested or been		
CC	transfected with the above apoptotic preparation or lysate, thus,		
CC	rendering the cell effective in presenting material expressed from		
CC	transfecting nucleic acid or material ingested to the immune system of a		
CC	mammal to elicit an anti-tumor immune response. The composition and		
CC	methods are useful for treating tumors or neoplastic diseases. The		
CC	present sequence represents a Staphylococcal enterotoxin E (SEE) protein		

PS Disclosure; Fig 6; 118pp; English.

XX The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's disease, periodontal diseases, cardiopulmonary diseases, cardiovascular diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-related diseases, and other immune disorders. The present sequence represents an Ig-574 fusion protein

XX SQ Sequence 592 AA;

Query Match 30.4%; Score 1069; DB 4; Length 592;
Best Local Similarity 37.9%; Pred. No. 3.5e-55;
Matches 254; Conservative 20; Mismatches 60; Indels 336; Gaps 9;

QY 1 EVOLQSGPDLVKPGASVKISKASGYSTGYTHMVKQSPGKLEWIGRINPNNGVTL 60
DB 20 EVOLQSGPDLVKPGASVKISKASGYSTGYTHMVKQSPGKLEWIGRINPNNGVTL 79

QY 61 NQKFKDKAILTVDKSSTTAYMELRSLTSDSAVYCARSTMTNYVMDYWGQTSVTVS 120
DB 80 NQKFKDKAILTVDKSSTTAYMELRSLTSDSAVYCARSTMTNYVMDYWGQTSVTVS- 138

QY 121 AKTTPSPVPLAPGSAQAQNSMTLGLVKGYPEPVTYTNWNSGSLSSGVHTFPVQLQSD 180
DB 139 ----- 138

QY 181 LYTSSSVTPSPSTWPSSTVTCNVAHPASSTKVDKIKVPRDSGGPSEKSEINEKDLRKK 240
DB 139 -----SGG----- 141

QY 241 SELOGTALGNLKIYYNKAITSSEKSAQDFTNTLLFKGFTGHPWYNLLDLGSTA 300
DB 142 ----- 141

QY 301 ATSEYEGSSVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLTEKKVPINLWDGKQ 360
DB 142 -----GGSGGGT-----GG----- 151

QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKQVQGLIVFHSSEGSTVS 420
DB 152 -----GG----- 153

QY 421 YDLFDAQQGVPTDLLRIYRDNNTISSTLSLSLYLTSTIVMTQTPTSLLSVAGDRVTIT 480
DB 154 -----SSIVMTQTPTFLLSVAGDRVTIT 176

QY 481 CKASQSVNDVAVYQKPGQPKLLISYTSRRVAGVDRFGSGGYGTDFTLTSSVQAE 540
DB 177 CKASQSVNDVAVYQKPGQPKLLISYTSRRVAGVDRFGSGGYGTDFTLTSSVQAE 236

QY 541 AAYVFCQDYNPPTFGGGTKLEIKRADA-APTVSIFFPSSEQLTSGGASVWVFLNFPY 599
DB 237 LAVYFCQDYNPPTFGGGTKLEIKRASKTGPSVFFLAPSSKTSGGTAALGCLVKDYFP 296

QY 600 KDINVKW-----IDGERQGVNLNSWTDQSDKSTYSMSSTLTLTVDKDEVERHNSYCEAT 655
DB 297 EPTVTSWNSGALTSVGHVTPAVLQS-----SGLYSLSSVTVTPSSSLGT-QTYICNVN 348

QY 656 HKTSTSPIVK 665
DB 349 HKPSNTKVDK 358

RESULT 23
AAW86003

ID AAW86003 standard; protein; 595 AA.

XX AAW86003;

AC 15-MAR-1999 (first entry)

XX Anti-5T4 single chain antibody 5T4Sabl.

DE Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;

XX monoclonal antibody; single chain antibody; mouse; human; 5T4Sabl.

XX Mus sp.

OS Homo sapiens.

OS Synthetic.

OS Chimeric.

XX W09855607-A2.

PN 10-DEC-1998.

XX 04-JUN-1998; 98WO-GB001627.

XX 04-JUN-1997; 97GB-00011579.

PR 20-JUN-1997; 97GB-00013150.

PR 04-JUL-1997; 97GB-00014230.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

PA Kingman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;

PI WPI; 1999-059910/05.

DR N-PSDB; AAV80291.

XX New vector encoding a tumour interacting protein for treating cancer - contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat cancer.

XX Example 1; Fig 1B; 82pp; English.

XX This is the amino acid sequence of a single chain antibody (Sabl), termed 5T4Sabl, comprising an scFv derived from murine monoclonal antibody 5T4 (see AAW86002) and the human g1 constant region. cDNA (see AAV80291) encoding the Sabl has been inserted into vector pCIneo to allow expression in mammalian cells. The trophoblast cell surface antigen defined by 5T4 is expressed at high levels on the cells of a wide variety of human tumours. The invention relates to a vector comprising a nucleotide sequence coding for a tumour interacting protein (TIP) and optionally a nucleotide sequence of interest (NOI) which encodes a protein of interest (POI), the vector being capable of delivering the NOI and/or POI to the tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The vector is used to treat cancer, and may also be used as a gene delivery system for introducing at least 1 gene encoding a TIP (preferably a tumour binding protein) into a haematopoietic cell lineage

XX SQ Sequence 595 AA;

Query Match 30.4%; Score 1069; DB 2; Length 595;
Best Local Similarity 37.9%; Pred. No. 3.5e-55;
Matches 254; Conservative 20; Mismatches 60; Indels 336; Gaps 9;

QY 1 EVOLQSGPDLVKPGASVKISKASGYSTGYTHMVKQSPGKLEWIGRINPNNGVTL 60
DB 23 EVOLQSGPDLVKPGASVKISKASGYSTGYTHMVKQSPGKLEWIGRINPNNGVTL 82

QY 61 NQKFKDKAILTVDKSSTTAYMELRSLTSDSAVYCARSTMTNYVMDYWGQTSVTVS 120
DB 83 NQKFKDKAILTVDKSSTTAYMELRSLTSDSAVYCARSTMTNYVMDYWGQTSVTVS- 141

QY 121 AKTTPSPVPLAPGSAQAQNSMTLGLVKGYPEPVTYTNWNSGSLSSGVHTFPVQLQSD 180
DB 142 ----- 141

QY 181 LYTSSSVTPSPSTWPSSTVTCNVAHPASSTKVDKIKVPRDSGGPSEKSEINEKDLRKK 240

Db	142	-----SGG-----	144	CC	heavy and light chains directed against enterotoxigenic Escherichia coli (STEC), in particular, ETEC of a strain possessing the K88 or K99 antigen. The heavy and light chain sequences are useful for producing transgenic plants, which express the K88 or K99 antibody. The transgenic plants are useful for producing animal feed, food product, animal feed additive, feed pre-mix or nutritional supplement and are also useful for treating or preventing enteric disease in an animal. The present sequence was used in an example from the invention.
Qy	241	SELQGTALGNLKQIYYNKAITSSEKSAQDLTNTLLPKGFTTGHVWYNDLLVLDGSTA	300	CC	
Db	145	-----	144	CC	
Qy	301	ATSEYEGSSVDLYGAYYGQAGGTPNKTAQMYGGVTLHDNNRLTEKKVPINLWIDGKQ	360	CC	
Db	145	-----GGSGGGT-----	154	CC	
Qy	361	TTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKQVORGLIVFHSSEGSTVS	420	CC	
Db	155	-----GG-----	156	CC	
Qy	421	YDLFDAQQYVPTLLRIYRDNNTTISSTLSISLYLYTTSIVMTQTPTSLVLSAGDRTIIT	480	CC	
Db	157	-----SSIVMTQTPTFLVLSAGDRTIIT	179	CC	
Qy	481	CKASQSVSNDAVYQKQPGSPKLLISYTSRAGVDPDFSGSGYGTDTFTLTSSVQAE	540	CC	
Db	180	CKASQSVSNDAVYQKQPGSPKLLISYTSRAGVDPDFSGSGYGTDTFTLTSSVQAE	239	CC	
Qy	541	AAVYFCQDYNPPTFGGKLEIKRADA-APTYSIPPPSSEQLTSGGASVVCFLNNFYP	599	CC	
Db	240	LAVYFCQDYNPPTFGGKLEIKRASTKPGSVFPLAPSSKSTSGGTAALGCLVKDYFP	299	CC	
Qy	600	KDINVKW-----IDGSRQNGVLNSWTQDQSKDSTYSMSSTLTLDKDYERHNSYTCEAT	655	CC	
Db	300	EPTVSNWNGALYSGVHTFPAVLQS-----SGLYSLSVVTVTPSSSLGT-QTYICNVN	351	CC	
Qy	656	HKTSTSPIVK 665		CC	
Db	352	HKPSNTKVDK 361		CC	
RESULT 24					
Id	ADR59118	standard; protein; 469 AA.			
Ac	ADR59118;				
Dt	18-NOV-2004	(first entry)			
De	Anti-K88/K99	antibody related protein, SEQ ID 69.			
Kw	Gastrointestinal; antibody; heavy chain; light chain; variable region; enterotoxigenic Escherichia coli; ETEC; K88 antigen; K99 antigen; animal food; enteric disease.				
Os	Mus sp.				
Xx	WO2004074491-A2.				
Pd	02-SEP-2004.				
Pf	16-FEB-2004; 2004WO-EP001427.				
Xx	18-FEB-2003; 2003US-0448429P.				
Pa	(SYGN) SYNGENTA PARTICIPATIONS AG.				
Pi	Brown D, Campos M, Dalmia B, Demarest S, Hansen G, Heifetz PB;				
Xx	WPI; 2004-635583/61.				
Xx	Novel immunoglobulin heavy chain comprising bovine CH3 or CH2 domain, murine CH2CH3 domain or human CH2CH3 domain, useful in treatment or prevention of enteric disease in animal.				
Ps	Claim 58; SEQ ID NO 69; 165pp; English.				
Xx	The present invention relates to coding sequences for mammalian antibody				

CC	heavy and light chains directed against enterotoxigenic Escherichia coli (ETEC), in particular, ETEC of a strain possessing the K88 or K99 antigen. The heavy and light chain sequences are useful for producing transgenic plants, which express the K88 or K99 antibody. The transgenic plants are useful for producing animal feed, food product, animal feed additive, feed pre-mix or nutritional supplement and are also useful for treating or preventing enteric disease in an animal. The present sequence was used in an example from the invention.	
XX		
SQ	Sequence 469 AA;	
Query Match 30.2%; Score 1064; DB 8; Length 469;		
Best Local Similarity 37.8%; Pred. No. 5.3e-55;		
Matches 252; Conservative 52; Mismatches 114; Indels 248; Gaps 13;		
QY	1	EVQLQQSGDPLVKGASVKISCKASGYFTGYVMHWKSPGKGLRWIGRINPNNGVTLY 60
DB	20	EVQLQQSGFELVKTAGSVKISCKADSYSLTDYVMHWKQSHGESLEWIGVINYNGATNY 79
QY	61	NQKFKDKATLTVDKSSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYMQGTSVTVSS 120
DB	80	NQKFKGKATFTVDTSSSTVTVMQFNSLTSEDSAVYYCVREALLRNYAMDYMQGTSVTVSS 139
QY	121	AKTTPSPVPLAPGSAQAQNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180
DB	140	AKTTPSPVPLAPGSAQAQNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 199
QY	181	LYTLSSSVTPSWSEVTTCNVAPASSTKVDKIVPRDSDGSPSEKSEINEKDLRKK 240
DB	200	LYTLSSSVTPSWSEVTTCNVAPASSTKVDKIVPRDCG----- 242
QY	241	SELQGTALGNLKOIYYNKAITSSEKSAQDLTNTLLPKGFTTGHVWYNDLLVLDGSTA 300
DB	243	: :

Db 293 -DVEVHTAQTPREQFNSTFRSVSELPIMHQDLWGKFKCRVNSAAPAPIEK----- 346
Qy 412 HSSEGSTVSYDLFDAQQGVPTLLRIYRDNNTTSSLSISLYLTTYSIVMTQTPTSLLV 471
Db 347 -----TISK----- 351
Qy 472 SAGDRVTITCKASQSVNDVAVYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
Db 352 ----- 351
Qy 532 TISSVQAEADAAYVFCQDYNPPTFGGKLEIKRADAAPTYSIFPPSSQOLTSGGASVV 591
Db 352 -----KGRPKAPQVYTIIPPEQMAKDKVSLT 378
Qy 592 CFLNNFYPKDINVKWKIDGSRQGVNSWTDODSKDSTYSMSSTLTLTKDEYERHNSVT 651
Db 379 CMITDFPEDITVEQWNGQPAEN-YKNTQPIMDT-DGSFYVYSKLVNQSKNWEAGNTFT 436
Qy 652 CEATHK 657
Db 437 CSVLHE 442

RESULT 31
ADW97139
ID ADW97139 standard; protein; 460 AA.

AC ADW97139;
XX
XX
XX
DT 21-APR-2005 (first entry)
DE Murine mAb 1021 heavy chain protein (alternate version).
XX
XX Screening; diagnosis; chemotherapy; therapy; cancer; cytostatic;
KW neoplasm; prostatitis; andrology; genitourinary disease; inflammation;
KW rheumatoid arthritis; antiarthritic; antirheumatic; immune disorder;
KW musculoskeletal disease; antiinflammatory; autoimmune disease;
KW immunosuppressive; cardiovascular disease; cardiovascular-gen.;
KW cerebrovascular ischemia; scarring; vulnery; infection;
KW myocardial infarction; cardant; neurological disease;
KW Alzheimers disease; neuroprotective; nootropic; degeneration;
KW hematological disease; organ transplant rejections;
KW graft versus host disease; developmental disorder; antibody.

XX Mus sp.

OS WO2005010049-A2.

XX PN 03-FEB-2005.

XX PD 06-JUL-2004; 2004WO-US018921.

XX PF 09-JUL-2003; 2003US-0485820P.

XX PR (ELIL) LILLY & CO ELI.

XX PA Bradley HM, Kikly KK, Lancaster JS, Rowlinson SW;

XX PI WPI; 2005-123130/13.

XX DR N-PSDB; ADW97103.

XX Binding composition for treating diseases e.g. cancer, is capable of
PT specifically binding to and neutralizing transforming growth factor (TGF)
PT beta 1, comprises binding sites of anti-TGF beta antibodies designated
PT 1021, 2471 and 3821.

XX Example 2; Page 90; 129pp; English.

XX The present invention relates to a binding composition which is capable
CC of specifically binding to and neutralizing transforming growth factor
CC (TGF) beta 1, comprises binding sites of anti-TGF beta 1 antibodies
CC designated 1021, 2471 and 3821. The invention is useful for diagnosing,
CC

CC preventing and treating diseases chosen from cell proliferative (e.g.
CC cancer), inflammatory (e.g. chronic prostatitis), autoimmune (e.g.
CC rheumatoid arthritis), cardiovascular (e.g. stroke, myocardial scarring,
CC infarction), neurological (e.g. Alzheimer's disease), fibrotic, blood
CC diseases (e.g. agammaglobulinemia), organ rejection, graft-versus-host
CC disease and developmental diseases. The present sequence is the murine
CC mAb 1021 heavy chain protein. This sequence is the alternate version of
CC ADW97104.

XX Sequence 460 AA;

Qy Query Match 29.6%; Score 1044; DB 9; Length 460;
Best Local Similarity 37.8%; Pred. No. 8e-54;
Matches 252; Conservative 52; Mismatches 110; Indels 252; Gaps 14;

Qy 1 EVOLQSGPDLVKPGASVKISKASGYSTGYMHVHKVSPGKGLGWIRINPNNGVTLY 60

Db 21 EVOLQSGPELVKPGASVKISKASGYTDTYMHVHKVSPGKGLGWIRINPNNGVTLY 80

Qy 61 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYVCARSTMITNYVMYDQGTSTVTSS 120

Db 81 NQKFKSKATLTVDNSSTAYMELRSLTSDSAVYVCVRG-----YWFATWGRGTLTIVST 136

Qy 121 AKTTPPSVYPLAPGSAATNSMTLGLCKLVKGYFPEPTVTWNSGSLSSGVHTTTPAVLQSD 180

Db 137 AKTTPSVYPLAPGSAATNSMTLGLCKLVKGYFPEPTVTWNSGSLSSGVHTTTPAVLQSD 196

Qy 181 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVKKIVPRDGGGPPSEKSEINEKDLRKK 240

Db 197 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVKKIVPRDGGGPPSEKSEINEKDLRKK 239

Qy 241 SELQGTALGNLQIYYNYSKAITSSSEKSDAQELTNTLLFKGPTGHPYNDLLVDLGSTA 300

Db 240 CRPCICTVPEVSSVFIPPK-----PKDVLITL----- 268

Qy 301 ATSEYEGSVLDLYGAYGYQCAGTTPNKTCMYGGVTLHDNNRLTEKKVPINLWDGKQ 360

Db 269 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 293

Qy 361 TTVPTDKVTSKEV-----TVELDLQARHLYHGK-FGL-YNSDSFGGKVGQRLIVF 411

Db 294 -DVEVHTAQTPREQFNSTFRSVSELPIMHQDLWGKFKCRVNSAAPAPIEK----- 347

Qy 412 HSSEGSTVSYDLFDAQQGVPTLLRIYRDNNTTSSLSISLYLTTYSIVMTQTPTSLLV 471

Db 348 -----TISK----- 352

Qy 472 SAGDRVTITCKASQSVNDVAVYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531

Db 353 ----- 352

Qy 532 TISSVQAEADAAYVFCQDYNPPTFGGKLEIKRADAAPTYSIFPPSSQOLTSGGASVV 591

Db 353 -----KGRPKAPQVYTIIPPEQMAKDKVSLT 379

Qy 592 CFLNNFYPKDINVKWKIDGSRQGVNSWTDODSKDSTYSMSSTLTLTKDEYERHNSVT 651

Db 380 CMITDFPEDITVEQWNGQPAEN-YKNTQPIMDT-DGSFYVYSKLVNQSKNWEAGNTFT 437

Qy 652 CEATHK 657

Db 438 CSVLHE 443

RESULT 32

ADQ14477
ID ADQ14477 standard; protein; 467 AA.

XX ADQ14477;

XX 07-OCT-2004 (first entry)

XX Mouse anti-human agonist Ab heavy chain.

Db 61 YNDLLVDKSGSDATNKYKGVLDYLGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTEEX 120
Qy 349 KVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGL 408
Db 121 XVQXBWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGL 180
Qy 409 IVPHSSEGSTVSYDLFDAQSQYPTDLLRIYRDNTTSSLSLSLYLYTT 458
Db 181 IVPHSSEGSTVSYDLFDAQSQYPTDLLRIYRDNTTSENWHDIDYLYTT 230

RESULT 34
AAE18377
ID AAE18377 standard; protein; 597 AA.
XX AAE18377;
AC AAE18377;
DT 07-MAY-2002 (first entry)
XX Human N-terminal DAV-1 heavy chain-mature TNF-alpha fusion protein.

XX Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;
KW cytotatic; vasotrophic; ophthalmological; tumour necrosis factor-alpha;
KW TNF-alpha; fusion protein.
XX Homo sapiens.
OS Synthetic.
OS Chimeric.

XX Key Location/Qualifiers
FH Region 1..439
FT /note= "N-terminal portion of DAV-1 heavy chain"
FT Region 441..597
FT /note= "Human mature TNF-alpha"
XX WO200204522-A2.
XX 17-JAN-2002.
XX 09-JUL-2001; 2001WO-EP007878.
XX 10-JUL-2000; 2000US-00613017.
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA (SCRI) SCRIPPS RES INST.

XX Nemerow GR, Li E;
XX WPI; 2002-171707/22.
DR New bifunctional molecules comprising an antibody or its antigen-binding
PT portion, and a targeting agent, useful for e.g. gene therapy, or for
PT promoting Adenoviral vector-mediated gene delivery to cells lacking av
PT integrins.
XX Claim 15; Page 98-99; 106pp; English.

XX The present invention relates to a bifunctional molecule comprising an
XX antibody or its antigen-binding portion, and a targeting agent where the
XX antibody specifically binds to an antigen in a protein that binds to av
XX integrin, and the targeting agent specifically binds to a cell surface
XX protein that activates the phosphatidylinositol 3 (PI3K) signalling
XX pathway. The bifunctional molecules are useful for gene therapy, for
XX promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking
XX av integrins, for enhancing Ad binding and internalisation, and in gene
XX delivery of by fibreless adenovirus particles. The bifunctional molecules
XX permit targeting of viral and bacterial vectors to cells that express
XX targeted receptors. Diseases that can be targeted include cancers,
XX vascular disorders, diabetic retinopathies, restenosis, ophthalmic
XX disorders, hyperproliferative disorders, and hormonal disorders. The

CC present sequence is human N-terminal DAV-1 heavy chain-mature tumour
CC necrosis factor-alpha (TNF-alpha) fusion protein which is used in the
CC invention
XX
SQ Sequence 597 AA;
Query Match 29.2%; Score 1028; DB 5; Length 597;
Best Local Similarity 37.2%; Pred. No. 9.7e-53;
Matches 253; Conservative 53; Mismatches 115; Indels 260; Gaps 15;

Qy 1 EVLOQSGDPLVKPGASVKISKASGYSTGYMHVWKSPGKGLIEWIRINPNNGVTLY 60
Db 20 EVLOQSGPELVKPGASVKISKASGYTFTDYNMHVWKSHGKSLIEWIGYIYKGGTGY 79
Qy 61 NQKFKDKATLTVDKSSTTAYMEIRSLTSDSAVYVCARSTMTINVMYWGQGSTVTVSS 120
Db 80 NQKFKSKATLTDTSSSNTAYMEIRSLTSDSAVYVCARG-----IAYWQGTSLTVSA 132

Qy 121 AKTTTPSVVPLAPGSAQAQNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTFPVQLSD 180
Db 133 AKTTTPSVVPLAPGSAQAQNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTFPVQLSD 192

Qy 181 LYTLSSSVTPSSTWPSSTVTCNVAHPASSTKVDKIVPRDGGSPSEKSEINEKDLRKK 240
Db 193 LYTLSSSVTPSSTWPSSTVTCNVAHPASSTKVDKIVPRDCG----- 235

Qy 241 SELQGTALGNLQIYYNSKAITSEKSDAQELTLLFKGFTGHPWYNDLLVDLGSTA 300
Db 236 CRPCICTVPESSVFIFPPK-----PKDVLITL----- 264

Qy 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTBEKKVPIINLWDGKQ 360
Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289

Qy 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQGLIVF 411
Db 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAIEK----- 343

Qy 412 HSSEGSTVSYDLFDAQSQYPTDLLRIYRDNTTSSLSLSISLYLYTTSIVMTQPTSLLV 471
Db 344 -----TISK----- 348

Qy 472 SAGDRVITITCKASQSVSNDVAVYQKPGQSKLLISYTSRYAGVPDRFSGGYGDTFTL 531
Db 349 ----- 348

Qy 532 TISSVQAEADAAYFCQDYNSPPTFGGKLEIKRADAAPTVISIPPPSEQLTSGGASVV 591
Db 349 -----KGRPKAPQVYTIPTPPKEQMAKDKVSLT 375

Qy 592 CFLNNFYPKDINVKMKIDGSEKQNGVLSNWTDDSKDSTYSMSSTLTLTCKDEVERHNSYT 651
Db 376 CMITDFFPEDITVEQWQNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNOKSNWEAGNTFI 433

Qy 652 CEATHKTSPTPIVKSFNRNES 672
Db 434 CSVLHE-----FVRSRRTPS 449

RESULT 35
ABG76352
ID ABG76352 standard; protein; 597 AA.
XX ABG76352;
AC ABG76352;

XX 23-OCT-2003 (revised)
DT 10-MAY-2003 (first entry)
XX Mouse DAV-1 heavy chain-mature human TNF-alpha fusion protein.
XX Human; bifunctional molecule; antigen-binding portion; alpha integrin;
KW cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;
KW signalling pathway; targeted gene therapy; delivery vector;

XX 08-OCT-1998. 98AU-00059701.
PD
PF 30-MAR-1998; 98AU-00059701.
PR 01-APR-1997; 97JP-00082953.
PR 25-JUN-1997; 97JP-00169088.
PR 08-OCT-1997; 97JP-00276064.
XX (SANY) SANKYO CO LTD.
XX Nobufusa S, Kimihisa I, Jun O, Masahiko O, Hideyuki H, Tohru T;
PI Hiroko Y, Akio S, Shin Y;
XX WPI; 1998-543440/01.
DR N-PSDB; AAV71029.
XX New antibodies and proteins bind conserved epitope of Fas antigen - used
PT to evaluate drugs in animal models and to treat Fas-associated diseases
PT e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis,
PT hepatitis and AIDS.
XX
PS Example 4; Page 187-188; 292pp; English.
XX This is the amino acid of the heavy chain of murine anti-human Fas
CC monoclonal antibody HFE7A. cDNA (see AAV70129) encoding the heavy chain
CC was obtained from HFE7A-secreting hybridoma (FERM BP-5828) RNA by RT-PCR
CC (see AAV70125-26). The invention provides humanised HFE7A antibodies (see
CC AAV83031-37) produced by CDR grafting. These antibodies are capable of
CC inducing apoptosis in abnormal cells expressing Fas, and of inhibiting
CC Fas-induced apoptosis in normal cells. They are used to evaluate, in
CC animal models, treatments of diseases that involve Fas/Fas ligand
CC interactions, and also to treat such diseases, including autoimmune
CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft
CC versus host disease, Sjogren syndrome, pernicious anaemia, Addison's
CC disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-
CC dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis,
CC AIDS and transplant rejection (all claimed). (Updated on 25-MAR-2003 to
CC correct DR field.)
XX
XX Sequence 464 AA;
Query Match 29.1%; Score 1025.5; DB 2; Length 464;
Best Local Similarity 36.2%; Pred. No. 1e-52;
Matches 243; Conservative 64; Mismatches 106; Indels 259; Gaps 14;
QY 1 EVLOQSGDPLVKGASVKLSCKASGYSTGYMHVVKQSPGKLEWIGRINPNNGVTLY 60
DB 20 QVLOQPGALVKGASVKLSCKASGYSTGYMHVVKQSPGKLEWIGRINPNNGVTLY 79
QY 61 NQFKDKATLTVDSKSTTAYMELRSITSEDSAVYICARS-TMITNTVMYVGQGSVTVS 119
DB 80 NQFKDKATLTVDSKSTTAYMELRSITSEDSAVYICARNRDYNNYFDWGGTIVTVS 139
QY 120 SAKTTPSVVPLAPGSAAGTNSMVTLCGLVKGYFPEPVTVMNSGLSSGVHFFPAVLQS 179
DB 140 SAKTTPSVVPLAPGSAAGTNSMVTLCGLVKGYFPEPVTVMNSGLSSGVHFFPAVLQS 199
QY 180 DLYTLSSSVTPSPSTPSEVTCNVAHPASSTVKDKKIIPRDSGGPSEKSEINEKDLRK 239
DB 200 DLYTLSSSVTPSPSTPSEVTCNVAHPASSTVKDKKIIPRDCG----- 243
QY 240 KSLOGTALGNLQIYYVNSKAITSEKSAQDLTNTLLFKGFTGHPWYNLLDLVLGSLT 299
DB 244 -KPCICTPEVSSVFIFPK-----PKDVLITL----- 272
QY 300 AATSEYSGSVLDYGYAYGYQCAAGTTPNKTACMYGGVTLHNNRLTEKKVPINLWIDGK 359
DB 273 -----TP-KVTCVVVDIS-----KDDPEVQPSWFVD-- 297

QY 360 QTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQGLIV 410
DB 298 --DVEVHTAQTPREQFNSTRSVSELPFIMQWNLNGKEFKCRVNSAAPPAPIEK---- 351
QY 411 FHSSEGSTVSYDLFDAQQGYPDTLLRIYRDNTTISSTLSLSISLYLTYTTSIVMTQTPTSL 470
DB 352 -----TISKT----- 356
QY 471 VSAGDRVTITCKASQSVSNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFT 530
DB 357 ----- 356
QY 531 LTISVVQAEADAAYVFCQDYNPPTFGGKTKLEIKRADAAPTYSIFPPSEQLTSGASV 590
DB 357 -----KGRKAPQVYITPPPKQMAKQVSL 382
QY 591 VCFLNFFPKDINVKWKIDGSRQN-----GVLNSWTDQSKDSTYSMSSTLTLTDEYE 645
DB 383 TCMTITDFFPEDITVEWMQNGQPAENYKNTQPIMNT-----NGSYFVYSKLVNQKSNWE 435
QY 646 RHNSYTCSEATHK 657
DB 436 AGNTFTCSVLHE 447
RESULT 37
AAB14747
ID AAB14747 standard; protein; 464 AA.
XX
AC AAB14747;
XX
DT 24-NOV-2000 (first entry)
XX Mouse anti-Fas antibody HFE7A heavy chain.
DE
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine;
XX complementarity determining region; CDR; human Fas; Fas ligand;
KW apoptosis modulator; programmed cell death; autoimmune disease; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis;
KW aplastic anaemia; pancytopenia; hepatitis; AIDS; graft rejection;
KW heavy chain.
XX
OS Mus musculus.
XX
PN JP20000169393-A.
XX
PD 20-JUN-2000.
XX
PF 30-SEP-1999; 99JP-00278301.
XX
PR 30-SEP-1998; 98JP-00276883.
XX
PA (SANY) SANKYO CO LTD.
XX
XX WPI; 2000-485645/43.
DR N-PSDB; AAV72108.
XX
PT Preventive or treating agent for the diseases caused by an abnormality in
PT the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas
PT antibody.
PS Example 4; Page 67-68; 139pp; Japanese.
XX The invention relates to compositions for the prevention or treatment or
CC diseases caused by an abnormality in the Fas/Fas ligand system containing
CC an anti-Fas antibody as the active component. The anti-Fas antibody is
CC either the murine anti-human Fas monoclonal antibody HFE7A, or a
CC humanised version of HFE7A containing identical CDRs (complementarity
CC determining regions) to antibody HFE7A. Via its interaction with Fas, the
CC antibody of the invention acts as a modulator of apoptosis. The
CC composition of the invention may therefore be used in the treatment or
CC prevention of conditions such as autoimmune diseases, allergy, atopy,
CC arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis,

Db 80 NQKFKGKATLTVDTSSTAYMQLSLLTSDSAVYYCARNRDYNNWYFDVWGTTGTTVTS 139
QY 120 SAKTTPPSYVPLAPGSAQTNSMVTLCGLVKGYPPEPVTVTWNSGSLSSGVHTFPFVAVLOS 179
Db 140 SAKTTPPSYVPLAPGSAQTNSMVTLCGLVKGYPPEPVTVTWNSGSLSSGVHTFPFVAVLOS 199
QY 180 DLYTLSSSVTVPSSTWPSSTVCNVAHPASSTKVDKKIYPRDSGGPSEKSEINEKDLRK 239
Db 200 DLYTLSSSVTVPSSTWPSSTVCNVAHPASSTKVDKKIYPRDCG----- 243
QY 240 KSELOQTALGNLKOIYYNSKAITSEKSGADQPLTNTLLFKGFTGHPWYNLLVDLGST 299
Db 244 -CKPCICTVPEVSSVFIFPPK-----PKDVLITL----- 272
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPINLWIDGK 359
Db 273 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV-- 297
QY 360 QTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQGRGLIV 410
Db 298 --DVEVHTAQTPREBQFNSSTFRSVSELPIMHQNWLNKGEKFCRVNSAAPPAIEK----- 351
QY 411 FHSSEGSTVSYDLFDAQGYPDTLRLIYRDNTTISSTLSLSLYLTTTSIVMTQTPTSL 470
Db 352 -----TISKT----- 356
QY 471 VSAGDRVTITCKASQSVSNDVAWYQKPGSPKLLISYTSRVRAGVDPDRFSGSGYGTDTFT 530
Db 357 ----- 356
QY 531 LTISSVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTYSIFPPSSEQLTSGASV 590
Db 357 -----KGRPKAPQYVYTIPTTPPKQMAKDKVSL 382
QY 591 VCFLNFPYKPDINVWKIDGSRQN-----GVLSNWTDDQSDKSTYSMSSTLTLTDEYE 645
Db 383 TCMITDFPEDITVEQWNGQPAENYKNTQPIMNT-----NGSYFVYSKLVNQSNE 435
QY 646 RHNSYTCEATHK 657
Db 436 AGNTFTCSVLHE 447

RESULT 39
ABB74912
ID ABB74912 standard; peptide; 464 AA.
XX ABB74912;
XX
XX
DT 30-APR-2002 (first entry)
DE Humanised anti-Fas antibody related peptide SEQ ID NO 29.
XX
XX Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;
KW heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic;
KW autoimmune disease; allergy; atopy.
XX
XX Homo sapiens.
OS
PN JP2001342149-A.
XX
PD 11-DEC-2001.
XX
PF 28-MAR-2001; 2001JP-00093243.
XX
PR 29-MAR-2000; 2000JP-00091144.
XX
XX (SANY) SANKYO CO LTD.
XX
XX WPI; 2002-145114/19.
DR
XX
XX Drug for preventing or treating e.g. autoimmune disease or allergy,
PT comprises humanized anti-Fas antibody.

XX
PS
XX
CC The invention relates to a preventive or treating agent for diseases
CC caused by abnormality in the Fas/Fas ligand system containing, as the
CC active component, an antibody having a light chain subunit and a heavy
CC chain subunit and an activity of combining specifically with mammalian
CC Fas and an activity of inducing apoptosis in a cell expressing Fas. The
CC agent has antiallergic, immunosuppressive and apoptotic activity and is
CC used for preventing and treating autoimmune diseases, allergy, atopy and
CC others. The present sequence is that of a peptide useful to the invention
XX
SQ Sequence 464 AA;
Query Match 29.1%; Score 1025.5; DB 5; Length 464;
Best Local Similarity 36.2%; Pred. No. 1e-52;
Matches 243; Conservative 64; Mismatches 106; Indels 259; Gaps 14;
QY 1 EVQLQQSGDLPVKPGASVKISKASGYFTGYVMHWKQSPGKGLEWIGRIINPNNGVTLY 60
Db 20 QVQLQQPGALVKPGASVKLSKASGYFTSYMQWVKQRPQGLEWIGELIDSDSYNY 79
QY 61 NQKFKGKATLTVDKSTTAYMELRSLTSDSAVYYCARS-TMITNYMDYWGOGTSTVTS 119
Db 80 NQKFKGKATLTVDTSSTAYMQLSLLTSDSAVYYCARNRDYNNWYFDVWGTTGTTVTS 139
QY 120 SAKTTPPSYVPLAPGSAQTNSMVTLCGLVKGYPPEPVTVTWNSGSLSSGVHTFPFVAVLOS 179
Db 140 SAKTTPPSYVPLAPGSAQTNSMVTLCGLVKGYPPEPVTVTWNSGSLSSGVHTFPFVAVLOS 199
QY 180 DLYTLSSSVTVPSSTWPSSTVCNVAHPASSTKVDKKIYPRDSGGPSEKSEINEKDLRK 239
Db 200 DLYTLSSSVTVPSSTWPSSTVCNVAHPASSTKVDKKIYPRDCG----- 243
QY 240 KSELOQTALGNLKOIYYNSKAITSEKSGADQPLTNTLLFKGFTGHPWYNLLVDLGST 299
Db 244 -CKPCICTVPEVSSVFIFPPK-----PKDVLITL----- 272
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPINLWIDGK 359
Db 273 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV-- 297
QY 360 QTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQGRGLIV 410
Db 298 --DVEVHTAQTPREBQFNSSTFRSVSELPIMHQNWLNKGEKFCRVNSAAPPAIEK----- 351
QY 411 FHSSEGSTVSYDLFDAQGYPDTLRLIYRDNTTISSTLSLSLYLTTTSIVMTQTPTSL 470
Db 352 -----TISKT----- 356
QY 471 VSAGDRVTITCKASQSVSNDVAWYQKPGSPKLLISYTSRVRAGVDPDRFSGSGYGTDTFT 530
Db 357 ----- 356
QY 531 LTISSVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTYSIFPPSSEQLTSGASV 590
Db 357 -----KGRPKAPQYVYTIPTTPPKQMAKDKVSL 382
QY 591 VCFLNFPYKPDINVWKIDGSRQN-----GVLSNWTDDQSDKSTYSMSSTLTLTDEYE 645
Db 383 TCMITDFPEDITVEQWNGQPAENYKNTQPIMNT-----NGSYFVYSKLVNQSNE 435
QY 646 RHNSYTCEATHK 657
Db 436 AGNTFTCSVLHE 447
RESULT 40
ABB74866
ID ABB74866 standard; peptide; 464 AA.
XX
XX ABB74866;
XX

Query Match		29.1%;	Score 1025.5;	DB 9;	Length 466;
Best Local Similarity		36.8%;	Pred. No. 1e-52;		
Matches		245;	Conservative	61;	Mismatches 112; Indels 251; Gaps 14;
QY	1	EVQLQSGDPLVKPGASVKISCKASGYFTGYMHVWVKSPGKGLEWIGRIINPNNGVTLY	60		
DB	20	QVQLQPGAEVLRPGASVKLSCKASGYFTSYWVWVKRPGGLEWIGNIYPSDSYTN	79		
QY	61	NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYYCARSTM----	117		
DB	80	NQKFKDKATLTVDKSSNTVMQLNSPTSDSAVYYCTRNGVEGYPHYAMYGQTSVT	139		
QY	118	VSAKTTTPSVPLAPGSAQTNSMTLGLVKGYPEPVTWNSGSLSSGVHTTFAVL	177		
DB	140	VSAKTTTPSVPLAPGSAQTNSMTLGLVKGYPEPVTWNSGSLSSGVHTTFAVL	199		
QY	178	QSDLYTLSSSVTPSSTWPTSETVTCNVAHPASSTKVYKIVPRDGGPSEKSEINEKDL	237		
DB	200	QSDLYTLSSSVTPSSTWPTSETVTCNVAHPASSTKVYKIVPRDCG-----	245		
QY	238	RKXSELOQTALGNLKOIYYNSKAITSSSEKSDAQFLTNTLLFKGFTGHPWYNDLLVDLG	297		
DB	246	---CKPCICTVPEVSSVFIFPPK-----PKDVLITL-----	274		
QY	298	STAATSEYEGSSVDLYGAYGYQCAGGTGNKTCMYGGVTLHDNNRLTBEKKVPINLWID	357		
DB	275	-----TP-KVTCVVVDIS-----KDDPEVQFSWFVD	299		
QY	358	GKQTTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQVQGL	408		
DB	300	----DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEPKCRVNSAAFPAPTEK--	353		
QY	409	IVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNNTTISLSLSLYLYTTSIVMTQPTS	468		
DB	354	-----TIKST-----	358		
QY	469	LLVSGDRVTITCKASQSVNDVAMVYQKPGQSPKLLISVTSRYAGVPRDFSGSGYGT	528		
DB	359	-----	358		
QY	529	FTLTISVQAEADAAYVFCQDYNPSPTFGGKLEIKRADAAPTIVFPPSSQLTSGGA	588		
Query Match		29.1%;	Score 1025.5;	DB 9;	Length 466;
Best Local Similarity		36.8%;	Pred. No. 1e-52;		
Matches		245;	Conservative	61;	Mismatches 112; Indels 251; Gaps 14;
QY	1	EVQLQSGDPLVKPGASVKISCKASGYFTGYMHVWVKSPGKGLEWIGRIINPNNGVTLY	60		
DB	20	QVQLQPGAEVLRPGASVKLSCKASGYFTSYWVWVKRPGGLEWIGNIYPSDSYTN	79		
QY	61	NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYYCARSTM----	117		
DB	80	NQKFKDKATLTVDKSSNTVMQLNSPTSDSAVYYCTRNGVEGYPHYAMYGQTSVT	139		
QY	118	VSAKTTTPSVPLAPGSAQTNSMTLGLVKGYPEPVTWNSGSLSSGVHTTFAVL	177		
DB	140	VSAKTTTPSVPLAPGSAQTNSMTLGLVKGYPEPVTWNSGSLSSGVHTTFAVL	199		
QY	178	QSDLYTLSSSVTPSSTWPTSETVTCNVAHPASSTKVYKIVPRDGGPSEKSEINEKDL	237		
DB	200	QSDLYTLSSSVTPSSTWPTSETVTCNVAHPASSTKVYKIVPRDCG-----	245		
QY	238	RKXSELOQTALGNLKOIYYNSKAITSSSEKSDAQFLTNTLLFKGFTGHPWYNDLLVDLG	297		
DB	246	---CKPCICTVPEVSSVFIFPPK-----PKDVLITL-----	274		
QY	298	STAATSEYEGSSVDLYGAYGYQCAGGTGNKTCMYGGVTLHDNNRLTBEKKVPINLWID	357		
DB	275	-----TP-KVTCVVVDIS-----KDDPEVQFSWFVD	299		
QY	358	GKQTTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQVQGL	408		
DB	300	----DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEPKCRVNSAAFPAPTEK--	353		
QY	409	IVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNNTTISLSLSLYLYTTSIVMTQPTS	468		
DB	354	-----TIKST-----	358		
QY	469	LLVSGDRVTITCKASQSVNDVAMVYQKPGQSPKLLISVTSRYAGVPRDFSGSGYGT	528		
DB	359	-----	358		
QY	529	FTLTISVQAEADAAYVFCQDYNPSPTFGGKLEIKRADAAPTIVFPPSSQLTSGGA	588		
DB	359	-----KGRPKASQVYTIIPPKEQMAKDKV	382		
QY	589	SVVCFLNPNPKDINKWKIDGSEKONGVUNSWTDQSDKDYTSMSSTLTITKDEYERIN	648		
DB	383	SLTCMITDFPEDITVEWQWQPAEN-YKNTQPIMDT-DGSYFVYKLVQKSNWEAGN	440		
QY	649	SYTCEATHK 657			
DB	441	TFTCSVLHE 449			
RESULT 42					
ADX39137					
XX	ID	ADX39137	standard; protein; 466 AA.		
XX	AC	ADX39137;			
XX	DT	21-APR-2005 (first entry)			
XX	DE	Mouse monoclonal antibody 4785 heavy chain SEQ ID 38.			
XX	KW	Monoclonal antibody; heavy chain; autoimmune disease; immunosuppressive;			
XX	KW	immune disorder; systemic lupus erythematosus; antiinflammatory;			
XX	KW	dermatological; dermatological disease; metabolic disorder;			
XX	KW	musculoskeletal disease; tumor necrosis factor receptor.			
OS	Mus sp.				
XX	PN	KR2004083918-A.			
XX	PD	06-OCT-2004.			

Db 359 -----KGRPKASQVYTIPTPKQMAKDV 382

Qy 589 SVVCELNNFVKDINVKWKIDGSEKQNGVLNSWTDODSKDSTYSMSSTLTTLTXDEVERHN 648

Db 383 SLTFCMTDFFPEDITVWQWNGQPAEN-YKNTQIPIMDT-DGSYFVYSKLVNQKSNWEAGN 440

Qy 649 SYTCEATHK 657

Db 441 TFTCSVLHE 449

RESULT 43

AAE18380

ID AAE18380 standard; protein; 613 AA.

XX

AC AAE18380;

DT 07-MAY-2002 (first entry)

XX Human N-terminal DAV-1 heavy chain-mature SCF fusion protein.

XX Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;

KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;

KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;

KW cytostatic; vasotropic; ophthalmological; stem cell factor; SCF;

fusion protein.

XX Homo sapiens.

OS Synthetic.

OS Chimeric.

XX

XX Key Location/Qualifiers

FT Region 1..438

FT /note= "N-terminal portion of DAV-1 heavy chain"

FT Region 439..449

FT /note= "Linker peptide"

FT Region 450..613

FT /note= "Human mature SCF"

XX

PN WO200204522-A2.

XX

PD 17-JAN-2002.

XX

PF 09-JUL-2001; 2001WO-EP007878.

XX

PR 10-JUL-2000; 2000US-00613017.

XX

PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PA (SCRI) SCRIPPS RES INST.

XX

PI Nemerow GR, Li E;

XX

XX WPI; 2002-171707/22.

XX

PT New bifunctional molecules comprising an antibody or its antigen-binding

PT portion, and a targeting agent, useful for e.g. gene therapy, or for

PT promoting Adenoviral vector-mediated gene delivery to cells lacking av

PT integrins.

XX

PS Claim 15; Page 102-103; 106pp; English.

XX

CC The present invention relates to a bifunctional molecule comprising an

CC antibody or its antigen-binding portion, and a targeting agent where the

CC antibody specifically binds to an antigen in a protein that binds to av

CC integrin, and the targeting agent specifically binds to a cell surface

CC protein that activates the phosphatidylinositol 3 (PI3K) signalling

CC pathway. The bifunctional molecules are useful for gene therapy, for

CC promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking

CC av integrins, for enhancing Ad binding and internalisation, and in gene

CC delivery of by fibreless adenovirus particles. The bifunctional molecules

CC permit targeting of viral and bacterial vectors to cells that express

CC targeted receptors. Diseases that can be targeted include cancers,

CC vascular disorders, diabetic retinopathies, restenosis, ophthalmic

CC disorders, hyperproliferative disorders, and hormonal disorders. The

CC present sequence is human N-terminal DAV-1 heavy chain-mature stem cell

CC factor (SCF) fusion protein which is used in the invention

XX

Sequence 613 AA;

Query Match 29.1%; Score 1024.5; DB 5; Length 613;

Best Local Similarity 37.3%; Pred. No. 1.6e-52;

Matches 250; Conservative 51; Mismatches 115; Indels 255; Gaps 14;

Qy 1 EVOLQSGPDLVKPGASVKISKASGYFTGYNMHWKQSPGKLEWIGRINPNNGVTL 60

Db 20 EVOLQSGPDLVKPGASVKISKASGYFTGYNMHWKQSPGKLEWIGRINPNNGVTL 79

Qy 61 NQKFKDKATLTVDKSSSTTAYMELSLTSEDVAVYYCARSTMTINYYMDYVQGGTSVTVSS 120

Db 80 NQKFKSKATLTVDKSSSTTAYMELSLTSEDVAVYYCARSTMTINYYMDYVQGGTSVTVSS 132

Qy 121 AKTTPSPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVTHTPFAVLQSD 180

Db 133 AKTTPSPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVTHTPFAVLQSD 192

Qy 181 LYTLSSTVPSSTWPSSETVTCNVAHPASTKVDKIVPRDSDGSPSEKSEINEKDLRKK 240

Db 193 LYTLSSTVPSSTWPSSETVTCNVAHPASTKVDKIVPRDSDGSPSEKSEINEKDLRKK 235

Qy 241 SELQGTALGNLKOIYYNKAITSSEKSAQDQFLNTLLPKGFTGHPWYNLLVDLGSTA 300

Db 236 CRPCICTVPEVSSVFIPPK-----PKDVLTITL----- 264

Qy 301 ATSEYEGSSVDLYGAYYGYQCAGGTNKTACMYGGVTLHDNNRLTBKVKPINLWIDGKQ 360

Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289

Qy 361 TTVPIDKVTSKKEV-----TVQELDLQARHLYHGK-FGL-YNSDSFGKVKQVGRGLIVF 411

Db 290 -DVEVHTAQTPREQFNSTFRSVSELPIMHQDLNGKEPKCRVNSAAPAPIEK----- 343

Qy 412 HSSEGSTVSYDLFDPAQOQVPTLLRIYRDNLTSTLSLSISLYLYTTSIVMTQPTSLLV 471

Db 344 -----TISKY----- 348

Qy 472 SAGDRVITITCKASQSVSNDAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTL 531

Db 349 ----- 348

Qy 532 TISSVQAEADAVYFCQDYNSPPTFGGTYKLEIKRADAAPTVPISFPSSSQTSGGASVV 591

Db 349 -----KGRPKAQVYTIPTPKQMAKDVSLT 375

Qy 592 CFLNNEFVKDINVKWKIDGSEKQNGVLNSWTDODSKDSTYSMSSTLTTLTXDEVERHNSYT 651

Db 376 CMITDFFPEDITVWQWNGQPAEN-YKNTQIPIMDT-DGSYFVYSKLVNQKSNWEAGNFTFI 433

Qy 652 CEATHKTSSTSP 662

Db 434 CSVLHSEFCRYP 444

RESULT 44

ABG76355

ID ABG76355 standard; protein; 613 AA.

XX

AC ABG76355;

XX

DT 23-OCT-2003 (revised)

DT 10-MAY-2003 (first entry)

XX

DE Mouse DAV-1 heavy chain-mature human SCF fusion protein.

XX Human; bifunctional molecule; antigen-binding portion; alpha integrin;

KW cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;

XX	PS	Example 10; SEQ ID NO 10; 269pp; English.	XX	Db	334	-----KGRPKAPQVYTIPTPPKQMAKDKVSLT	360
XX	CC	The invention describes a non-murine antibody (I) that competes with	XX	Qy	592	CFLNNFYPKDIINVKWIKIDGSEONGVLNSWTODSDKSTYSMSSTLTTLTDEYERHNSYT	651
XX	CC	monoclonal antibody RX1 for binding to macrophage colony stimulating	XX	Db	361	CMITDFPDDITVEMQWNGQPAEN-YKNTQPIMDT-DGSYFVYKLVNPKVQSNWEAGNTFT	418
XX	CC	factor (M-CSF) by more than 75%, where the monoclonal antibody RX1 has	XX	Qy	652	CEATHK 657	
XX	CC	the heavy chain and light chain amino acid sequences having a fully	XX	Db	419	CSVLRE 424	
XX	CC	defined 447 amino acids (SEQ ID No. 2) and 214 amino acids (SEQ ID No. 4)					
XX	CC	sequences given in the specification, respectively. (I) is useful for					
XX	CC	preventing a subject afflicted with a disease that causes or contributes					
XX	CC	to osteolysis, where the antibody effectively reduces the severity of					
XX	CC	bone loss associated with the disease. The disease is chosen from					
XX	CC	metabolic bone diseases associated with relatively increased osteoclast					
XX	CC	activity, including endocrinopathies, hypercalcemia, deficiency states,					
XX	CC	chronic diseases, and hereditary diseases, cancer, osteoporosis,					
XX	CC	osteopetrosis, inflammation of bone associated with arthritis and					
XX	CC	rheumatoid arthritis, periodontal disease, fibrous dysplasia, and/or					
XX	CC	Paget's disease. (I) is useful for preventing or treating metastatic					
XX	CC	cancer. Antibodies of the invention are useful for preventing or reducing					
XX	CC	bone loss; osteolysis; metastatic cancer to bone and cancer. (I) is					
XX	CC	useful for manufacturing a medicament for preventing or reducing bone					
XX	CC	loss in a patient exhibiting osteolysis, manufacturing a medicament for					
XX	CC	treating a patient afflicted with a disease that causes or contributes to					
XX	CC	osteolysis, and metastatic cancer to bone in a patient suffering from					
XX	CC	metastatic cancer, for manufacturing a medicament for treating a patient					
XX	CC	having cancer. (I) in synergistic combination, is useful for preparing a					
XX	CC	medicament for treating a patient exhibiting osteolysis. This is the					
XX	CC	amino acid sequence of macrophage colony stimulating factor (M-CSF)					
XX	CC	specific murine antibody 5H4 heavy chain.					
XX	Qy	Sequence 441 AA;					
XX	PS	Query Match					
XX	CC	Best Local Similarity 29.1%; Score 1023.5; DB 9; Length 441;					
XX	CC	Matches 249; Conservative 53; Mismatches 113; Indels 251; Gaps 15;					
XX	Qy	1 EVLOQSGDPLVKPGASVKISCKASGYSTFTGYMHVYKQSPGKLEWIGRINPNNGVTLY 60					
XX	Db	1 EIQLQSGDPLVKTGTSTKISCKASGYSTFTGYPMHWYKQSGKLEWIGYISCYNGDTNY 60					
XX	Qy	61 NQFKDKATLTVDKSTTAYMEIRSLTSDSAYYCARSTMTITNYMDYNGQSTSTVSS 120					
XX	Db	61 NONFKGATFTVDTSTSTAYMQNSTSDSAYYCARSTMTITNYMDYNGQSTSTVSS 117					
XX	Qy	121 AKTTTPSVPLAPGSAQAQNSMTLGLVKGYPEPVTVTWNSGSLSSGVHTPPAVLQSD 180					
XX	Db	118 AKTTTPSVPLAPGSAQAQNSMTLGLVKGYPEPVTVTWNSGSLSSGVHTPPAVLQSD 177					
XX	Qy	181 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRDGGPSEKSEINEKDLRKK 240					
XX	Db	178 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRDGGPSEKSEINEKDLRKK 220					
XX	Qy	241 SELQGTALGNLKIYYNYSKAITSSSEKADQFTNTLLPKGFTTGHFWYNDLLVDLGSTA 300					
XX	Db	221 CKPCICTVPEVSVSVFIPPPK-----PKDVLITL----- 249					
XX	Qy	301 ATSEYEGSSVDLYGAYYQCAGTGNKTAATGGVTLTDHNNRLTBEKKVPINLWIDGKQ 360					
XX	Db	250 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 274					
XX	Qy	361 TTVPIDKVTSSKEV-----TVQELDLQARHLYHGK-FGL-YNSDSFGKGVQORGLVFP 411					
XX	Db	275 -DVEVHTAQTPREEQFNSTFRSVSELPIMHODWLNKGEKFCRVNSAAFPAPTEK----- 328					
XX	Qy	412 HSEGSSTVSLDPAQOQYPTLLRIYRDNNTTSSLSLSLSLYTTSIVMTQFTSLLV 471					
XX	Db	329 -----TISKT----- 333					
XX	Qy	472 SAGDRVITTCASQSVSNDAVYQKPGQPKLLISYTSRYAGVDPFRSGSGYGTDFTL 531					
XX	Db	334 ----- 333					
XX	Qy	532 TISSVOAEDAANYFCQDYNSPPTFGGKTKLEIKRADAAPTYSIFPPPSQSLTSGGASVV 591					

XX	PS	Example 10; SEQ ID NO 10; 269pp; English.	XX	Db	334	-----KGRPKAPQVYTIPTPPKQMAKDKVSLT	360
XX	CC	The invention describes a non-murine antibody (I) that competes with	XX	Qy	592	CFLNNFYPKDIINVKWIKIDGSEONGVLNSWTODSDKSTYSMSSTLTTLTDEYERHNSYT	651
XX	CC	monoclonal antibody RX1 for binding to macrophage colony stimulating	XX	Db	361	CMITDFPDDITVEMQWNGQPAEN-YKNTQPIMDT-DGSYFVYKLVNPKVQSNWEAGNTFT	418
XX	CC	factor (M-CSF) by more than 75%, where the monoclonal antibody RX1 has	XX	Qy	652	CEATHK 657	
XX	CC	the heavy chain and light chain amino acid sequences having a fully	XX	Db	419	CSVLRE 424	
XX	CC	defined 447 amino acids (SEQ ID No. 2) and 214 amino acids (SEQ ID No. 4)					
XX	CC	sequences given in the specification, respectively. (I) is useful for					
XX	CC	preventing a subject afflicted with a disease that causes or contributes					
XX	CC	to osteolysis, where the antibody effectively reduces the severity of					
XX	CC	bone loss associated with the disease. The disease is chosen from					
XX	CC	metabolic bone diseases associated with relatively increased osteoclast					
XX	CC	activity, including endocrinopathies, hypercalcemia, deficiency states,					
XX	CC	chronic diseases, and hereditary diseases, cancer, osteoporosis,					
XX	CC	osteopetrosis, inflammation of bone associated with arthritis and					
XX	CC	rheumatoid arthritis, periodontal disease, fibrous dysplasia, and/or					
XX	CC	Paget's disease. (I) is useful for preventing or treating metastatic					
XX	CC	cancer. Antibodies of the invention are useful for preventing or reducing					
XX	CC	bone loss; osteolysis; metastatic cancer to bone and cancer. (I) is					
XX	CC	useful for manufacturing a medicament for preventing or reducing bone					
XX	CC	loss in a patient exhibiting osteolysis, manufacturing a medicament for					
XX	CC	treating a patient afflicted with a disease that causes or contributes to					
XX	CC	osteolysis, and metastatic cancer to bone in a patient suffering from					
XX	CC	metastatic cancer, for manufacturing a medicament for treating a patient					
XX	CC	having cancer. (I) in synergistic combination, is useful for preparing a					
XX	CC	medicament for treating a patient exhibiting osteolysis. This is the					
XX	CC	amino acid sequence of macrophage colony stimulating factor (M-CSF)					
XX	CC	specific murine antibody 5H4 heavy chain.					
XX	Qy	Sequence 441 AA;					
XX	PS	Query Match					
XX	CC	Best Local Similarity 29.1%; Score 1023.5; DB 9; Length 441;					
XX	CC	Matches 249; Conservative 53; Mismatches 113; Indels 251; Gaps 15;					
XX	Qy	1 EVLOQSGDPLVKPGASVKISCKASGYSTFTGYMHVYKQSPGKLEWIGRINPNNGVTLY 60					
XX	Db	1 EIQLQSGDPLVKTGTSTKISCKASGYSTFTGYPMHWYKQSGKLEWIGYISCYNGDTNY 60					
XX	Qy	61 NQFKDKATLTVDKSTTAYMEIRSLTSDSAYYCARSTMTITNYMDYNGQSTSTVSS 120					
XX	Db	61 NONFKGATFTVDTSTSTAYMQNSTSDSAYYCARSTMTITNYMDYNGQSTSTVSS 117					
XX	Qy	121 AKTTTPSVPLAPGSAQAQNSMTLGLVKGYPEPVTVTWNSGSLSSGVHTPPAVLQSD 180					
XX	Db	118 AKTTTPSVPLAPGSAQAQNSMTLGLVKGYPEPVTVTWNSGSLSSGVHTPPAVLQSD 177					
XX	Qy	181 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRDGGPSEKSEINEKDLRKK 240					
XX	Db	178 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRDGGPSEKSEINEKDLRKK 220					
XX	Qy	241 SELQGTALGNLKIYYNYSKAITSSSEKADQFTNTLLPKGFTTGHFWYNDLLVDLGSTA 300					
XX	Db	221 CKPCICTVPEVSVSVFIPPPK-----PKDVLITL----- 249					
XX	Qy	301 ATSEYEGSSVDLYGAYYQCAGTGNKTAATGGVTLTDHNNRLTBEKKVPINLWIDGKQ 360					
XX	Db	250 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 274					
XX	Qy	361 TTVPIDKVTSSKEV-----TVQELDLQARHLYHGK-FGL-YNSDSFGKGVQORGLVFP 411					
XX	Db	275 -DVEVHTAQTPREEQFNSTFRSVSELPIMHODWLNKGEKFCRVNSAAFPAPTEK----- 328					
XX	Qy	412 HSEGSSTVSLDPAQOQYPTLLRIYRDNNTTSSLSLSLSLYTTSIVMTQFTSLLV 471					
XX	Db	329 -----TISKT----- 333					
XX	Qy	472 SAGDRVITTCASQSVSNDAVYQKPGQPKLLISYTSRYAGVDPFRSGSGYGTDFTL 531					
XX	Db	334 ----- 333					
XX	Qy	532 TISSVOAEDAANYFCQDYNSPPTFGGKTKLEIKRADAAPTYSIFPPPSQSLTSGGASVV 591					

SQ	Sequence 456 AA;	
	Query Match 29.1%; Score 1023.5; DB 5; Length 456; Best Local Similarity 37.4%; Pred. No. 1.3e-52; Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;	
QY	1 EVOLQSGPDLVKPGASVKISKASGYSTGYMHVWKSPGKLEWIGRINPNNGVTLY 60	KW penton base monoclonal antibody.
DB	20 EVOLQSGPDLVKPGASVKISKASGYSTGYMHVWKSHGKSLWIGVIYPYKGGTY 79	XX Mus sp.
QY	61 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYYCARSTMTITNYVMDYWGQTSVTSS 120	XX US2002164333-A1.
DB	80 NQKFKSKATLTDDSSNTAYMELRSLTSDSAVYYCARG-----IAYWQGTLTVTSA 132	XX 07-NOV-2002.
QY	121 AKTTSPSVPLAPGSAQAQNSMTLGLVKGYPPPEPTVTWNSGSLSSGVHPTPAVLQSD 180	XX 10-JUL-2000; 2001US-00903327.
DB	133 AKTTSPSVPLAPGSAQAQNSMTLGLVKGYPPPEPTVTWNSGSLSSGVHPTPAVLQSD 192	XX 10-JUL-2000; 2000US-00613017.
QY	181 LYTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVDDKIIVPRDGGPSEKSEINEKDLRKK 240	XX 10-JUL-2000; 2000US-0325781P.
DB	193 LYTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVDDKIIVPRDCG----- 235	XX (SCRI) SCRIPPS RES INST.
QY	241 SELQGTALGNLQIYYNNSKAITSSSEKADQFLTNTLLFKGFTGHPWYNLLVDLGSTA 300	XX Nemerow GR, Li E;
DB	236 CKPCTVPEVSSVFIPPK-----PKDVLITL----- 264	XX WPI; 2002-171707/22.
QY	301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEKKVPINLWDGKQ 360	XX DR N-PSDB; ABX12744.
DB	265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV--- 289	XX New bifunctional molecules comprising an antibody or its antigen-binding portion, and a targeting agent, useful for e.g. gene therapy, or for promoting Adenoviral vector-mediated gene delivery to cells lacking av integrins.
QY	361 TTVPIDKVTSSKEV-----TVQELDLQARHYLHGK-FGL-YNDSDFGGKVQORGLIVF 411	XX Claim 10; Page 30-31; 49pp; English.
DB	290 -DVEVTAQTQPREEQFNSTFRSVSELPMHQDLNGKEFKCVNSAAPAPIEK----- 343	XX The present invention relates to a bifunctional molecule comprising an antibody or its antigen-binding portion, and a targeting agent. The antibody specifically binds to an antigen in a protein that binds to alpha integrin, and the targeting agent specifically binds to a cell surface protein that activates the phosphatidylinositol-3-OH kinase (PI3K) signalling pathway. The bifunctional molecules are useful for targeted gene therapy using targeting delivery vectors, such as adenoviral gene delivery particles. The bifunctional molecules are useful for treating viral infections, rheumatoid arthritis, cancers, cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic disorders, hyperproliferative disorders, and hormonal disorders. The present sequence represents mouse DAV-1 heavy chain, penton base monoclonal antibody
QY	412 HSSEGSTSVSYDLFDAQGVPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQTPTSLLV 471	XX SQ Sequence 456 AA;
DB	344 -----TISK----- 348	Query Match 29.1%; Score 1023.5; DB 5; Length 456; Best Local Similarity 37.4%; Pred. No. 1.3e-52; Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;
QY	472 SAGDRVTITCKASQSVNDVAVYQQPGQSKLLISYTSRYAGVDPDRSGSGYGTDFTL 531	QY 1 EVOLQSGPDLVKPGASVKISKASGYSTGYMHVWKSPGKLEWIGRINPNNGVTLY 60
DB	349 ----- 348	DB 20 EVOLQSGPDLVKPGASVKISKASGYTFTDYNMHVWKSHGKSLWIGVIYPYKGGTY 79
QY	532 TISSVQAEAAVYFCQDYNPPFTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVV 591	QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYYCARSTMTITNYVMDYWGQTSVTSS 120
DB	349 -----KGRPKAPQVYIIPPEQQAQKDVSLT 375	DB 80 NQKFKSKATLTDDSSNTAYMELRSLTSDSAVYYCARG-----IAYWQGTLTVTSA 132
QY	592 CFLNFPYKIDINVKWKIDGSRQGVNSWTDQSDKSTYSMSSTLTLTCKDEYERHNSYT 651	QY 121 AKTTSPSVPLAPGSAQAQNSMTLGLVKGYPPPEPTVTWNSGSLSSGVHPTPAVLQSD 180
DB	376 CMITDFPEDIIVQWQNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNOKSNWEAGNTFI 433	DB 133 AKTTSPSVPLAPGSAQAQNSMTLGLVKGYPPPEPTVTWNSGSLSSGVHPTPAVLQSD 192
QY	652 CEATHK 657	QY 181 LYTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVDDKIIVPRDGGPSEKSEINEKDLRKK 240
DB	434 CSVLHE 439	DB 193 LYTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVDDKIIVPRDCG----- 235
RESULT 47		QY 241 SELQGTALGNLQIYYNNSKAITSSSEKADQFLTNTLLFKGFTGHPWYNLLVDLGSTA 300
ABG76345		DB 236 CKPCTVPEVSSVFIPPK-----PKDVLITL----- 264
ID ABG76345	standard; protein; 456 AA.	QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEKKVPINLWDGKQ 360
XX		DB 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV--- 289
AC	ABG76345;	QY 361 TTVPIDKVTSSKEV-----TVQELDLQARHYLHGK-FGL-YNDSDFGGKVQORGLIVF 411
CC		DB 290 -DVEVTAQTQPREEQFNSTFRSVSELPMHQDLNGKEFKCVNSAAPAPIEK----- 343
DT	10-MAY-2003 (first entry)	QY 412 HSSEGSTSVSYDLFDAQGVPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQTPTSLLV 471
DE	Mouse DAV-1 heavy chain monoclonal antibody.	DB 344 -----TISK----- 348
XX		QY 472 SAGDRVTITCKASQSVNDVAVYQQPGQSKLLISYTSRYAGVDPDRSGSGYGTDFTL 531
KW	Mouse; bifunctional molecule; antigen-binding portion; alpha integrin;	DB 349 ----- 348
KW	cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;	QY 532 TISSVQAEAAVYFCQDYNPPFTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVV 591
KW	signalling pathway; targeted gene therapy; delivery vector;	DB 349 -----KGRPKAPQVYIIPPEQQAQKDVSLT 375
KW	adenoviral gene delivery particle; viral infection; cancer;	QY 592 CFLNFPYKIDINVKWKIDGSRQGVNSWTDQSDKSTYSMSSTLTLTCKDEYERHNSYT 651
KW	rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;	DB 376 CMITDFPEDIIVQWQNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNOKSNWEAGNTFI 433
KW	restenosis; ophthalmic disorder; hyperproliferative disorder;	QY 652 CEATHK 657
KW	hormonal disorder; virucide; antiinflammatory; antirheumatic;	DB 434 CSVLHE 439
KW	antiarthritic; ophthalmologic; DAV-1 heavy chain;	

Db 290 -DVEVHTAQTPREQFNSTFRSVSELPIMHQDLNGKEFKCRVNGAAPPAPIEK----- 343
 QY 412 HSSEGSTSVSYDLFDAQOGYPTLLRIYRDNTTISSTLSLSLYLTTTSIVMTQPTSLIV 471
 Db 344 -----TISKT----- 348
 QY 472 SAGDRVITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
 Db 349 ----- 348
 QY 532 TISSVQAEADAANVFCQDQYNSPPTFGGGTKLEIKRADAAPTIVFPPSSBQLTGGASVV 591
 Db 349 -----KGRPKAPQVYTIPTPPKEQMAKDKVSLT 375
 QY 592 CFLNNEYPKIDINVKWKIDGSRQNGVLNSWTDQSKDSTYSMSSTLTLTDEYERHNSYT 651
 Db 376 CMITDFPEDIITVEWQNGQPAEN-YKNTQPIMDT-DGSYFVYKLVNQSKNWEAGNFTI 433
 QY 652 CEATHK 657
 Db 434 CSVLHE 439
 RESULT 48
 AEB96754
 ID AEB96754 standard; protein; 456 AA.
 AC AEB96754;
 DT 20-OCT-2005 (first entry)
 DX DAV-1 antibody heavy chain.
 DE Gene therapy; cancer; vascular disease; diabetic retinopathy; restenosis;
 KW ocular disease; hyperproliferation; hormone metabolism disorder;
 KW cytostatic; vasotropic; antidiabetic; ophthalmological; metabolic-gen.;
 KW DAV-1; heavy chain; antibody.
 OS Synthetic.
 OS WO2005075506-A1.
 PN 18-AUG-2005.
 PD 29-DEC-2004; 2004WO-1B004324.
 PF 09-JAN-2004; 2004US-0535199P.
 PR (SCRI) SCRIPPS RES INST.
 PA Nemerow GR, Li E;
 PI WPI; 2005-555928/56.
 DR New modified adenovirus fiber protein comprising a fiber shaft and a
 PT modified knob, useful for treating cancer, vascular disorders, diabetic
 PT retinopathies, restenosis and vascular, ophthalmic, hyperproliferative or
 PT hormonal disorders.
 XX Example 1; SEQ ID NO 28; 250pp; English.
 XX The invention relates to a modified adenovirus fiber protein comprising a
 CC fiber shaft that contains a sufficient number of shaft repeats to permit
 CC trimerization in the absence of a fiber knob or in the absence of an
 CC extrinsic trimerization domain, and optionally a modified knob, where, if
 CC the knob is included, it is modified to remove or disable the
 CC trimerization domain of the knob. The invention also relates to a
 CC modified adenovirus fiber protein comprising a modified knob, where the
 CC modification of the knob removes or disables a trimerization domain of
 CC the knob, and the modified fiber trimerizes a nucleic acid molecule
 CC comprising a sequence of nucleotides that encodes the modified adenovirus
 CC fiber protein, a cell comprising the nucleic acid, an adenovirus particle
 CC comprising the modified fiber, a composition formulated for

CC administration to a subject, comprising the adenovirus particle,
 CC detargeting an adenoviral vector particle comprising producing the
 CC adenoviral particle, where the binding of the particle to a native
 CC receptor is reduced or eliminated as compared to binding of a particle
 CC containing the unmodified fiber, introducing the adenoviral particle into
 CC cells, introducing the cells into a subject and administering the
 CC composition to the subject. The modified adenovirus fiber protein is
 CC useful for treating cancer, vascular disease, diabetic retinopathy,
 CC restenosis, ocular diseases, hyperproliferative disorders and hormonal
 CC disorders. This sequence represents a DAV-1 antibody heavy chain used in
 CC the scope of the invention.
 XX
 SQ Sequence 456 AA;
 Query Match 29.1%; Score 1023.5; DB 9; Length 456;
 Best Local Similarity 37.4%; Pred. No. 1.3e-52;
 Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;
 QY 1 EVLOQSGDPLVKPGASVKISKASGYSTFGYGMHWKQSPGKLEWIGRINPNNGVTLY 60
 Db 20 EVLOQSGDPLVKPGASVKISKASGYSTFGYGMHWKQSPGKLEWIGRINPNNGVTLY 79
 QY 61 NOKFKDKATLTVDKSSSTAYMELRSITSEDSAVYYCARSTMTITNYVMDYMGQGSTVTSVS 120
 Db 80 NOKFKSKATLTDDSSNTAYMELRSITSDASAVYICARG-----IAYMGQGTLTVTVA 132
 QY 121 AKTTPPSVYPLAPGSAQTNSMVTGLCLVKGYPEPPTVTWNSGSLSSGVTHTPAVLQSD 180
 Db 133 AKTTPPSVYPLAPGSAQTNSMVTGLCLVKGYPEPPTVTWNSGSLSSGVTHTPAVLQSD 192
 QY 181 LYTLSSTVTPSPSTWSPSETVTCNVAHPASSTKVKKIIPRDSGPGSEKSEINEKDLRKK 240
 Db 193 LYTLSSTVTPSPSTWSPSETVTCNVAHPASSTKVKKIIPRDSGPGSEKSEINEKDLRKK 235
 QY 241 SELQGTALGNLQIYYVYNSKAITSSSEKADQFLNTLLFKGPTGHPWYNLLVDLGSTA 300
 Db 236 CKPCICTVPEVSSVFIPPK-----PKDVLITL----- 264
 QY 301 ATSEYEGSSVDLYGAYYGYQCAGGTENKTCACMYGGVTLHNNRLTBEEKVPIINLWIDGKQ 360
 Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSMFVD--- 289
 QY 361 TTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVGQGLIVF 411
 Db 290 -DVEVHTAQTPREQFNSTFRSVSELPIMHQDLNGKEFKCRVNGAAPPAPIEK----- 343
 QY 412 HSSEGSTSVSYDLFDAQOGYPTLLRIYRDNTTISSTLSLSLYLTTTSIVMTQPTSLIV 471
 Db 344 -----TISKT----- 348
 QY 472 SAGDRVITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
 Db 349 ----- 348
 QY 532 TISSVQAEADAANVFCQDQYNSPPTFGGGTKLEIKRADAAPTIVFPPSSBQLTGGASVV 591
 Db 349 -----KGRPKAPQVYTIPTPPKEQMAKDKVSLT 375
 QY 592 CFLNNEYPKIDINVKWKIDGSRQNGVLNSWTDQSKDSTYSMSSTLTLTDEYERHNSYT 651
 Db 376 CMITDFPEDIITVEWQNGQPAEN-YKNTQPIMDT-DGSYFVYKLVNQSKNWEAGNFTI 433
 QY 652 CEATHK 657
 Db 434 CSVLHE 439
 RESULT 49
 AAE18379
 ID AAE18379 standard; protein; 493 AA.
 XX
 AC AAE18379;
 XX

CC present sequence is human N-terminal DAV-1 heavy chain-mature inaeulin
CC growth factor-1 (IGF-1) fusion protein which is used in the invention
XX
SQ Sequence 510 AA;

Query Match 29.1%; Score 1023.5; DB 5; Length 510;
Best Local Similarity 37.4%; Pred. No. 1.5e-52;
Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;

QY 1 EVQLQSGDPLVKPGASVKISKASGYFTGYMHVVKSPGKLEWIGRIINPNNGVTLV 60
Db EVQLQSGPELVKPGASVKISKASGYFTDYNMHVVKSHGKSLWIGVYIPYKGGTGY 79

QY 61 NQKFKDKATLVVDKSTTAYMELRSLTSDSAVYYCARSTMTINYMDYWGQSTVTVSS 120
Db NQKFKSKATLTDTSSNTAYMELRSLTSDSAVYYCARG-----IAYWGQSTLVTVSA 132

QY 121 AKTTTPSVVPLAPGSAQTNSMTVTLGCLVKGYPPEPTVTWNSGSLSSGVHTFPVQLQSD 180
Db AKTTTPSVVPLAPGSAQTNSMTVTLGCLVKGYPPEPTVTWNSGSLSSGVHTFPVQLQSD 192

QY 181 LYTLSSTVTPSPSTWPSSETVTCNVAHPASSTKVDDKIIVPRDGGPSEKSEINEKDLRKK 240
Db LYTLSSTVTPSPSTWPSSETVTCNVAHPASSTKVDDKIIVPRDCG-----235

QY 241 SELOQTALGNLKIYYNYSKAITSSSEKSDAQFLNTLLFKGPTGHPWYNDLLVLGSTA 300
Db CKPCICTVPEVSSVFIFFPK-----PKDVLITL-----264

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db TP-KVTCVVVDIS-----KODPEQSWFVD---289

QY 361 TTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQGLIYF 411
Db DVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAPIEK-----343

QY 412 HSEGSTVSYDLFDAQQGVPTDLLRIYRDNVTISSTLSLSLYLYTTSIVMTQTFPSLLV 471
Db TISKT-----348

QY 472 SAGDRVITTKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
Db 349 -----348

QY 532 TISSVQAEADAAYFCQDYNPPTFGGKTLEIKRADAAPTVISIPPPSEQLTSGGASVV 591
Db 349 -----KGRPKAPQVVTIIPPKEQWAKDKVSLT 375

QY 592 CFLNPNPKDINVKWIDGSRONGVLNSWTDQSDKDYTSMSSTLTTLTKDEYERHNSYT 651
Db 376 CMITDFPEDITVEMQWQPAEN-YKNTQPIMDT-DGSFYFVYSKLVNQSNWEAGNTFI 433

QY 652 CEATHK 657
Db 434 CSVLHE 439

RESULT 52
ABG76353
ID ABG76353 standard; protein; 510 AA.
XX
AC ABG76353;
XX
DT 23-OCT-2003 (revised)
DT 10-MAY-2003 (first entry)
DE Mouse DAV-1 heavy chain-mature human IGF-1 fusion protein.
XX
KW Human; bifunctional molecule; antigen-binding portion; alpha integrin;
KW cell surface protein; phosphatidylinositol-3-OH kinase; p13K;
KW signalling pathway; targeted gene therapy; delivery vector;
KW adenoviral gene delivery particle; viral infection; cancer;

KW rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;
KW restenosis; ophthalmic disorder; hyperproliferative disorder;
KW hormonal disorder; virucide; antiinflammatory; antirheumatic;
KW antiarthritic; ophthalmological; DAV-1 antibody heavy chain; IGF-1;
KW insulin-like growth factor-1; mouse.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX US2002164333-A1.
XX 07-NOV-2002.
XX 10-JUL-2001; 2001US-00903327.
XX 10-JUL-2000; 2000US-00613017.
PR 10-JUL-2000; 2000US-0325781P.
XX (SCRI) SCRIPPS RES INST.
PA
XX
PI Nemerow GR, Li E;
XX WPI; 2002-171707/22.
XX
XX New bifunctional molecules comprising an antibody or its antigen-binding portion, and a targeting agent, useful for e.g. gene therapy, or for promoting Adenoviral vector-mediated gene delivery to cells lacking av integrins.
XX
XX Example 2; Page 39-41; 49pp; English.
XX
CC The present invention relates to a bifunctional molecule comprising an antibody or its antigen-binding portion, and a targeting agent. The antibody specifically binds to an antigen in a protein that binds to alpha integrin, and the targeting agent specifically binds to a cell surface protein that activates the phosphatidylinositol-3-OH kinase (PI3K) signalling pathway. The bifunctional molecules are useful for targeted gene therapy using targeting delivery vectors, such as adenoviral gene delivery particles. The bifunctional molecules are useful for treating viral infections, rheumatoid arthritis, cancers, cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic disorders, hyperproliferative disorders, and hormonal disorders. The present sequence represents a fusion protein with mouse DAV-1 antibody heavy chain. (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 510 AA;

Query Match 29.1%; Score 1023.5; DB 5; Length 510;
Best Local Similarity 37.4%; Pred. No. 1.5e-52;
Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;

QY 1 EVQLQSGDPLVKPGASVKISKASGYFTGYMHVVKSPGKLEWIGRIINPNNGVTLV 60
Db EVQLQSGPELVKPGASVKISKASGYFTDYNMHVVKSHGKSLWIGVYIPYKGGTGY 79

QY 61 NQKFKDKATLVVDKSTTAYMELRSLTSDSAVYYCARSTMTINYMDYWGQSTVTVSS 120
Db NQKFKSKATLTDTSSNTAYMELRSLTSDSAVYYCARG-----IAYWGQSTLVTVSA 132

QY 121 AKTTTPSVVPLAPGSAQTNSMTVTLGCLVKGYPPEPTVTWNSGSLSSGVHTFPVQLQSD 180
Db AKTTTPSVVPLAPGSAQTNSMTVTLGCLVKGYPPEPTVTWNSGSLSSGVHTFPVQLQSD 192

QY 181 LYTLSSTVTPSPSTWPSSETVTCNVAHPASSTKVDDKIIVPRDGGPSEKSEINEKDLRKK 240
Db LYTLSSTVTPSPSTWPSSETVTCNVAHPASSTKVDDKIIVPRDCG-----235

QY 241 SELOQTALGNLKIYYNYSKAITSSSEKSDAQFLNTLLFKGPTGHPWYNDLLVLGSTA 300
Db CKPCICTVPEVSSVFIFFPK-----PKDVLITL-----264

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
SQ

Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289
Qy 361 TTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNDSDFGGKVORGLIVF 411
Db 290 -DVEVHTAQTPREQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPAPIEK----- 343
Qy 412 HSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTTSIVMTQPTSLLV 471
Db 344 -----TISK----- 348
Qy 472 SAGDRVITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
Db 349 ----- 348
Qy 532 TISSVOAEDAAVYFCQDYNPPTFGGKLEIKRADAAPTIVSIFPPSSEQLTSGGASVV 591
Db 349 -----KGRPKAPQVYTIPPPKEQMAKDKVSLT 375
Qy 592 CFLNNFPYKIDINVKWIKDGSERQGVNSWTDQSDKSTYSMSSTLTLTKDEYERHNSYT 651
Db 376 CMITDFPEDITVEMQWQPAEN-YKNTQPIMDT-DGSYFVYVKLVNOKSNWEAGNTFI 433
Qy 652 CEATHK 657
Db 434 CSVLHE 439
RESULT 53
AAE18372
ID AAE18372 standard; protein; 438 AA.
AC AAE18372;
DT 07-MAY-2002 (first entry)
DE Human penton base monoclonal antibody, DAV-1 heavy chain fragment.
KW Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;
KW cytostatic; vasotropic; ophthalmological.
OS Homo sapiens.
XX WO200204522-A2.
XX 17-JAN-2002.
XX 09-JUL-2001; 2001WO-EP007878.
XX 10-JUL-2000; 2000US-00613017.
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX (SCRI) SCRIPPS RES INST.
XX Nemerow GR, Li E;
XX WPI; 2002-171707/22.
XX N-PSDB; AAE18372.
XX New bifunctional molecules comprising an antibody or its antigen-binding
XX portion, and a targeting agent, useful for e.g. gene therapy, or for
XX promoting adenoviral vector-mediated gene delivery to cells lacking av
XX integrins.
XX Claim 10; Page 96; 106pp; English.
XX The present invention relates to a bifunctional molecule comprising an
XX antibody or its antigen-binding portion, and a targeting agent where the
XX antibody specifically binds to an antigen in a protein that binds to av
XX integrin, and the targeting agent specifically binds to a cell surface

CC protein that activates the phosphatidylinositol 3 (PI3K) signalling
CC pathway. The bifunctional molecules are useful for gene therapy, for
CC promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking
CC av integrins, for enhancing Ad binding and internalisation, and in gene
CC delivery of by fibreless adenovirus particles. The bifunctional molecules
CC permit targeting of viral and bacterial vectors to cells that express
CC targeted receptors. Diseases that can be targeted include cancers,
CC vascular disorders, diabetic retinopathies, restenosis, ophthalmic
CC disorders, hyperproliferative disorders, and hormonal disorders. The
CC present sequence is human penton base monoclonal antibody, DAV-1 heavy
CC chain fragment
XX
SQ Sequence 438 AA;
Query Match 29.0%; Score 1022.5; DB 5; Length 438;
Best Local Similarity 37.4%; Pred. No. 1.4e-52;
Matches 249; Conservative 50; Mismatches 111; Indels 255; Gaps 14;
Qy 1 EVLOQSGDPLVKPGASVKISKASGYSTGYMHVVKSPGKLEWIGRINPNNGVTLY 60
Db 20 EVLOQSGDPLVKPGASVKISKASGYSTGYMHVVKSPGKLEWIGRINPNNGVTLY 79
Qy 61 NQKFKDKATLTVDKSTTAYMELSLTSEDSAVVYCARSTMITNYMDYMGQSTSVTVSS 120
Db 80 NQKFKDKATLTVDKSTTAYMELSLTSEDSAVVYCARSTMITNYMDYMGQSTSVTVSS 132
Qy 121 AKTTPSPVYPLAPGSAATNSMVTGLCLVKGYFPEPTVTWNSGSLSSGVHTTFAVLQSD 180
Db 133 AKTTPSPVYPLAPGSAATNSMVTGLCLVKGYFPEPTVTWNSGSLSSGVHTTFAVLQSD 192
Qy 181 LYTLSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKK 240
Db 193 LYTLSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKK 235
Qy 241 SELQGTALGNLQIYYVNSKAITSESEKADQELTLLFKGPTTGHVWYNDLLVDLGSTA 300
Db 236 CRPKICTVPEVSSVFIFPPK-----PKDVLITL----- 264
Qy 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMGVGTLHNNRLTBEKKVPINLWDGKQ 360
Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289
Qy 361 TTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNDSDFGGKVORGLIVF 411
Db 290 -DVEVHTAQTPREQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPAPIEK----- 343
Qy 412 HSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTTSIVMTQPTSLLV 471
Db 344 -----TISK----- 348
Qy 472 SAGDRVITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
Db 349 ----- 348
Qy 532 TISSVOAEDAAVYFCQDYNPPTFGGKLEIKRADAAPTIVSIFPPSSEQLTSGGASVV 591
Db 349 -----KGRPKAPQVYTIPPPKEQMAKDKVSLT 375
Qy 592 CFLNNFPYKIDINVKWIKDGSERQGVNSWTDQSDKSTYSMSSTLTLTKDEYERHNSYT 651
Db 376 CMITDFPEDITVEMQWQPAEN-YKNTQPIMDT-DGSYFVYVKLVNOKSNWEAGNTFI 433
Qy 652 CEATHK 656
Db 434 CSVLH 438
RESULT 54
ABG76347
ID ABG76347 standard; protein; 438 AA.
XX
AC ABG76347;
XX

Db 301 STYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDE 360
 QY 272 FITN-----TLLFKGFTGHPWYNDLLVLDGSTR-ATSEYEGSS--VDLYGAYVGYQCAGG 324
 Db 361 LTKNQVSLTCLVKGFYP-----SDIAVEWESNGPENNYKTTTPVLDSDGSFPLYSKL-- 413
 QY 325 TNKTKACMYGGV---TLHD--NNRLTEEK-----KVPINLWIDGKQTTVP 364
 Db 414 TVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGCGGGGGGGGQVQLVQSGAEVKKP 473
 QY 365 IDKVKTSKLE-----EVTQELDLQARHYLHGKFLGYNLSDSFSGKVGORGLI 409
 Db 474 GSSVKVSCRAGVFTFYVYLHWVRQPGCGLEWGMWGIYPCNVHAQYN-EKFKGRV----- 527
 QY 410 VFHSSEGSTVVDLFDQAQGYPTLRIYRDNTTISSTLSLSLYL-----TT----- 458
 Db 528 -----TITADKSTAYMELSLR--SEDTAVVYCARSWEGFFYWGQGTITVTVSSGG 577
 QY 459 -----SIVMTQPTSLVLSAGDRVTITCKASQSVNDVAVYQCKPGQSPKLL 505
 Db 578 GSGGGGGGGGSDIQMTQSPSLASVGDVRVTITCKASQVGINVAVYQCKPGKAPKSL 637
 QY 506 ISYTSRYAGVPRFSGSGYGTDTLTITISVQAEADAAYFCQDYNPSPTFGGQTKLEIK 565
 Db 638 ISSASYRSGVPRFSGSGYGTDTLTITISLQPEDFATYFCQYDYPTFGGQTKVEIK 697

RESULT 57
 AAY39452
 ID AAY39452 standard; protein; 206 AA.
 XX
 AC AAY39452;
 XX
 DT 19-NOV-1999 (first entry)
 XX
 DE Antibody ABX-CBL light chain sequence.
 XX
 KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
 KW organ transplant rejection disease; lymphoma; pancreatic disease;
 KW autoimmune disease; inflammatory disease; arthritis; binding site.
 XX
 OS Homo sapiens.
 XX
 PN WO9945031-A2.
 XX
 PD 10-SEP-1999.
 XX
 PF 03-MAR-1999; 99NO-US0004583.
 XX
 PR 03-MAR-1998; 98US-00034607.
 PR 03-FEB-1999; 99US-00244253.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
 XX
 DR WPI; 1999-540816/45.
 XX
 PT New monoclonal antibody, used for treating e.g. graft versus host
 PT disease, cancers, autoimmune diseases and inflammatory diseases.
 XX
 PS Disclosure; Page 58; 245pp; English.
 XX
 CC This sequence represents the light chain of the antibody ABX-CXL. The
 CC invention relates to a monoclonal antibody (MAB) with an isotype that
 CC fixes complement and a variable region that binds to the epitope on CD147
 CC bound by the IgM MAB ABX-CBL, providing that the antibody is not CBL1.
 CC The MAB can selectively kill activated T-cells, activated B-cells or
 CC resting or activated monocytes. The products and methods can be used for
 CC treating diseases involving activated T-cells or B-cells or monocytes,
 CC e.g. graft versus host disease (GVHD), organ transplant rejection

CC diseases (e.g. renal transplant, ocular transplant), cancers (e.g.
 CC cancers of the blood (e.g. leukaemia's and lymphomas) and pancreatic),
 CC autoimmune diseases (e.g. lupus), and inflammatory diseases (e.g.
 CC arthritis)
 XX
 SQ Sequence 206 AA;
 Query Match 28.9%; Score 1018; DB 2; Length 206;
 Best Local Similarity 95.1%; Pred. No. 1.1e-52; Indels 0; Gaps 0;
 Matches 193; Conservative 4; Mismatches 6;
 QY 469 LLVSAGDRVTITCKASQSVNDVAVYQCKPGQSPKLLISYTSRYAGVPRFSGSGYGT 528
 Db 3 LLVSAGDRVTITCKASQSVNDVAVYQCKPGQSPKLLIYASNRYTGVDRFTGSGYGT 62
 QY 529 FTLTISVQAEADAAYFCQDYNPSPTFGGQTKLEIKRADAAPTIVSIFPPSSQLTSGGA 588
 Db 63 FTLTISVQAEADLAVYFCQDYSSPYTFGGQTKLEIKRADAAPTIVSIFPPSSQLTSGGA 122
 QY 589 SVVCFLNFPYKIDINVVKWIKDGSERQNGVLNSWTDQSKDSTYSMSSTLTLTCKDEYERHN 648
 Db 123 SVVCFLNFPYKIDINVVKWIKDGSERQNGVLNSWTDQSKDSTYSMSSTLTLTCKDEYERHN 182
 QY 649 SYTCEATHKTSPIVKSFNRNE 671
 Db 183 SYTCEATHKTSPIVKSFNRNE 205
 RESULT 58
 AAR66758
 ID AAR66758 standard; protein; 465 AA.
 XX
 AC AAR66758;
 XX
 DT 01-SEP-1995 (first entry)
 XX
 DE Anti-tobacco mosaic virus monoclonal Ab heavy chain.
 XX
 KW Tobacco mosaic virus; TMV; monoclonal antibody; heavy chain;
 KW virus-resistant plants; biofarming.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Peptide /label= leader
 FT Peptide 20..465
 FT Domain /label= mat_peptide
 FT Domain 20..128
 FT Domain /note= "variable heavy domain"
 FT Domain 129..141
 FT Domain /note= "J heavy 4 domain"
 FT Domain 142..465
 FT Domain /note= "constant heavy domain"
 XX
 PN JP06319396-A.
 XX
 PD 22-NOV-1994.
 XX
 PF 07-MAY-1993; 93JP-00131208.
 XX
 PR 07-MAY-1993; 93JP-00131208.
 XX
 PA (NISB) JAPAN TOBACCO INC.
 PA (KURS) KURARAY CO LTD.
 XX
 DR WPI; 1995-040220/06.
 DR N-PSDB; AAQ79930.
 XX
 PT Transformed plant producing animal-derived anti-virus antibody - esp.
 PT tobacco plants producing anti-tobacco mosaic virus monoclonal antibody.
 XX
 PS Example 2; Page 14-15; 26pp; Japanese.

Db	355	-----KGRPKAPQVYTIPTPKQWAKDKVSL	380
QY	591	VFPLNNFYPKDINVKWIKDSEQRQGVLSWTDQSDKSTYSMSSTLTUTKDEYERHSY	650
Db	381	TCMITDFPDDITVEWQWQPAEN-YKNTQPIMDT-DGSYFYVSKLVNQSNWEAGNTF	438
QY	651	TCEATHK	657
Db	439	TCSVLHE	445
RESULT 60			
ID	ADQ07409	standard; protein; 701 AA.	
XX	AC	ADQ07409;	
XX	DT	07-OCT-2004 (first entry)	
DE	hCBE11	monospecific-1 antibody construct mature heavy chain.	
XX	XX	tumour volume; lymphotoxin-beta receptor; LT-beta-R; agonist; antibody; chemotherapeutic; supra-additive; inhibition; cytostatic; gene therapy; cancer; mature heavy chain; hCBE11 monospecific-1.	
KW	OS	Homo sapiens.	
OS	OS	Synthetic.	
XX	PN	WO2004058183-A2.	
PN	PD	15-JUL-2004.	
XX	XX	22-DEC-2003; 2003WO-US041243.	
PF	XX	20-DEC-2002; 2002US-0435185P.	
PR	XX	(BIOG-) BIOGEN IDEC MA INC.	
PA	XX	Lepage D, Gill A;	
PI	XX	WPI; 2004-525785/50.	
DR	DR	N-PSDB; ADQ07408.	
XX	XX	Inhibiting tumor volume comprising administering an amount of a lymphotoxin-beta receptor agonist or antibody and a chemotherapeutic agent (e.g. gemcitabine or adriamycin).	
PT	PT	Disclosure; SEQ ID NO 8; 161pp; English.	
XX	XX	The invention relates to a novel method for inhibiting tumour volume. The method comprises administering an amount of a lymphotoxin-beta receptor (LT-beta-R) agonist or antibody and an amount of at least one chemotherapeutic agent, where the administration of the LT-beta-R agonist or antibody and the chemotherapeutic agent results in supra-additive inhibition of the tumour. The invention further relates to a pharmaceutical composition comprising an amount of an LT-beta-R agonist and at least one chemotherapeutic agent, and a pharmaceutical carrier, which upon administration to a subject results in supra-additive inhibition of a tumour. The lymphotoxin-beta receptor agents have cytostatic activity. Gene therapy may be used in the tumour inhibition method. The method is useful for inhibiting tumour volume or for treating cancer. The lymphotoxin-beta receptor agonist and the chemotherapeutic agent are useful for preparing a medicament for the treatment of cancer, which upon administration to a subject results in supra-additive inhibition of a tumour. This sequence represents the mature heavy chain of the hCBE11 monospecific-1 antibody construct for use in the tumour volume inhibition method of the invention.	
CC	CC	Sequence 701 AA;	
Query Watch	28.6%;	Score 1006;	DB 8; Length 701;
Best Local Similarity	34.9%;	Pred. No. 2.4e-51;	
Matches	256;	Conservative 94; Mismatches 183;	Indels 200; Gaps 21;

QY	1	EVQLQSGPDLVKGASVKISKASGYFTGYMHWVKOSPGKLEWIGRINPNNGVTLY	60
Db	1	EVQLVESGGGLVKPGGSLRLSCAASGFTSDYIMWFROAPGRGLEWVATISDGGSYTY	60
QY	61	NQFKDKATLTVDKSTTAYMELRLSITSDSAVYICARSTMITNYVMDYWGQTSYTVSS	120
Db	61	PDSVKGRFTISRDNAKNSLYLQWSSLRAEDTAVYICAREENGNYFYFDYWGQTTTVSS	120
QY	121	AKTTPPSVYPLAPGAAQNSMWTGLCLVKGFPEPPTVTVWNSGSLSSGVHFPVAVLQSD	180
Db	121	ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDFPEPPTVTVWNSGALTSGVHTFPVAVLQSS	180
QY	181	-LYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKKIVPRDS-----GG	224
Db	181	GLYSLSVVTVPSSSLGTQYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPCPAPPELLGG	240
QY	225	PS-----EKSEEI-----NEKLRKKSEIQGTALGNLK---QIYYYN	258
Db	241	PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	300
QY	259	S-----KATTSSE-----KSADQ	271
Db	301	STYRVSVLTVLHQDLNGKEYCKVSKNKKALPAPIETKISKAKGQPREPQVYTLPPSRDE	360
QY	272	FLTN-----TLLPKGFTGHPWYNDLLVDLGSTA-ATSEYEGSS--VDLYGAYYVQCAGG	324
Db	361	LTQNQVSLTCLVKGYF-----SDIAVESNGQPENNYKTPPVLDSDGSFELYSKL--	413
QY	325	TPNKTACMYGGV---TLHD--NNRLTEEK-----KVPINLWIDGKQTTVP	364
Db	414	TVDKSRWQGNVFCVSMHEALHNHYTKLSLSPGGGGGGGGSEVQLVESGGGLVKP	473
QY	365	IDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDFGGKVQRGL-IVFHSSEGSTVSYDL	423
Db	474	GGSLR-----LSCAASGFTFDYMYWFRQAPGK---GLEWVATISDGGSYTY--	518
QY	424	FDAQGYPTDLLRIYRDNNTTISSTLSLSLYLVTTS-----	459
Db	519	-----YDPSV---KGRFTISRDNKNSLYLQWSSLRAEDTAVYICAREENGNYFYFDY	568
QY	460	-----IVMTQTPTSLVLSAGDRVTITCKASQSVSNDA	492
Db	569	WQGGTTVTTVSSGGGGGGGGSDIQMTQSPSSLSASVGRVTITCKAGODIKSYLS	628
QY	493	WYQKPGQSPKLLISYTSRYAGVDRPSGSGYGTDTLTITSSVQAEADAIVFCQDQYNS	552
Db	629	WYQKPGKAPKLLIYYATRLADGVPSRFSFGSGGSDYTLTITSLQPEDFATYYCLOGHES	688
QY	553	PPTFGGGTKLEIK	565
Db	689	PWTFGGGTKLEIK	701
RESULT 61			
ID	ADQ12186	standard; protein; 701 AA.	
XX	AC	ADQ12186;	
XX	DT	07-OCT-2004 (first entry)	
DE	hCBE11	monospecific-1 antibody.	
XX	XX	lymphotoxin-beta receptor; LT-abgr-R; Cytostatic; cancer; tumour; hCBE11; huBHA10.	
KW	OS	Homo sapiens.	
OS	XX	WO2004058191-A2.	
PN	XX	15-JUL-2004.	

QY 1 EVOLQSGDPLVKPGASVKISKASGYSTGYVHMVVKSPGKGLWIGRINPNNGVTLY 60
DB 21 EVOLQSGGAALMRPGSVVKISKSGSGYTTDTYTMHVKQSHAKSLEWIGLITFFYGDALY 80
QY 61 NOKFKDKATLTVDKSTTAYMELRLSTSDSAVYICARSTMITNYVMDYWGQGTSTVVS 120
DB 81 NOKFKDKATLTVDKSSSTAYMELARLTSDSAIYYCTRGRLRGPFPAYWGQGTLTVISA 140
QY 121 AKTTPSPVPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVMNSGSLSSGVHFFPAVLQSD 180
DB 141 AKTTPSPVPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVMNSGSLSSGVHFFPAVLQSD 200
QY 181 LYTLLSSVTPSPSTWSPSETVTCNVAHPASSTKVKKIVPRDGGPSEKSENEKDLRKK 240
DB 201 LYTLLSSVTPSPSTWSPSETVTCNVAHPASSTKVKKIVPRDCG----- 243
QY 241 SELQGTALGNLQIYYVYNSKAITSEKSAQDLTNTLLFKGPTGHPWYNLLVLDLGSTA 300
DB 244 CKPCICTVPEVSSVFPPK-----PKDVLITL----- 272
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTBEKKVPLNLMWDGKQ 360
DB 273 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD-- 297
QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQRCGLIYF 411
DB 298 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPAPIEK----- 351
QY 412 HSSEGSTVSYDLFDAQGQVPTLLRIYRDNNTTISSTLSLSISLYLYTTSIVMTQTPTSLIV 471
DB 352 -----TISK----- 356
QY 472 SAGDRVITITCKASQSVSNDAVYQKPGQSKLLISYTSRYAGVDRFSGSGYGTDFTL 531
DB 357 ----- 356
QY 532 TISSVQAEADAANYFCQDYNSTPFGGKTLEIKRADAAPTYSIFPPSSEQLTSGGASVV 591
DB 357 -----KGRPKAPQVYTIPTPPKEQWAKDKVSLT 383
QY 592 CFLNFPYKIDINVKWKIDGSRQNGVLNWSWTDQSDKSTYSMSSTLTLTCKDEYERHNSYT 651
DB 384 CMITDFPEDITVEQWQNGQPAEN-YKNTQPIMDT-DGSYFYVYSKLVQKSNWEAGNTFT 441
QY 652 CEATHK 657
DB 442 CSVLHE 447

RESULT 63
ADN97521
ID ADN97521 standard; protein; 700 AA.

XX AC ADN97521;
XX DT 01-JUL-2004 (first entry)
XX DE Artificial protein construction protein #19.
XX KW artificial protein; propeptide; protein engineering; antibody.
XX OS Unidentified.
XX PN WO2004031362-A2.
XX PD 15-APR-2004.
XX PF 03-OCT-2003; 2003WO-US031420.
XX PR 03-OCT-2002; 2002US-0415940P.
XX PA (LARG-) LARGE SCALE BIOLOGY CORP.

XX Reini SJ, Edwards P;
XX WPI; 2004-330170/30.
XX N-PSDB; ADN97520.
XX New artificial proprotein comprises three peptide sequences, useful for
XX artificial multimeric protein engineering in eukaryotes.
XX Example 14; SEQ ID NO 94; 244pp; English.
XX The invention relates to an artificial proprotein comprising three
XX peptide sequences: a first peptide sequence of interest, a propeptide
XX sequence attached to the C-terminus of the first peptide sequence of
XX interest, and a second peptide of interest attached to the C-terminus of
XX the propeptide sequence. The artificial proprotein and polynucleotides
XX are useful for artificial multimeric protein engineering, e.g. antibodies
XX and antibody fragments in eukaryotes. This sequence corresponds to a
XX protein used in the generation of the protein of the invention.
XX Sequence 700 AA;

Query Match 28.4%; Score 1000; DB 8; Length 700;
Best Local Similarity 36.8%; Pred. No. 5.5e-51;
Matches 242; Conservative 54; Mismatches 131; Indels 230; Gaps 11;
QY 1 EVOLQSGDPLVKPGASVKISKASGYSTGYVHMVVKSPGKGLWIGRINPNNGVTLY 60
DB 257 QVLOQSGPELVKPGASLKLSTASGFKTIYIHWKORPQGLEWIGRIYPTNYTRY 316
QY 61 NOKFKDKATLTVDKSTTAYMELRLSTSDSAVYICARSTMITNYVMDYWGQGTSTVVS 120
DB 317 DKFQDKATITADTSNTAYLQVSLTSEDYVYCSRWGGDGFYAMDYWGQASVTVS 376
QY 121 AKTTPSPVPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVMNSGSLSSGVHFFPAVLQSD 180
DB 377 AKTTPSPVPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVMNSGSLSSGVHFFPAVLQSD 436
QY 181 LYTLLSSVTPSPSTWSPSETVTCNVAHPASSTKVKKIVPRDGGPSEKSENEKDLRKK 240
DB 437 LYTLLSSVTPSPSTWSPSETVTCNVAHPASSTKVKKIVPRDCG----- 479
QY 241 SELQGTALGNLQIYYVYNSKAITSEKSAQDLTNTLLFKGPTGHPWYNLLVLDLGSTA 300
DB 480 -----CKPC 483
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTBEKKVPLNLMWDGKQ 360
DB 484 ICTVPEVSSVFIF-----PPK-----PKDVLITLITPKV 512
QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRLVHFHSEGSTVS 420
DB 513 TCVVVD-----ISKDDPEVQ-----FS 529
QY 421 YDLFDAQGOYPTLLRIYRDNNTTISSTLSLSISLYLYTTSIVMTQTPTSLLSAGDRVIT 480
DB 530 WFDVDDVEVHTAQTPREEQFNSTFRSV-----ELPIMHQD----- 565
QY 481 CKASQSVSNDAVYQKPGQSKLLISYTSRYAGVDRFSGSGYGTDFTLTSSVQAE 540
DB 566 -----WLNDDKEFKC-----RVNSAAPPAPIEKTIS----- 590
QY 541 AAVYFCQDYNSTPFGGKTLEIKRADAAPTYSIFPPSSEQLTSGGASVCFNNFPYK 600
DB 591 -----KTKGRPKAPQVYTIPTPPKEQWAKDKVSLTCTMITDFFPE 628
QY 601 DINVKWKIDGSRQNGVLNWSWTDQSDKSTYSMSSTLTLTCKDEYERHNSYTCATHK 657
DB 629 DITVEQWQNGQPAEN-YKNTQPIMDT-DGSYFYVYSKLVQKSNWEAGNTFTCSVLHE 683

RESULT 64
AAW85692

Db	138	SGGGSGGGSGGGSGD	IQMTQSPS-----SL	SASVGRDVTITCRASODISSYLNWYQQ	191	
Qy	154	---PEPVTVTNWNSGSLSSGVHTFP	AVLQSDLYTLSSSVTPVPSSTWPS	ETVTCNVAHP-	207	
Db	192	KPGKAPKLLIYYTSLHSGV---	PRFSGSGSGTDFTFI--SSLP	EDIATYYCQGNLT	247	
Qy	208	----ASSTKVDKKIIVPRDSGGP	SEKEEINEKDLRKGLOQTALGNL	KQIYYVNSKAIT	263	
Db	248	PYTFQGGTKVEIKGGGGSGGGSG	GGGVD-----SQVQLQESGP	GLVLR-----	291	
Qy	264	SSEKSADQFLNTLLFKGF--	PTGHPWYNDDLVLGSLTAATSEY	EGSSVDLYCAYGYQC	321	
Db	292	-----PSQTLSTLCTVSGYSIT	SDHAW-----SWVRQPPG	RGLG-----WIGY--	329	
Qy	322	AGGTPNKTAACMGVGT	LHD---NNRLTB	EKKVPINLWIDGKQTTVPID	KVTSKKEVTWQ	378
Db	330	-----ISYSGITTYNPSL	KSRVTMLR-----	-----DTSKNQ	QFSLR	360
Qy	379	ELDLQAR-----HYLHGK	FGLYNSDSFGGKVQRGLIV	FHSSSEGSTVSYDL	FDAGQGYPTDL	434
Db	361	LSSVTAADTAVYCARSLART	TAMDYWG--QGSLVT	VSSGGGGSGGGSGGGG	GGG-----	411
Qy	435	LRIYRDNTTISLSLSISLY	TTTSIVMTQTPFSLLSVAG	DRVTITCKASQSVSNDV	AVNY	494
Db	412	-----SDIQMTQSPSSL	SASVGRDVTITCRASODISSY	LNWY	448	
Qy	495	QOKPGOSPKLLISYTS	SRVAGVDRFSGSGYCTDFT	LTISSSVQAE	DAAVFCQDYN	554
Db	449	QOKPKAKPKLLIYTSR	LHSGVPSFGSGSGTDFT	FISSLP	EDIATYYCQGNLT	508
Qy	555	TFGGGTGLEIKRADAA	PTVSPPPSSEQLTSGGAS	VVCFLN	NFYPKDINVKWIDG	614
Db	509	TFGGGTKEIKRTVAAP	SVFIFFPPSDEQLKSGT	ASVVCCLNNFY	PREAKVQMKVDNALQS	568
Qy	615	NGVLNSWTDQDSK	STYSMSSTLTLTKDEYER	HNSYTCEATHKTSPT	PIVKSFN	672
Db	569	GNSQESVTEQDSK	STYSLSSTLTLSKADY	EKHKVYACEVTHQGL	SSPVTKSFNRGES	626
RESULT 67						
AAW86002						
ID	AAW86002 standard; protein; 243 AA.					
XX	AAW86002;					
XX	15-MAR-1999 (first entry)					
DT	Murine anti-5T4 antigen monoclonal antibody scFv.					
XX	Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;					
KW	monoclonal antibody; single chain antibody; scFv; mouse; 5T4scFv.1.					
XX	Mus sp.					
OS	Synthetic.					
OS	Chimeric.					
XX	Key					
XX	Location/Qualifiers					
FT	Misc-difference 169					
FT	/note= "encoded by GDT"					
XX	WO9855607-A2.					
XX	10-DEC-1998.					
XX	04-JUN-1998; 98WO-GB001627.					
XX	04-JUN-1997; 97GB-00011579.					
PR	20-JUN-1997; 97GB-00013150.					
PR	04-JUL-1997; 97GB-00014230.					
XX	(OXFO-) OXFORD BIOMEDICA UK LTD.					
XX						

Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
WPI; 1999-059910/05.
N-PSDB; AAV80290.

New vector encoding a tumour interacting protein for treating cancer -
contains a desired nucleotide sequence and/or protein which recognises
tumours, and is used as a gene delivery system to treat cancer.

Example 1; Fig 1A; 82pp; English.

This amino acid sequence comprises an scFv, termed 5T4scFv.1, comprising
the heavy chain variable region (VH) from the murine 5T4 monoclonal
antibody followed by a 15-amino acid flexible linker and the light chain
variable region (VL) of the mouse 5T4 antibody. The trophoblast cell
surface antigen defined by monoclonal antibody 5T4 is expressed at high
levels on the cells of a wide variety of human tumours. 5T4scFv.1 DNA
(see AAV80290) can be used to construct single-chain antibodies (see
AAW86003) and scFv fusion constructs (see AAW86004-05). The invention
relates to a vector comprising a nucleotide sequence coding for a tumour
interacting protein (TIP) and optionally a nucleotide sequence of
interest (NOI) which encodes a protein of interest (POI), the vector
being capable of delivering the NOI and/or POI to the tumour recognised
by the TIP. Delivery can be in vivo or ex vivo. The vector is used to
treat cancer, and may also be used as a gene delivery system for introducing
at least 1 gene encoding a TIP (preferably a tumour binding protein) into
a haematopoietic cell lineage

Sequence 243 AA;

Query Match 27.6%; Score 972.5; DB 2; Length 243;
Best Local Similarity 40.1%; Pred. No. 6.6e-50;
Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

Qy 1 EVQLQSGDPLVKGASVKISCKASGSPFGYVHWVKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVQLQSGDPLVKGASVKISCKASGSPFGYVHWVKQSPGKLEWIGRINPNNGVTLY 60

Qy 61 NQPKDKATLTVDKSTTAYMELRSLTSEDSAVYCARSTMIINYMDYWGQGTSTVTVSS 120
Db 61 NQPKDKATLTVDKSTTAYMELRSLTSEDSAVYCARSTMIINYMDYWGQGTSTVTVSS 119

Qy 121 AKTTPSPVYPLAFGSAQAQTNMVTGLCLVKGYFPEPVTVTVNSGSLSSGHHPTFPAVLQSD 180
Db 120 ----- 119

Qy 181 LYTLSSTVTPSTWPSSETVTCNVAHPASTKVDKKIIPRDSGGPSEKSEINEKDLRKK 240
Db 120 -----SGG----- 122

Qy 241 SELQGTALGNLKQIYYVNSKAITSSSEKSADQFLNTLLPKGFFTGHWPYNDLLVDLGSTA 300
Db 123 ----- 122

Qy 301 ATSEYEGSSVDLYGAVYGOCAGGTPNKTAICYGGVTLLHDNNRLTEBKKVPINLWIDGKQ 360
Db 123 -----GGSGGGGT-----GG----- 132

Qy 361 TTVPIDKVTSKBEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEGSTVS 420
Db 133 ----- 134

Qy 421 YDLFDAQGGYPTDLLRIYRDNNTTISSTSLGISLVLYTSTVMTQTPTSLVLSAGDRVIT 480
Db 135 -----SSIVMTQTPTFLVLSAGDRVIT 157

Qy 481 CKASQSVSNDVAVYQKPGQSPKLLISYTSR YAGVPDRFSGSGYGTFTLTISVQAED 540
Db 158 CKASQSVSNDVAVYQKPGQSPKLLISYTSR YAGVPDRFSGSGYGTFTLTISLQAED 217

Qy 541 AAVFCQDYNVSPPTFGGGTKLEIKR 566
Db 218 LAVVFCQDYNVSPPTFGGGTKLEIKR 243

RESULT 68
AA42294
ID AA42294 standard; protein; 243 AA.
AC AA42294;
XX
DT 06-DEC-1999 (first entry)
XX
DE Anti-5T4 secreted single chain antibody Fv fragment.
XX
KW Cytochrome; targeting; localisation; cancer; tumour; prodrug; reduction;
KW nucleus.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9945127-A2.
XX
XX 10-SEP-1999.
PD
XX 05-MAR-1999; 99WO-GB000674.
PF
XX 06-MAR-1998; 98GB-00004841.
PR 19-AUG-1998; 98GB-00018103.
PR 29-JAN-1999; 99GB-00002081.
XX
(OXFO-) OXFORD BIOMEDICA UK LTD.
PA Stratford IJ, Patterson AV, Kingman SM, Kan O, Griffiths L;
PI Mitrophanous K;
XX
XX WPI; 1999-551046/46.
DR N-PSDB; AA219786.
XX
XX New prodrug activating agent targeted to selected cells or tissues,
PT particularly hypoxic cells, for treating e.g. tumors.
XX
XX Example 9; Fig 3; 187pp; English.
PS
XX This sequence represents an example of a secreted single chain antibody
CC Fv fragment (in this case, directed against the 5T4 antigen), which is
CC involved in transcellular localisation. A secreted single chain antibody
CC Fv fragment can be fused to cytochrome P450 reductase (P450R) derivatives
CC such as anchorless P450R (AA42287) or FN fragment (AA42288). This
CC enables the fusion protein to be delivered to other cells where it is
CC then transported to the nucleus. Many drugs' sites of action are in the
CC nucleus, rather than the cytoplasm, where P450R normally functions. P450R
CC or its derivatives can be used to activate prodrugs to their active form
CC via reduction. Administration of a prodrug is useful where the active
CC drug may be metabolised before it reaches its site of action or where the
CC active drug is cytotoxic, e.g., anticancer drugs. Targeted delivery of
CC such prodrug activators allows a reduction in dose of the prodrug, and
CC thus of systemic side-effects. P450R derivative fusion proteins, or
CC vectors that express them, are specifically used to treat tumours, or
CC inflammation, atherosclerosis and muscular dystrophy, but may also be
CC used to treat many other conditions, e.g., cerebral malaria, rheumatoid
CC arthritis, or conditions associated with hypoxia, ischaemia or
CC hypoglycemia, or to deliver antibiotics, antiviral agents, analgesics,
CC anaesthetics, anti-inflammatories, antineoplastic agents and diagnostic
CC agents
XX
SQ Sequence 243 AA;
Query Match 27.6%; Score 972.5; DB 2; Length 243;
Best Local Similarity 40.1%; Pred. No. 6.6e-50;
Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;
QY 1 EVQLQSGDPLVKPGASVKISKASGYSFTGYIMHWVKQSPGKLEWIGRINPNNGVTLV 60
DB 1 EVQLQSGDPLVKPGASVKISKASGYSFTGYIMHWVKQSHGKSLIEWIGRINPNNGVTLV 60

QY 61 NOKEKDKATLTVDKSSSTTAYMELRSITSDSAVYYCARSTMTINYYMDYWGQGTSTVTS 120
DB 61 NOKFKDKAILTVDKSSSTTAYMELRSITSDSAVYYCARSTMTINYYMDYWGQVTSTVS- 119
QY 121 AKTTPSPVYFLAPGSAQAQTNMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTPAPVLQSD 180
DB 120 ----- 119
QY 181 LYTSSSVTVSPSTWPSSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEEINEKDLRKK 240
DB 120 -----SGG----- 122
QY 241 SELQGTALGNLQIYYNNSKAITSSSEKADQFLTNLLFKGPFTGHPWYNDLLVDLGSTA 300
DB 123 ----- 122
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPKTACMYGGVTLHDNNRLTBEKKVPIINLWDGKQ 360
DB 123 -----GGSGGGT----- 132
QY 361 TTVPIDKVKTSKEVTYQELDLQARHYLHGKFGLYNSDSFGKVKQGLVIFHSSSESTVS 420
DB 133 -----GG----- 134
QY 421 YDLFDAQGOYPTDLLRIYRDNTTISSTLSLSLYTTSIVMTQTPTSLLSVSGDRVIT 480
DB 135 -----SSIVMTQTPTFLLSVSGDRVIT 157
QY 481 CKASQSVSNDAVYQOKPQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTSSVOAED 540
DB 158 CKASQSVSNDAVYQOKPQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTSSVOAED 217
QY 541 AAVYFCQDYNSPPTFGGSKLEIKR 566
DB 218 LAVYFCQDYNSPPTFGGSKLEIKR 243
RESULT 69
AA427407
ID AA427407 standard; protein; 243 AA.
XX
AC AA427407;
XX
DT 23-NOV-1999 (first entry)
XX
DE 5T4 scFv antibody signal peptide.
XX
KW Prodrug; localization domain; tumor-selective antibody; cytochrome P450;
KW prodrug activating domain; modified hematopoietic stem cell; MHC; tumor;
KW inflammation; atherosclerosis; muscular dystrophy; cerebral malaria;
KW rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; tumor antigen;
KW 5T4 scFv.
XX
OS Unidentified.
XX
PN WO9945126-A2.
XX
XX 10-SEP-1999.
PD
XX 05-MAR-1999; 99WO-GB000672.
PF
XX 06-MAR-1998; 98GB-00004841.
PR 19-AUG-1998; 98GB-00018103.
PR 29-JAN-1999; 99GB-00002081.
XX
(OXFO-) OXFORD BIOMEDICA UK LTD.
PA Stratford IJ, Patterson AV, Kingman SM, Kan O, Griffiths L;
PI Mitrophanous K;
XX
XX WPI; 1999-540852/45.
DR N-PSDB; AA207810.
XX

PT New produg activating agent targeted to selected cells or tissues,
 PT particularly hypoxic cells, for treating e.g. tumors or inflammation.
 XX
 XX
 XX Example 9; Fig 3F; 149pp; English.
 CC The invention provides a new produg activating agent that comprises: (i)
 CC a localization domain (LD); other than a tumor-selective antibody) and a
 CC produg activating domain (PAD); (ii) at least one nucleic acid encoding
 CC a cytochrome P450 and under control of at least one constitutive or
 CC inducible expression control sequence or (iii) a modified hematopoietic
 CC stem cell (MHSC) containing at least one nucleic acid encoding a PAD and
 CC under control of elements as in (ii). The produg activating agent or
 CC vectors that express them, are specifically used to treat tumors,
 CC inflammation, atherosclerosis and muscular dystrophy, but may also be
 CC used to treat many other conditions, e.g. cerebral malaria, rheumatoid
 CC arthritis, or conditions associated with hypoxia, hypoglycemia or
 CC ischemia, or to deliver antibiotics, antiviral agents, analgesics,
 CC anesthetics, anti-inflammatories, antineoplastic agents and diagnostic
 CC agents. LD optimize activity of PAD, e.g. by delivering it to selected
 CC locations or by delivering it to neighboring cells (bystander effect),
 CC and allow a reduction in dose of produg, and thus of systemic side-
 CC effects. Nucleic acids encoding the agent may be expressed selectively in
 CC hypoxic cells. The present sequence represents the single chain variable
 CC antibody fragment against the tumor antigen 5T4 (5T4 scFv). 5T4 scFv is
 CC used in the construction of a fusion protein comprising 5T4 scFv and a
 CC human P450 reductase derivative alp450R
 XX
 XX SQ Sequence 243 AA;

Query Match 27.6%; Score 972.5; DB 2; Length 243;
 Best Local Similarity 40.1%; Pred. No. 6.6e-50;
 Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVQLQSGDPLVPGASVKISCKASGYSFTGYIMHWVKQSPGKLEWIGRINPNNVTLY 60
 DB 1 EVQLQSGDPLVPGASVKISCKASGYSFTGYIMHWVKQSPGKLEWIGRINPNNVTLY 60
 QY 61 NQKFKDKATLVDRKSTTAYMELSLTSDSAVYICARSTMTITNYMDYMGQSTVTVSS 120
 DB 61 NQKFKDKATLVDRKSTTAYMELSLTSDSAVYICARSTMTITNYMDYMGQSTVTVSS 119
 QY 121 AKTTPSVYPLAGSAAQNTSMVTLGLVKGYFPEPVTVTWNSGSLSSGVHTPAVLQSD 180
 DB 120 ----- 119
 QY 181 LYTLSSTVTPSPSTPSETVTCNVAPASSTKVDKIVPRDSGSPSEKSEINEKDLRKK 240
 DB 120 -----SGG----- 122
 QY 241 SELQGTALGNLKIYYNSKAITSEKSAQDPLTLLFKGFTGHPWYNDLLVLDGSTA 300
 DB 123 ----- 122
 QY 301 ATSEYEGSSVDLYGAYGYQCAGTPNKTACMTGGVTLHDNNRLTEBKVPINLWIDGKQ 360
 DB 123 -----GGSGGGT-----GG----- 132
 QY 361 TTPVIDKVTSKKEVTQELDLQARHVLHCKFGLYNSDSFGKVGQRLIVPHSSEGSTVS 420
 DB 133 -----GG----- 134
 QY 421 YDLFDAQQGVPTLLRIYRDNMTTISSTLSISLYLTYTTSIVMTQTPTSLVLSAGDRVIT 480
 DB 135 -----SSIVMTQTPTFLVLSAGDRVIT 157
 QY 481 CKASQSVNSDVAVYQKPGSPKLLISYTSRAGVDPDRFGSGGYGHDFTLTLSVQAE 540
 DB 158 CKASQSVNSDVAVYQKPGSPKLLISYTSRAGVDPDRFGSGGYGHDFTLTLSVQAE 217
 QY 541 AAVYFCQDYNSPPTFGGKLEIKR 566
 DB 218 LAVYFCQDYNSPPTFGGKLEIKR 243

RESULT 70
 AAB83835

ID AAB83835 standard; protein; 243 AA.

XX AAB83835;

AC AAB83835;

DT 23-JUL-2001 (first entry)

DE Amino acid sequence of a 5T4 scFv designated 5T4ScFv.1.

XX Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
 KW hypersensitivity; autoimmune disease; central nervous system disorder;
 KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
 KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
 KW Helicobacter-related disease; immune disorder.

OS Synthetic.

OS Mus sp.

XX Key Location/Qualifiers

FT Misc-difference 169

FT /note= "Ala encoded by GDT"

XX WO200136486-A2.

XX 25-MAY-2001.

XX 13-NOV-2000; 2000WO-GB004317.

XX 18-NOV-1999; 99WO-GB003859.

PR 15-FEB-2000; 2000GB-00003527.

PR 02-MAR-2000; 2000GB-00005071.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Kingman A, Kingman SM, Bebbington CR, Carroll MW, Ellard FM;

PI Myers KA;

XX WPI; 2001-343805/36.

DR N-PSDB; AAF69729.

XX Use of single chain antibody capable of recognizing a disease associated
 PT molecule for manufacturing a medicament for preventing and/or treating a
 PT disease condition associated with disease associated molecule.

XX Claim 3; Fig 1; 118pp; English.

CC The specification describes the use of a single chain antibody (ScFv),
 CC which is capable of recognizing a disease associated molecule in the
 CC manufacture of a medicament for the prevention and treatment of a disease
 CC condition. The ScFv antibody is useful in the manufacture of a
 CC medicament, for affecting a disease in vivo, for preparing a
 CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
 CC treatment of a disease. The ScFv antibody is also useful for treating
 CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
 CC diseases, cancers, central nervous system disorders including Parkinson's
 CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
 CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
 CC related diseases, and other immune disorders. The present sequence the VH and
 CC VL regions from murine 5T4 monoclonal antibody, joined by a linker
 CC sequence

SQ Sequence 243 AA;

Query Match 27.6%; Score 972.5; DB 4; Length 243;

Best Local Similarity 40.1%; Pred. No. 6.6e-50;

Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVQLQSGDPLVPGASVKISCKASGYSFTGYIMHWVKQSPGKLEWIGRINPNNVTLY 60

DB 1 EVQLQSGDPLVPGASVKISCKASGYSFTGYIMHWVKQSPGKLEWIGRINPNNVTLY 60

PT New vector encoding a tumour interacting protein for treating cancer -
PT contains a desired nucleotide sequence and/or protein which recognises
PT tumours, and is used as a gene delivery system to treat cancer.
XX
PS Example 5; Fig 2; 82pp; English.
XX This is the amino acid sequence of B7-1.5T4.1, a fusion protein
CC comprising the extracellular domain (amino acids 1-215) of human co-
CC stimulatory molecule B7-1 joined via a flexible peptide linker to an scFv
CC (see AAW86002) derived from murine 5T4 monoclonal antibody. B7-1.5T4.1
CC cDNA (see AAV80292) can be inserted into vector pCI to allow expression
CC of the fusion protein in mammalian cells. The trophoblast cell surface
CC antigen defined by 5T4 is expressed at high levels on the cells of a wide
CC variety of human tumours. The invention relates to a vector comprising a
CC nucleotide sequence coding for a tumour interacting protein (TIP) and
CC optionally a nucleotide sequence of interest (NOI) which encodes a
CC protein of interest (POI), the vector being capable of delivering the NOI
CC and/or POI to the tumour recognised by the TIP. Delivery can be in vivo
CC or ex vivo. The vector is used to treat cancer, and may also be used as a
CC gene delivery system for introducing at least 1 gene encoding a TIP
CC (preferably a tumour binding protein) into a haematopoietic cell lineage.
CC B7-1 is expected to bind specifically to CD28 and CTLA-4 present on human
CC T-cells
XX
SQ Sequence 488 AA;

Query Match 27.5%; Score 967.5; DB 2; Length 488;
Best Local Similarity 40.0%; Pred. No. 3e-49;
Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVLOQSGDPLVKPGASVKISKASGYFTGYNMHWKSPGKLEWIGRINPNNGVTL 60
DB 247 EVLOQSGDPLVKPGASVKISKASGYFTGYNMHWKSPGKLEWIGRINPNNGVTL 306
QY 61 NQKFKDKATLTVDKSTTAYMELRLTSDSAVYCARSTMTITNYMDYWGQTSVTSS 120
DB 307 NQKFKDKATLTVDKSTTAYMELRLTSDSAVYCARSTMTITNYMDYWGQTSVTSS - 365
QY 121 AKTTPPSVPLAPGSAQTNSMVTGLVKGYFPEPTVTWNSGSLSSGVHTPPAVLQSD 180
DB 366 ----- 365
QY 181 LYTSSVTPSPSTWSEVTCNVHPASTKVKIVPRDSGGPSEKSEINEKDLRKK 240
DB 366 -----SGG----- 368
QY 241 SELQGTALGNLKOIYYNSKAITSEKSADQFLTNLLPKGFTTGHWPYNDLLVDLGSTA 300
DB 369 ----- 368
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTBEKVPINLWIDGKQ 360
DB 369 -----GGSGGGT----- 378
QY 361 TTVPIDKVTSKKEVTVQELDLQARHLHGKFLGYNDSFGKQVQKGLIVFHSSEGSTVS 420
DB 379 -----GG----- 380
QY 421 YDLFDAQGYPTDLLRIYRDNNTTISLSLSILYLTYSIVMTQTPTSLVSGADRVTLT 480
DB 381 -----SSIVMTQTPTFLVVSAGDRVTLT 403
QY 481 CKASQSVNDVAVYQKPGSPKLLISYTSRYSAGVDPDRFGSGYGTDFTLTSSVQAE 540
DB 404 CKASQSVNDVAVYQKPGSPKLLISYTSRYSAGVDPDRFIGSGYGTDFTLTSSVQAE 463
QY 541 AAVYFCQDYNSPPTFGGKLEIK 565
DB 464 LAVYFCQDYNSPPTFGGKLEIK 488

RESULT 73
AAB83836

ID AAB83836 standard; protein; 488 AA.
XX AC AAB83836;
XX DT 23-JUL-2001 (first entry)
XX DE Amino acid sequence of a B7-1.5T4.1 fusion protein.
XX KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
XX hyper-sensitivity; autoimmune disease; central nervous system disorder;
XX Parkinson's disease; periodontal disease; cardiopulmonary disease;
XX cardiovascular disease; gastrointestinal disorder; infection; diabetes;
XX Helicobacter-related disease; immune disorder.
XX OS Synthetic.
XX OS Mus sp.
XX OS Homo sapiens.
XX PN WO200136486-A2.
XX PD 25-MAY-2001.
XX PF 13-NOV-2000; 2000WO-GB0004317.
XX PR 18-NOV-1999; 99WO-GB003859.
XX PR 15-FEB-2000; 2000GB-00003527.
XX PR 02-MAR-2000; 2000GB-00005071.
XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX PI Kingeman A, Kingeman SM, Bebbington CR, Carroll MW, Ellard FM;
PI Myers KA;
XX DR WPI: 2001-343805/36.
XX DR N-PSDB; AAF89730.
XX PT Use of single chain antibody capable of recognizing a disease associated
XX molecule for manufacturing a medicament for preventing and/or treating a
XX disease condition associated with disease associated molecule.
XX PS Claim 3; Fig 2; 118pp; English.
XX CC The specification describes the use of a single chain antibody (ScFv),
XX which is capable of recognizing a disease associated molecule in the
XX manufacture of a medicament for the prevention and treatment of a disease
XX condition. The ScFv antibody is useful in the manufacture of a
XX medicament, for affecting a disease in vivo, for preparing a
XX pharmaceutical composition, for in vivo imaging and/or for adjuvant
XX treatment of a disease. The ScFv antibody is also useful for treating
XX inflammatory diseases including arthritis, hyper-sensitivity, autoimmune
XX diseases, cancers, central nervous system disorders including Parkinson's
XX disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
XX diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
XX related diseases, and other immune disorders. The present sequence
XX represents a B7-1.5T4.1 fusion protein. This comprises the N-terminus of
XX the 5T4 ScFv is fused after amino acid 215 of human B7-1
SQ Sequence 488 AA;

Query Match 27.5%; Score 967.5; DB 4; Length 488;
Best Local Similarity 40.0%; Pred. No. 3e-49;
Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVLOQSGDPLVKPGASVKISKASGYFTGYNMHWKSPGKLEWIGRINPNNGVTL 60
DB 247 EVLOQSGDPLVKPGASVKISKASGYFTGYNMHWKSPGKLEWIGRINPNNGVTL 306
QY 61 NQKFKDKATLTVDKSTTAYMELRLTSDSAVYCARSTMTITNYMDYWGQTSVTSS 120
DB 307 NQKFKDKATLTVDKSTTAYMELRLTSDSAVYCARSTMTITNYMDYWGQTSVTSS - 365
QY 121 AKTTPPSVPLAPGSAQTNSMVTGLVKGYFPEPTVTWNSGSLSSGVHTPPAVLQSD 180

Db 366 ----- 365
QY 181 LYTSSSVTPSSWPSETVTCNVAHPASSTKVDDKIVPRDGGPSEKSEINEKDLRKK 240
Db 366 ----- 368
QY 241 SELQGTALGNLQKIYYVNSKAITSSSEKADQFLTNLLFKGPFTHGHPWYNDLLVDLGSTA 300
Db 369 ----- 368
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEBEKVPINLWIDGKQ 360
Db 369 ----- 378
QY 361 TTVPIDKVKTSKEVTVQELDLQARHLHGKFGLYNSDSFGGKVGRLIVFHSSEGSTVS 420
Db 379 ----- 380
QY 421 YDLFDAQGQYPTDLLRIYRDNTTISSTLSISLYLTTSIVMTQTPTSLLSVAGDRVTIT 480
Db 381 ----- 403
QY 481 CKASQSVNDVAVYQKPGQSPKLLISYTSRRYAGVDPDRFSGSGYGTDTFTLTSSVQAE 540
Db 404 CKASQSVNDVAVYQKPGQSPKLLISYTSRRYAGVDPDRFSGSGYGTDTFTLTSSVQAE 463
QY 541 AAVYFCQDYNPPTFGGKLEIK 565
Db 464 LAVYFCQDYNPPTFGGKLEIK 488

RESULT 74
ABU07262
ID ABU07262 standard; protein; 488 AA.
XX
AC ABU07262;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1963.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX

PS
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 488 AA;
Query Match 27.5%; Score 967.5; DB 6; Length 488;
Best Local Similarity 40.0%; Pred. No. 3e-49;
Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;
QY 1 EVQLQSGPDLVKPGASVKISCKASGYSTGYMHVWVKQSPCKGLEWIGRINPNNGVTLY 60
Db 247 EVQLQSGPDLVKPGASVKISCKASGYSTGYMHVWVKQSHGKSLIEWIGRINPNNGVTLY 306
QY 61 NOKFKDKATLTVDKSTTAYMELRLTSDSDSAVYVCARSTMTITNYMDYWGQTSVTSS 120
Db 307 NOKFKDKATLTVDKSTTAYMELRLTSDSDSAVYVCARSTMTITNYMDYWGQTSVTSS- 365
QY 121 AKTTPPSVYPLAPGSAATNSMTVLGCLVKGYFPEPTVTWNSSGSLSSGVHTFPAVLQSD 180
Db 366 ----- 365
QY 181 LYTSSSVTPSSWPSETVTCNVAHPASSTKVDDKIVPRDGGPSEKSEINEKDLRKK 240
Db 366 ----- 368
QY 241 SELQGTALGNLQKIYYVNSKAITSSSEKADQFLTNLLFKGPFTHGHPWYNDLLVDLGSTA 300
Db 369 ----- 368
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEBEKVPINLWIDGKQ 360
Db 369 ----- 378
QY 361 TTVPIDKVKTSKEVTVQELDLQARHLHGKFGLYNSDSFGGKVGRLIVFHSSEGSTVS 420
Db 379 ----- 380
QY 421 YDLFDAQGQYPTDLLRIYRDNTTISSTLSISLYLTTSIVMTQTPTSLLSVAGDRVTIT 480
Db 381 ----- 403
QY 481 CKASQSVNDVAVYQKPGQSPKLLISYTSRRYAGVDPDRFSGSGYGTDTFTLTSSVQAE 540
Db 404 CKASQSVNDVAVYQKPGQSPKLLISYTSRRYAGVDPDRFSGSGYGTDTFTLTSSVQAE 463
QY 541 AAVYFCQDYNPPTFGGKLEIK 565
Db 464 LAVYFCQDYNPPTFGGKLEIK 488
RESULT 75
ABU07253
ID ABU07253 standard; protein; 488 AA.
XX
AC ABU07253;
XX

DT 29-JAN-2003 (first entry)
XX Human expressed protein tag (EPT) #1954.
DE
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX Homo sapiens.
XX WO200278524-A2.
PN 10-OCT-2002.
XX 28-MAR-2002; 2002WO-US009671.
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
PA Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
DR New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX Example 2; SEQ ID NO 1954; 134pp; English.

Search completed: February 15, 2006, 20:13:13
Job time : 225.229 secs

QY 181 LYTSSSVTPSPSTWPSSTVTCNVAHPASSTKVDKIVPRDGGPSEKSEINEKDLRKK 240
Db 366 -----SGG----- 368
QY 241 SELQGTALGNLKOIYYNNSKAITSSSEKSADQFLTNLLPKGFTGHPWYNDLLVDLGSTA 300
Db 369 ----- 368
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db 369 -----GGSGGGT-----GG----- 378
QY 361 TTVPIDKVKTSKEVTVBELDLQARHYLHGKFLGYNLSDSFGGKVQRLIVFHSSEGSTVS 420
Db 379 -----GG----- 380
QY 421 YDLFDAQQVPTDLLRIYRDNTTISSTLSISLYTTTSIVMTQTPTSLIVSAGDRVTIT 480
Db 381 -----SSIVMTQTPTFLVLSAGDRVTIT 403
QY 481 CKASQSVSNDVAVYQOKPGOSPKLLISYTSRVRAGVDRFSGSGYGTDFLTITSSVOAED 540
Db 404 CKASQSVSNDVAVYQOKPGOSPTLLISYTSRVRAGVDRFSGSGYGTDFLTITSSVOAED 463
QY 541 AAVYFCQDDYNSPPTFGGTTKLEIK 565
Db 464 LAVYFCQDDYNSPPTFGGTTKLEIK 488

Query Match 27.5%; Score 967.5; DB 6; Length 488;
Best Local Similarity 40.0%; Pred. No. 3e-49;
Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVOLQSGDPLVKGASVKISCKASGYFTGYMHWVKQSPGKLEWIGRINPNNGVTL 60
Db 247 EVOLQSGDPLVKGASVKISCKASGYFTGYMHWVKQSHGKSLWIGRINPNNGVTL 306
QY 61 NQKFKDKAILTVDKSSTAYMELRSLTSDSAVYCARSTMTNYVMDYWGQTSVTSS 120
Db 307 NQKFKDKAILTVDKSSTAYMELRSLTSDSAVYCARSTMTNYVMDYWGQTSVTSS- 365
QY 121 AKTPPSVPLAPGSAQAQNSMTLGLVKGYFPEPTVTWNSGSLSSGVHTFPVLQSD 180
Db 366 ----- 365

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:13:35 ; Search time 38.6122 Seconds
(without alignments)
1674.542 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522

Sequence: 1 EVQLQQSGDPLVPGASVKI.....EATHKTSTSPIVKSPNRNES 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

PIR 80:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1107	31.4	257	A28179	enterotoxin E prec
2	1036.5	29.4	225	S37484	Ig kappa chain - m
3	973	27.6	446	S40295	Ig gamma-2a chain
4	952	27.0	220	A31790	Ig kappa chain V r
5	951.5	27.0	469	S37483	Ig gamma-2a chain
6	948	26.9	257	A28664	enterotoxin A prec
7	931	26.4	548	S38864	Ig epsilon chain C
8	929	26.4	246	S38950	Ig gamma chain - m
9	926	26.3	214	S68212	Ig kappa chain (Ma
10	918	26.1	260	C89984	enterotoxin P (imp
11	914.5	26.0	219	S52028	Ig kappa chain - m
12	914	26.0	214	PC4202	monoclonal antibod
13	910.5	25.9	219	PC4203	Ig kappa chain (mo
14	903.5	25.7	219	S16112	Ig kappa chain V r
15	900.5	25.6	474	G2MS11	Ig gamma-2b chain
16	896.5	25.5	219	S38865	Ig kappa chain - m
17	892	25.3	218	JC5810	monoclonal antibod
18	890.5	25.3	221	S49220	Ig gamma-1 chain -
19	886.5	25.2	217	S42772	Ig kappa chain - m
20	880	25.0	218	S68241	Ig kappa chain V r
21	878.5	24.9	235	S25058	Ig kappa chain - m
22	876.5	24.9	225	JL0029	Ig kappa chain pre
23	875	24.8	234	S14237	Ig kappa chain pre
24	874	24.8	234	S01320	Ig kappa chain pre
25	873	24.8	475	S01321	Ig gamma-2b chain
26	870	24.7	444	PC4436	monoclonal antibod
27	857	24.3	210	A56169	Ig kappa chain V r
28	853	24.2	240	S06084	Ig kappa chain pre
29	808	22.9	220	S68211	Ig heavy chain (Ma

30	737.5	20.9	213	2	S68213	Ig heavy chain (Ma
31	715	20.3	231	2	PC4155	Ig gamma-2b chain
32	702.5	19.9	215	2	JE0244	Ig kappa chain NIG
33	700.5	19.9	549	2	S04845	Ig heavy chain pre
34	695.5	19.7	215	2	JE0242	Ig kappa chain NIG
35	683.5	19.4	254	2	B31790	Ig heavy chain V r
36	679.5	19.3	215	2	JE0243	Ig kappa chain NIG
37	675	19.2	230	2	S33161	Ig kappa chain - s
38	673.5	19.1	470	2	S22080	Ig heavy chain pre
39	663.5	18.8	197	2	S29593	Ig kappa chain (WM
40	661.5	18.8	241	2	S69131	Ig heavy chain (DO
41	659.5	18.7	215	2	A23746	Ig kappa chain V-I
42	658	18.7	216	2	JE0241	Ig kappa chain Am3
43	619.5	17.6	472	2	S31459	Ig gamma-1 heavy c
44	611	17.3	220	2	A49444	Ig gamma-1 chain -
45	611	17.3	258	2	A33953	enterotoxin D prec
46	595.5	16.9	627	2	S14683	Ig mu chain precu
47	591	16.8	178	2	PT0219	Ig kappa chain V-C
48	570.5	16.2	229	2	A20969	Ig kappa chain pre
49	562	16.0	178	2	S29594	Ig gamma chain (WM
50	561	15.9	126	2	I54782	gene Pvt-1a/Ig-Ck
51	560.5	15.9	151	2	PL0011	Ig heavy chain pre
52	557	15.8	324	1	GLMS	Ig gamma-1 chain C
53	557	15.8	393	1	KLMSM	Ig gamma-1 chain C
54	556	15.8	106	1	KLMS	Ig kappa chain C r
55	556	15.8	268	2	A56446	Ig heavy chain V r
56	550	15.6	326	2	PS0017	Ig gamma-1 chain C
57	539	15.3	322	2	PS0019	Ig gamma-2a chain
58	536	15.2	288	2	S29690	Ig heavy chain VDJ
59	530	15.0	170	2	A35944	Ig gamma-2a chain
60	529.5	15.0	249	2	S41374	single chain Fv an
61	527	15.0	150	2	PN0444	Ig heavy chain V r
62	516.5	14.7	585	2	A46507	Ig alpha chain - c
63	514	14.6	120	2	A49982	Ig heavy chain V r
64	513.5	14.6	238	2	A49633	Ig lambda-like cha
65	510.5	14.5	166	2	PL0012	Ig heavy chain pre
66	506	14.4	139	2	A27609	Ig heavy chain V r
67	503	14.3	128	2	I37267	Ig heavy chain V r
68	502	14.3	135	2	PS0057	Ig heavy chain pre
69	495.5	14.1	568	2	A34891	Ig heavy chain pre
70	495	14.1	128	2	C37267	Ig heavy chain V r
71	492	14.0	139	2	PS0024	Ig heavy chain pre
72	491.5	14.0	330	1	G2MSA	Ig gamma-2a chain
73	491.5	14.0	399	1	G2MSAM	Ig gamma-2a chain
74	489.5	13.9	125	2	S20639	Ig heavy chain V r
75	488	13.9	120	2	S41394	Ig heavy chain V r
76	485.5	13.8	125	2	PH0100	Ig heavy chain V r
77	483	13.7	287	4	PC4402	pelB leader/Ig hea
78	482	13.7	114	2	S26319	Ig heavy chain V r
79	481.5	13.7	117	1	MHMS4E	Ig heavy chain V r
80	481.5	13.7	140	2	T01407	Ig heavy chain (my
81	481	13.7	139	1	MHMS18	Ig heavy chain pre
82	480.5	13.6	117	1	MHMSJ5	Ig heavy chain V r
83	480	13.6	118	1	MHMS38	Ig heavy chain V r
84	480	13.6	126	2	S31930	Ig gamma chain pre
85	479.5	13.6	116	2	S55542	Ig heavy chain V r
86	479	13.6	112	2	S09957	Ig heavy chain V-D
87	479	13.6	122	2	PH0887	Ig heavy chain V r
88	479	13.6	405	1	G2MSBM	Ig gamma-2b chain
89	478.5	13.6	233	2	JC5322	p53 specific singl
90	478	13.6	117	2	PL0237	Ig heavy chain V r
91	478	13.6	131	2	S65537	Ig heavy chain V r
92	477	13.5	92	2	B45837	Ig gamma-1 chain C
93	477	13.5	117	2	B27563	Ig heavy chain V r
94	477	13.5	122	2	E37267	Ig heavy chain V r
95	477	13.5	137	2	H32513	Ig heavy chain pre
96	475	13.5	117	2	PL0235	Ig heavy chain V r
97	475	13.5	119	2	F30502	Ig heavy chain V r
98	474.5	13.5	119	2	PH0099	Ig heavy chain V r
99	474	13.5	141	2	PL0076	Ig heavy chain pre
100	473.5	13.4	119	2	B53285	Ig heavy chain V a
101	473	13.4	128	2	A37267	Ig heavy chain V r
102	473	13.4	152	2	S30751	Ig kappa chain pre

103	472.5	13.4	120	2	S25175	Ig heavy chain V r	176	442.5	12.6	123	2	G48677	Ig heavy chain V-D
104	472	13.4	106	1	X1RTA	Ig kappa chain C r	177	442	12.5	111	2	S25024	Ig heavy chain V r
105	471	13.4	120	2	B22769	Ig heavy chain V r	178	442	12.5	111	2	S25032	Ig heavy chain V r
106	469	13.3	107	2	S26320	Ig heavy chain V r	179	442	12.5	112	2	S40502	Ig heavy chain V r
107	468.5	13.3	123	2	S20646	Ig heavy chain V r	180	441.5	12.5	117	2	S01822	Ig heavy chain V-D
108	468	13.3	123	2	PL0234	Ig heavy chain V r	181	441	12.5	111	2	S25033	Ig heavy chain V r
109	468	13.3	120	2	E45722	anti-glycoprotein	182	441	12.5	111	2	S25047	Ig heavy chain V r
110	468	13.3	144	2	B30502	Ig heavy chain V r	183	440.5	12.5	136	2	PL0208	Ig heavy chain pre
111	467.5	13.3	121	2	H37266	Ig heavy chain V r	184	440.5	12.5	140	2	PH1484	Ig heavy chain V r
112	467	13.3	335	1	G2MSAB	Ig gamma-2a chain	185	440	12.5	120	2	S09956	Ig heavy chain V-D
113	466	13.2	120	2	F45722	anti-glycoprotein	186	439.5	12.5	135	2	PH1493	Ig heavy chain V r
114	465	13.2	118	2	S38717	Ig heavy chain V r	187	439.5	12.5	136	2	B47159	Ig heavy chain V r
115	465	13.2	233	2	S29577	Ig light chain - r	188	439.5	12.5	140	2	PH1488	Ig heavy chain V r
116	464.5	13.2	121	2	F37266	Ig heavy chain V r	189	439.5	12.5	231	2	S25738	Ig lambda chain -
117	464.5	13.2	592	2	S25705	Ig mu chain - shee	190	439.5	12.5	235	2	S25750	Ig lambda chain -
118	464	13.2	136	2	JL00077	Ig heavy chain pre	191	439	12.5	111	2	S25045	Ig heavy chain V r
119	464	13.2	572	2	B46529	Ig y heavy chain (192	439	12.5	123	2	S60067	Ig heavy chain V r
120	463.5	13.2	140	2	PH1482	Ig heavy chain V r	193	438.5	12.5	121	2	S40551	Ig heavy chain V r
121	463	13.1	509	2	S17597	Ig delta chain (WI	194	438.5	12.5	233	2	S25752	Ig lambda chain -
122	462	13.1	113	2	S55535	Ig heavy chain V r	195	438	12.4	115	2	B25924	Ig kappa chain pre
123	461.5	13.1	121	2	A26405	Ig heavy chain V r	196	437.5	12.4	119	2	PH1521	Ig heavy chain V r
124	461.5	13.1	123	2	F48677	Ig heavy chain V-D	197	437.5	12.4	138	1	HVMS17	Ig heavy chain pre
125	461	13.1	113	2	S55534	Ig heavy chain V r	198	437.5	12.4	216	2	S29258	Ig lambda chain V
126	461	13.1	171	2	S23623	Ig heavy chain V r	199	437.5	12.4	329	2	S00847	Ig gamma-2c chain
127	460.5	13.1	138	2	PH0105	anti-digoxin trans	200	437	12.4	109	2	S25038	Ig heavy chain V r
128	460	13.1	127	2	S04577	Ig kappa chain pre	201	437	12.4	111	2	S25034	Ig heavy chain V r
129	459.5	13.0	117	2	S03305	Ig heavy chain V r	202	437	12.4	118	2	S36265	Ig heavy chain V r
130	459.5	13.0	122	2	S20643	Ig heavy chain V r	203	437	12.4	249	2	S69340	Ig heavy chain VHI
131	459.5	13.0	138	2	S21810	Ig heavy chain V r	204	436.5	12.4	140	2	S26318	Ig heavy chain V r
132	459	13.0	119	2	A24672	Ig heavy chain pre	205	436.5	12.4	140	2	S04575	Ig heavy chain pre
133	458.5	13.0	111	2	PH0990	Ig heavy chain V r	206	436.5	12.4	233	2	S25747	Ig lambda chain -
134	458.5	13.0	138	2	S32513	Ig heavy chain pre	207	436	12.4	107	2	D53285	Ig kappa chain V a
135	458	13.0	115	2	A54378	Ig heavy chain V r	208	436	12.4	110	2	PH0995	Ig heavy chain V r
136	458	13.0	117	2	S25176	Ig heavy chain V r	209	436	12.4	120	2	F28195	Ig heavy chain V r
137	458	13.0	122	2	S24287	Ig heavy chain V r	210	436	12.4	213	2	S21066	Ig lambda chain V
138	457.5	13.0	123	2	E48677	Ig heavy chain V-D	211	435.5	12.4	121	2	PL0281	Ig heavy chain V r
139	457	13.0	106	1	K1RTB	Ig kappa chain C r	212	434	12.3	116	2	S26309	Ig heavy chain V r
140	455	12.9	110	2	PH1000	Ig heavy chain V r	213	434	12.3	217	2	JE0246	Ig lambda chain NI
141	454.5	12.9	118	2	S38565	Ig heavy chain V r	214	433.5	12.3	119	2	PH1520	Ig heavy chain V r
142	454.5	12.9	118	2	PL0200	anti-DNA autoantib	215	433.5	12.3	120	2	S03471	Ig heavy chain V-D
143	454.5	12.9	139	2	S03077	Ig heavy chain V r	216	433	12.3	102	2	S42176	Ig gamma chain V r
144	454.5	12.9	138	2	S45249	Ig heavy chain pre	217	433	12.3	111	2	S25051	Ig heavy chain V r
145	454	12.9	113	2	S25041	Ig heavy chain V r	218	433	12.3	113	2	S55533	Ig heavy chain V r
146	454	12.9	137	1	G2MS43	Ig heavy chain pre	219	433	12.3	115	2	PL0238	Ig heavy chain V r
147	453.5	12.9	113	2	PH0974	Ig heavy chain V r	220	433	12.3	120	1	MHMS15	Ig heavy chain V r
148	453.5	12.9	140	2	PH1489	Ig heavy chain V r	221	432.5	12.3	118	2	PL0231	Ig heavy chain V r
149	453	12.9	116	2	S53751	antibody Fab Jel 1	222	432.5	12.3	118	2	A24754	Ig heavy chain V r
150	452.5	12.8	119	2	S20640	Ig heavy chain V r	223	432.5	12.3	135	2	PH1492	Ig heavy chain V r
151	452	12.8	111	2	S25048	Ig heavy chain V r	224	432.5	12.3	231	2	S25753	Ig lambda chain -
152	452	12.8	235	2	S20000	Ig light chain pre	225	432	12.3	113	2	S55528	Ig heavy chain V r
153	450.5	12.8	140	1	HVMSG7	Ig heavy chain pre	226	431.5	12.3	111	2	PH0994	Ig heavy chain V r
154	450	12.8	115	2	C27563	Ig heavy chain V r	227	431.5	12.3	114	2	S20707	Ig heavy chain V r
155	450	12.8	118	2	S37201	Ig heavy chain V r	228	431.5	12.3	119	2	PH1502	Ig heavy chain V r
156	450	12.8	232	2	S25756	Ig heavy chain V r	229	431	12.2	111	2	S25054	Ig heavy chain V r
157	449.5	12.8	233	2	S25744	Ig lambda chain -	230	431	12.2	111	2	S25031	Ig heavy chain V r
158	448.5	12.7	111	2	PH0992	Ig heavy chain V r	231	431	12.2	145	2	PL0014	Ig kappa chain pre
159	447	12.7	108	2	PH0975	Ig heavy chain V r	232	430.5	12.2	140	2	PH1483	Ig heavy chain V r
160	447	12.7	113	2	S25044	Ig heavy chain V r	233	430	12.2	113	2	S55532	Ig heavy chain V r
161	446	12.7	118	2	K30560	Ig heavy chain V r	234	429.5	12.2	140	2	PH1486	Ig heavy chain V r
162	446	12.7	109	2	G28195	Ig heavy chain V r	235	429.5	12.2	140	2	PH1498	Ig heavy chain V r
163	446	12.7	333	2	PS0018	Ig gamma-2b chain	236	429.5	12.2	231	2	S25751	Ig lambda chain -
164	445.5	12.6	105	2	PH0978	Ig heavy chain V r	237	429	12.2	111	2	S25030	Ig heavy chain V r
165	445.5	12.6	121	2	A21854	Ig heavy chain V r	238	429	12.2	113	2	S55531	Ig heavy chain pre
166	445.5	12.6	131	2	A21472	Ig heavy chain pre	239	429	12.2	135	2	A30577	Ig heavy chain V r
167	445	12.6	111	2	S25052	Ig heavy chain V r	240	428.5	12.2	110	2	S26317	Ig lambda chain (B
168	444.5	12.6	109	2	PH0973	Ig heavy chain V r	241	428.5	12.2	216	2	A42193	Ig heavy chain V r
169	444.5	12.6	111	2	PH0993	Ig heavy chain V r	242	428	12.2	97	2	PH1137	Ig heavy chain V r
170	444.5	12.6	117	2	JC3269	PL7-6 antibody hea	243	427.5	12.1	114	2	A27563	Ig heavy chain V r
171	444.5	12.6	228	2	S25575	Ig light chain - r	244	427.5	12.1	119	2	PH1504	Ig heavy chain V r
172	444	12.6	111	2	S25055	Ig heavy chain V r	245	427.5	12.1	119	2	PH1512	Ig heavy chain V r
173	444	12.6	1005	2	T18537	Ig heavy chain - c	246	427.5	12.1	235	2	S05270	Ig lambda chain pr
174	443	12.6	107	2	S09964	Ig kappa chain V-J	247	427	12.1	111	2	S25040	Ig heavy chain V r
175	443	12.6	108	2	PH0977	Ig heavy chain V r	248	427	12.1	118	2	PL0084	Ig heavy chain V r

Db 200 LYTSSSVTVTSWPSSQITCNVAHPASSTKVDKIEPR-----GPTIKPCP----- 247

QY 241 SELQGTALGNLKOIYYNSKAITSSSEKADQFLTNLLFKGFFTGHPWYNLDLVLGSTA 300

Db 248 ----- 247

QY 301 ATSEYEGSSVDLYGAYGYQCAGTGNKTCMVGTVLHNNRLTEBKKVPINLWIDGKQ 360

Db 248 -----PKCPAPN-----LLGGPSVF----- 263

QY 361 TTVPIDKVKTSKKEVTVQELDLQARHVLHGKFGLYNSDSFGGKVORGLIVPHSSEGSTVS 420

Db 264 -----IFPPKIKOVIMI-----SLSPVIT 282

QY 421 YDLFDAQQGYPDTLRLRIYRDNTTISSTLSISLYLTTISVMQTPTPTSLLSVAGDRVTIT 480

Db 283 CVVDVSEDDPD-----VQISWFWANNVEHTAQTI----- 313

QY 481 CKASQSVSNDAVMYQQKPGQSKLLISYTSRYAGVDPDRFSGSGYGTDFTLTISVQAE 540

Db 314 -----HREDYNSTLRV----- 325

QY 541 AAVYFCQDYNSPPTFGGKLEIKRAD-----AAPTVSIFPPSSSEQLT 584

Db 326 SALPIQHODMWSKEF-----KCKVNNKDLPAPIERTISKPGSVRAPQVTVLPPPEEMT 381

QY 585 SGGASVVCFLNNFYPKDINVKKIDGSEKQ-----GVLSNWDQDSKDSYMSSTLTL 639

Db 382 KKQVTLTCMVDWPDIEDIYVETWNGKTELNYKTEPVLDS-----DGSYFWYKLRV 434

QY 640 TKDEYERHNNYTCETHK-TSTSPIVKSFNR 669

Db 435 EKKNWVERNSYSCSVVHEGLHNNHTTKFSR 465

RESULT 6

A28664

Enterotoxin A precursor - Staphylococcus aureus

C;Species: Staphylococcus aureus

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C;Accession: A28664; A29566

R;Betley, M.J.; Mekalanos, J.J.

J. Bacteriol. 170, 34-41, 1988

A;Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.

A;Reference number: A28664; MUID:88086892; PMID:3335483

A;Accession: A28664

A;Molecule type: DNA

A;Residues: 1-257 <BET>

A;Cross-references: UNIPROT:P13163; UNIPARC:UPI000012A273; GB:M18970; NID:g153120; PIDN:

A;Experimental source: strain FR1337

R;Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.

J. Biol. Chem. 262, 7006-7013, 1987

A;Title: Complete amino acid sequence of staphylococcal enterotoxin A.

A;Reference number: A29566; MUID:87222293; PMID:3584106

A;Accession: A29566

A;Molecule type: protein

A;Residues: 25-241,'S',243-257 <HUA>

A;Cross-references: UNIPARC:UPI00001766F5

C;Genetics:

A;Gene: entA

A;Map position: 6

C;Superfamily: enterotoxin B

Query Match 26.9%; Score 948; DB 2; Length 257;

Best Local Similarity 76.4%; Pred. No. 1.5e-42;

Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKADQFLTNLLFKGFFTG 285

Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHQFLQHTILFKGFFTD 84

QY 286 HPWYNLDLVLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTCMVGTVLHNNRLT 345

Db 85 HSWYNLLVDFDSKOIVDKYKGGKVDLYGAYGYQCAGTGNKTCMVGTVLHNNRLT 144

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHVLHGKFGLYNSDSFGGKVQ 405

Db 145 EEKVPINLWIDGKQNTVPLETVKTKNKNVTYQELDLQARRYLOEKYLNYSNDFDGKVQ 204

QY 406 RGLIVPHSSEGSTVSVDLFDQAQQYDPDTLLRIYRDNTTISSTLSISLYLTT 458

Db 205 RGLIVHTSTEPSVNYDLFQAQQYSGNTLLRIYRDNKTINSENMHIDIVLYTS 257

RESULT 7

S38864

Ig epsilon chain C region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001

C;Accession: S38864

R;Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A;Description: Combination of a defined specificity and desired isotype by cloning of an

A;Reference number: S38864

A;Accession: S38864

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-548 <KIP>

A;Cross-references: UNIPARC:UPI00001165CC; EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PI:

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;353-421/Domain: immunoglobulin homology <IMM>

Query Match 26.4%; Score 931; DB 2; Length 548;

Best Local Similarity 35.0%; Pred. No. 2.9e-41;

Matches 241; Conservative 83; Mismatches 186; Indels 178; Gaps 19;

QY 1 EVLOQOSGPDLVKPGASVKISKASGYFTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60

Db 1 QVKLESGGDLVKPGSLKSLCAASGLTFSSYKMSWRQIPDKLEWVATISSGGITYY 60

QY 61 NQKFKDKATLVDKSSTTAYMELRSLTSEDSAVYCARSTMITNYVMYDYGQTSVTSS 120

Db 61 PDSVKGRFTISRDNAKNTLYLQMSLSKSEDTAMYYCARQGVSTMIRFAYWGQGLTVTSA 120

QY 121 AKTTPSVVPLAPGSAQNTNSMTLGLVKGYPPEVTVTNWNSLSGSHVHTPAVLQSD 180

Db 121 GKTTPSVVPLAPGSAQNTNSMTLGLVKGYPPEVTVTNWNSLSGSHVHTPAVLQSD 180

QY 181 LYTSSSVTVPSSTWPSSETVCNVAHPASSTKVDKIVPRDSG-----GPSEKSEET--- 232

Db 181 LYTSSSVTVPSSTWPSSETVCNVAHPASSTKVDKIVPRDCGCKPCIVPESSVFIFPP 240

QY 233 NEKDLRKSELO-----GTALGNLKOIYYNSKAITSSSEKADQFLTNLLFKGFFTG 286

Db 241 KPKDVLTRSTIQLCYFIYGHILNDVSVWLMDREITDT-----LAQTVLIK----- 287

QY 287 PWYNLDLVLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTCMVGTVLHNNRLTE 346

Db 288 -----EEGLASTCSKLNITEQQMMSESTFCK-----VTSQVDYLAH 326

QY 347 EKKVPINLWIDGKQTV-----PIDKVKTSKKEVTVQELDLQARHVLHGKFGLYNSD 398

Db 327 TRCP-----DHEPRGVITYLPPSPDLIYQNGAPKLTCLVVDLESEKVN----- 372

QY 399 SFGKVQVORGLIVPHSSEGSTVSVDLFDQAQQYDPDTLLRIYRDNTTISSTLSISLYLTT 458

Db 373 -----VTWNQEKTSVS-----ASQWYTK-----HNNNATTSITSI----- 403

QY 459 SIWMTQPTSLLSVAGDRVTITCKASQSVSNDAVMYQQKPGQSKLLISYTSRYAGVDP 518

Db 404 -----LPVAKD-----WIE----- 413

QY 519 RFGSGYGTDFTLTISVQAEAAVYFCQDYNSS--PPTFGGQTKLEIKRADAPTVSIF 576

Db 414 -----GYG-----YQCIVDHPDFPKPIVRSITKTPGQR--SAPEYVVF 449

```
QY 577 PPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDS--YSMS 634
Db 450 PPEEE-SDKRTLTLCLIONFFPEDISVOMLGGKLSNSQHSSTTPLLKNSGNSRGGFFIP 508
QY 635 STLTLTDKDEYERHNSYTCBATHKTS 662
Db 509 SRLVAKTLWTQRKQFTCCVIHEALQKP 536

RESULT 8
S38950
Ig gamma chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S38950
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bi
Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha
A:Reference number: S38950; MUID:94128242; PMID:8297501
A:Accession: S38950
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-246 <KLE>
A:Cross-references: UNIPARC:UPI0000176F3B
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 26.4%; Score 929; DB 2; Length 246;
Best Local Similarity 78.5%; Pred. No. 1.3e-41;
Matches 179; Conservative 18; Mismatches 25; Indels 6; Gaps 2;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYSTFTYMMHWKQSPGKLEWIGRIINPNNGVTLY 60
Db 1 QIQLQSGDPLVKPGASVKISCKASGYSTFTDYIHWKQRPGEGLWIGWIYPGSGNTKY 60

QY 61 NQKFKDKATLTVDKSSTTAYMELRSITSDSAVYVCARSTMTNVMYMGQGSTVTS 120
Db 61 NEKFKDKATLTVDTSSTAYMQSSITSDSAVFCARG---GKFANDYMGQGSTVTS 117

QY 121 AKTTPSPVPLAPGSAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGHTFPAVLQSD 180
Db 118 AKTTPSVPLAPVCGDITGSSVTLGCLVKGYFPEPVTVTWNSGSLSSGHTFPAVLQSD 177

QY 181 LYTLSSTVTPSSTWSETVTCNVAHPASSTKVDKIIVRDSCGPSEK 228
Db 178 LYTLSSTVTPSSTWSPSQSITCNVAHPASSTKVDKIEPR---GPTIK 222

RESULT 9
S68212
Ig kappa chain (Mab03-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C:Accession: S68212
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68212
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-214 <TAK>
A:Cross-references: UNIPARC:UPI000017697E; EMBL:D29668
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 26.3%; Score 926; DB 2; Length 214;
Best Local Similarity 83.1%; Pred. No. 1.6e-41;
Matches 177; Conservative 16; Mismatches 14; Indels 6; Gaps 1;

QY 460 IVMTQTPTSLVLSAGDRVITTCASQSVSND-----VAMVQKQPGQSPKLLISYTSRY 513
Db 2 IVMTQSPSSLAMVGQKVMTSKSSQSLNSRNQKVLAWYQKPGQSPKLLVYFPASTR 61
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QY 514 AGVPRFSSGSGYGTDFTLTISSVQAEADAAVFCQDYNSPPTFGGCTKLEIKRAADAPTV 573
Db 62 SGVPRFPGSGSGTDFTLTISTVQAEADLADYFCQHYSTPTFGGCTKLEIKRAADAPTV 121
QY 574 SIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYSTSM 633
Db 122 SIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYSTSM 181
QY 634 SSTLTLTDKDEYERHNSYTCBATHKTSPIVKS 666
Db 182 SSTLTLTDKDEYERHNSYTCBATHKTSPIVKS 214

RESULT 10
C89984
enterotoxin p [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: C89984
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: C89984
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <KUR>
A:Cross-references: UNIPROT:Q99SU3; UNIPARC:UPI000000C7F8A; GB:BA000018; PID:g13701743; P;
A:Experimental source: strain N315
C:Genetics:
A:Gene: sep
C:Superfamily: enterotoxin B

Query Match 26.1%; Score 918; DB 2; Length 260;
Best Local Similarity 73.0%; Pred. No. 5.4e-41;
Matches 170; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 226 SKSSEINEKDLRKSELGQTALGNLQIYYNYSKAITSSSEKSAQDFLTNTLLFKGFFTG 285
Db 28 SKSSEINGKDLQKSELQGTALSNLRQTYHNGSAIIENKESNDQFLKNTILFNDFFTG 87

QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAVYGYOCAGGTGNKTCACMGYGVTLHDNNRLT 345
Db 88 HQWYNDLLVDLGSKDGTANIYKGGKVDLYGVYGYQCTGTPFKTACMGYGVTLHDNNQLE 147

QY 346 EEKVPINLWIDGKQTTVPIDKVTSSKKEVTVQELDLQARHYLHGKFLGYNDSFGGRVQ 405
Db 148 EEKVPINLWIDGKQNTVPLGTVTNKKEVTVQELDLQSRHYLHETVNTYNTDAFNGKIQ 207

QY 406 RGLIVPHSSEGTYSVDLPDAQGVPTDLLRIYRNTTISSTLSLSLYLYTT 458
Db 208 RGLIEFHPSSGSDVGLFPGAQGVPTQLRIYRDNKTIKSNMHIDIYLYTT 260

RESULT 11
S52028
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S52028
R:van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkee, W.G.; Schots, A.;
submitted to the EMBL Data Library, August 1994
A:Description: Coordinate expression of antibody subunit genes yields high levels of fun
A:Reference number: S52028
A:Accession: S52028
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <VAN>
A:Cross-references: UNIPARC:UPI0000114B22; EMBL:L35138; NID:G522336; PID:AAA67525.1; PII
C:Superfamily: immunoglobulin V region; immunoglobulin homology
```


RESULT 29

S68211
IG heavy chain (Mab13-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 20-Jun-2000
C;Accession: S68211
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A;Reference number: S68211; MUID:96085223; PMID:7498516
A;Accession: S68211
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-220 <TAK>
A;Cross-references: UNIPARC:UPI000011B261; EMBL:D29669; NID:g473956; PIDN:BA06140.1; PT
A;Note: the sequence of residues 1-4, 213-220 and the corresponding nucleotide sequence
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;136-200/Domain: immunoglobulin homology <IMM>

Query Match 22.9%; Score 808; DB 2; Length 220;
Best Local Similarity 70.2%; Pred. No. 2.3e-35;
Matches 153; Conservative 24; Mismatches 37; Indels 4; Gaps 2;
QY 6 QSGPDLVKPGASVKISKASGYFTGYMHVWKQSPGKLGLEWIG--RINPNNGVTLYNQK 63
DB 2 ESGGGLVRPNSLKLISCLTSGFTFSNRMHWRQPPGKRLIEWIAVITVKSNDYGAAYES 61
QY 64 FKDKATLTVDKSSSTTAYMELRSLTSDSAVYICARSTMTITNYVDYWGQGTSTVTVSSAKT 123
DB 62 VRGRFTISRDDKSSVYLNWRNREEDTAYYICRFPW--YAMDCWGQGTSTVIVSSAKT 119
QY 124 TPSPVYPLAPGSAQAQTNSMTVTLGCLVKGYPEPPTVYTNWNSGSLSSGVVHTTTPAVLQSDLYT 183
DB 120 TPSPVYPLAPGSAQAQTNSMTVTLGCLVKGYPEPPTVYTNWNSGSLSSGVVHTTTPAVLQSDLYT 179
QY 184 LSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRD 221
DB 180 LSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRD 217

RESULT 30

S68213
IG heavy chain (Mab03-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jul-1997 #sequence_revision 17-Sep-1997 #text_change 31-Dec-2004
C;Accession: S68213
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A;Reference number: S68213; MUID:96085223; PMID:7498516
A;Accession: S68213
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-213 <TAK>
A;Cross-references: UNIPROT:Q91Z05; UNIPARC:UPI0000176F3F; EMBL:D29667
C;Superfamily: immunoglobulin homology
F;137-201/Domain: immunoglobulin homology <IMM>

Query Match 20.9%; Score 737.5; DB 2; Length 213;
Best Local Similarity 64.7%; Pred. No. 1e-31;
Matches 139; Conservative 29; Mismatches 44; Indels 3; Gaps 1;
QY 2 VQLQSQGPDLVKPGASVKISKASGYFTGYMHVWKQSPGKLGLEWIGRINPNNGVTLYN 61
DB 2 VQLVESGGGLVQPGGSKLSCAASGFTFSFGHHWRQRAPEKLEWVAIYSSGSSSIYA 61
QY 62 QKPKDKATLTVDKSSSTTAYMELRSLTSDSAVYICARSTMTITNYVDYWGQGTSTVTVSSA 121
DB 62 DTVKGRFTISRDRPNKNTFLQMTSLASEDTAMTYICARSWLLP---FDYWGQGTTLTVSSA 118
QY 122 KTTTPSVYPLAPGSAQAQTNSMTVTLGCLVKGYPEPPTVYTNWNSGSLSSGVVHTTTPAVLQSD 191
DB 119 KTTTPSVYPLAPGCGDTTSGSVTLGCLVKGYFPESVTVYTNWNSGSLSSSVHTTTPALLQSG 178

QY 182 YTLSSSVTPSPSTWSPSETVTCNVAHPASSTKVDK 216
DB 179 YTMSSSVTPSPSTWSPSQVTCTCSVAHPASSTTVDKK 213

RESULT 31

PC4155
IG gamma-2b chain V-C region Mab823 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
C;Accession: PC4155
R;Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
Gene 169, 237-239, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mor
A;Reference number: PC4155; MUID:96194809; PMID:8647454
A;Accession: PC4155
A;Molecule type: mRNA
A;Residues: 1-231 <KWA>
A;Cross-references: UNIPARC:UPI00001157CB; GB:U28970; NID:g1262180; PIDN:AAC52489.1; PID
A;Note: This protein has unusual amino acid compared with the conserved sequences of mou
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;1-231/Product: heavy chain #status predicted <MAT>
F;98-102/Region: unique D sequence
F;103-119/Region: V region
F;139-203/Domain: immunoglobulin homology <IMM>

Query Match 20.3%; Score 715; DB 2; Length 231;
Best Local Similarity 60.9%; Pred. No. 1.6e-30;
Matches 137; Conservative 29; Mismatches 55; Indels 4; Gaps 2;
QY 1 EVQLVDSGPDLVKPGASVKISKASGYFTGYMHVWKQSPGKLGLEWIGRINPNNGVTLY 60
DB 1 EVQLVESGPGLVAPQSLSITCTVSGFSLTDYGVSMIRQPPGKLGLEWGIWA--GGSTFY 59
QY 61 NQFKDKATLTVDKSSSTTAYMELRSLTSDSAVYICARSTMTITNYVDYWGQGTSTVTVSS 120
DB 60 NSALKSRLSINKDNKSKQVFLKMNLSLHTDNTANYCYCKHEDRYDWFVDMGAGTTVTVSS 119
QY 121 AKTTTPSVYPLAPGSAQAQTNSMTVTLGCLVKGYPEPPTVYTNWNSGSLSSGVVHTTTPAVLQSD 180
DB 120 AKTTTPSVYPLAPRCGDTTSGSVTLGCLVKGYFPESVTVYTNWNSGSLSSSVHTTTPALLQSG 179
QY 181 LYTLSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRDSSGP 225
DB 180 LYTMSSSVTPSPSTWSPSQVTCTCSVAHPASSTTVDKKLEP---SGP 221

RESULT 32

JE0244
IG kappa chain NIG2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0244
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takada, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy
A;Reference number: JE0243
A;Accession: JE0244
A;Molecule type: protein
A;Residues: 1-215 <ALI>
A;Cross-references: UNIPARC:UPI0000176982
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 19.9%; Score 702.5; DB 2; Length 215;
Best Local Similarity 62.1%; Pred. No. 6.7e-30;
Matches 133; Conservative 36; Mismatches 42; Indels 3; Gaps 2;
QY 460 IVMTQPTSLVVSAGDRVTITCKASQSVNDVAWYQKQSPKLLISYTSRSSVAGVPDR 519
DB 2 VLTQSPATLSVSPGSRATLSCSRASQSVHSNLAWYQKQPGQPRLLIYRASTRATGIPAR 61

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 19.4%; Score 683.5; DB 2; Length 254;
 Best Local Similarity 63.8%; Pred. No. 8e-29;
 Matches 146; Conservative 22; Mismatches 48; Indels 13; Gaps 8;

QY 1 EVOLQSGDPLVPGASVKLSCKASGVSFTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
 DB 1 EVOLVESGGLVPGGSLKLSCAASGFSFGYMSWVRQTPDKRLEWVATISNGGGYTY 60

QY 61 NQFKDKATLVNKSSTAYMELRSLTSDSAVYICARSTMTIYMYDMYQGQTSVTSS 120
 DB 61 PDSVKGRTISLNAKNTLVQMSLSDSAMYICARRRYDENGFAYMGQGLVTVSA 120

QY 121 AKTTTPSVYPLAP--GSAATQNSMVTGLCLVKGVFPFPTV-TW----NSGSLSSG-VHT 172
 DB 121 AKTTAPSVYPLAPVCGXXDTTGSSTVLGLCLVKGVFPFPTVLTWXXXNKSLSGSGVHT 180

QY 173 FPAVLQS--DLYTLSSSVTPSS--TWP-SETVT--CNVAHPASSTKVDKK 216
 DB 181 FPAVLQSXXDLYTLSSSVTVTSSXTWPSQSIIXCNVAHPASSTKVDKK 229

RESULT 36
 JE0243
 Ig kappa chain NIG93 precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C;Accession: JE0243
 R;Alim, M.A.; Hara, Y.; Hoesain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
 submitted to JIPID, November 1998
 A;Description: A new subgroup of k type light chains (Vk) identified in cases of AL amy
 A;Reference number: JE0243
 A;Accession: JE0243
 A;Molecule type: protein
 A;Residues: 1-215 <Ali>
 A;Cross-references: UNIPARC:UPI0000176984
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 19.3%; Score 679.5; DB 2; Length 215;
 Best Local Similarity 61.0%; Pred. No. 1e-28;
 Matches 130; Conservative 33; Mismatches 49; Indels 1; Gaps 1;

QY 460 IVMTQPTSLVSGADRVITICKASQSVNDVAWYQKPGQSKLLISYTSRYAGVPDR 519
 DB 2 IVMTQSPATLSVPGERATLSCKASQSVATVVMYQKLGQAPRLLIYDASTATGVPAR 61

QY 520 FSGSGYGTDTLTITSSVQAEAAVYFCQDYNPPTFGGQTKLEIKRAD-AAPTSTIFPP 578
 DB 62 FSGSGSGTEFTLTITSLQSEDFAIYQCQHNAPPTFGQTKVETKRTVAAPSVFIFPP 121

QY 579 SSQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTDQDSKSTYSMSSTLT 638
 DB 122 SDEQLKSGTASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTDQDSKSTYSMSSTLT 181

QY 639 LTQDEYERHNSYTCETHKTSPIVKSFNRE 671
 DB 182 LSKADYKHKVYACEVTHQGLSSPVTXSNRGE 214

RESULT 37
 S33161
 Ig kappa chain - sheep
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
 C;Accession: S33161
 R;Foley, R.C.; Beh, K.J.
 submitted to the EMBL Data Library, July 1990
 A;Description: Isolation and characterisation of sheep kappa light chain cDNA.
 A;Reference number: S33161
 A;Accession: S33161
 A;Status: preliminary

A;Molecule type: mRNA
 A;Residues: 1-230 <FOL>
 A;Cross-references: UNIPARC:UPI0000113789; EMBL:X54110; NID:g297103; PIDN:CAA38046.1; PFI
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F;143-212/Domain: immunoglobulin homology <IMM>

Query Match 19.2%; Score 675; DB 2; Length 230;
 Best Local Similarity 59.4%; Pred. No. 2e-28;
 Matches 126; Conservative 37; Mismatches 49; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVSGADRVITICKASQSVNDVAWYQKPGQSKLLISYTSRYAGVPDR 519
 DB 18 IQVTFSSLSASLTERSVITCTOSVSNLYWYQKPGQAPKLLIYYATRLHTDVPSR 77

QY 520 FSGSGYGTDTLTITSSVQAEAAVYFCQDYNPPTFGGQTKLEIKRAD-AAPTSTIFPPS 579
 DB 78 FSGSGSGTDTLTITSLNLEANDTATYCLQVESYFLAFGGGTNVEIKRSDQPSVFLFKPS 137

QY 580 SEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTDQDSKSTYSMSSTLT 639
 DB 138 EEQLRTGTVSVVCLVNDFFPKDINVKVKVDGVTQNSFNQSFDTQDSKSTYSLSSTLT 197

QY 640 TKDEYERHNSYTCETHKTSPIVKSFNRE 671
 DB 198 SSSEYQSHNAYACEVSHKSLPTALVKFSFNKNE 229

RESULT 38
 S22080
 Ig heavy chain precursor (B/Mt.4A.17.H5.A5) - bovine
 A;Alternate names: Ig gamma-1 chain C region (clone 8.10)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C;Accession: S22080; S06610; A31303
 R;Sanders, P.G.
 submitted to the EMBL Data Library, November 1991
 A;Reference number: S22080
 A;Accession: S22080
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-470 <SAN>
 R;Cross-references: UNIPARC:UPI0000116007; EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g
 Mol. Immunol. 26, 841-850, 1989
 A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma
 A;Reference number: S06610; MUID:90097956; PMID:2513487
 A;Accession: S06610
 A;Molecule type: DNA
 A;Residues: 142-470 <SYM>
 A;Cross-references: UNIPARC:UPI0000176F36; EMBL:X16701
 A;Note: the sequence was determined from the germline gene
 C;Genetics:
 A;Gene: Ig CH gamma-1
 A;Introns: 98/1; 111/1; 221/1
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: glycoprotein; heterotrimer; immunoglobulin; membrane protein
 F;161-225/Domain: immunoglobulin homology <IMM>
 F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.1%; Score 673.5; DB 2; Length 470;
 Best Local Similarity 28.1%; Pred. No. 5.7e-28;
 Matches 187; Conservative 78; Mismatches 161; Indels 239; Gaps 18;

QY 1 EVOLQSGDPLVPGASVKLSCKASGVSFTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
 DB 20 QVQLRESGSLVKPSQTLSTCTVSGFSJSSYALTWVRQAPGKALEWVGIT--SGGTYY 78

QY 61 NQFKDKATLVNKSSTAYMELRSLTSDSAVYICARST---MITNYMDYMQGQTSVT 117
 DB 79 NPALKSRLSITKSNKSKQSVLSVSSVTPTATYICARSTYGEVGDGAIADAGQGLVT 138

QY 118 VSSAKTTPSVYPLAPGSAQAQTNMSMTLGLCLVKGVFPFPTVTVNWSGLSSGVHTFPAVL 177

Db	139	VSSASTTAKVYPLSSCCGKSSVTTLGCLVSSYMPPEVPTVWNSGALKSGVHTPEAVL	198
Qy	178	QSD-LYTLSSSVTPSTPSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKD	236
Db	199	QSSGLYLSLSSVTPGSGT-SGQFTTCNVAHPASSTKVDKAVDPTCKPSPC-----D	248
Qy	237	LRKKSLOGTALGNLQIYYNSKAITSEKSAQDLTWLLFKPGFTGHPWYNDLLVDL	296
Db	249	CCPPPELPGG-----PSVFIFPPKP-----KDTLT-----ISGTPEVTCVVVDV	287
Qy	297	GSTAATSEYEGSSVDLYGAYVYQACAGTGNKTACMYGVVTLHDNNRLTEKKVPINLWI	356
Db	288	G-----HD-----DEVKFSWFV	300
Qy	357	DGKQ-----TTVPIDKVKTSKEVTVQELDLQARHYLHGKFLGYNSSDFGKRVQRLIVPH	412
Db	301	DVEVNTATTKPREQFNSTYRV-VSALRIQHDMTGK-----EFCKVH-----	345
Qy	413	SSEGSTVSVDLFDACQOQYPTLLRIYRDNTTISSTLSLSLYLYTTSIVMTQTPTSLLVS	472
Db	346	-NEG-----LPAPIVR-----TISRT-----	360
Qy	473	AGDRVTTTCKASQSVNDVAWYQKPGQPKLLISYTSRKYAGVPDRFSGSGYGTDFTLT	532
Db	361	-----KGPARPQ-----	368
Qy	533	ISSVQAEAAVFCQDYNSPPFTFGGKTKLEIKRADAAPTIVSIFPPSSQOLTSGGASVVC	592
Db	369	-----VVVLAPPQBELSKSTVSLTC	388
Qy	593	FLNNFPKIDINVWKIDGSRQGVNLNSWTDQDSKDSYMSSTLTTLTKDEYERHNSYTC	652
Db	389	MVTSFYEDYIAVEWQRNGQPESDKYGTTPQLQDADSSYFLYSLKLVDRNSWQEGDTYC	448
Qy	653	EATHK	657
Db	449	VNWE	453
RESULT 39			
S29593			
Ig kappa chain (WM65) - mouse (fragment)			
C:Species: Mus musculus (house mouse)			
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000			
A:Accession: S29593			
R:Seymour, R.			
submitted to the EMBL Data Library, February 1991			
A:Reference number: S29593			
A:Accession: S29593			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-197 <SEY>			
A:Cross-references: UNIPARC:UPI0000115F08; EMBL:X57856; NID:G52588; PIDN:CAA40991.1; PID			
C:Superfamily: immunoglobulin V region; immunoglobulin homology			
C:Keywords: heterotetramer; immunoglobulin			
Query Match 18.8%; Score 663.5; DB 2; Length 197;			
Best Local Similarity 72.9%; Pred. No. 6.4e-28;			
Matches 132; Conservative 16; Mismatches 28; Indels 5; Gaps 2;			
Qy	460	IWVTOPTTSLVYSGDRVTITCKASQSV--SND--VAWYQKPGQSPKLLISYTSRVA	514
Db	17	IWVTOAAPISVTPGSGASISCKSSLLHSNGDTLYWFLQKPGQSPQLLIYRMSNLAS	76
Qy	515	GVPDRFSGSGYGTDFLTITSSVQAEAAVYFCQDYNSPPTFGGKTKLEIKRADAAPTYS	574
Db	77	GVPDRFSGSGSTSLRISRVEADVGFVFCQHLEYPYTFGGGKTKLEIKRADAAPTYS	136
Qy	575	IPPPSEQLTSGGASVVCFLNNFPKIDINVWKIDGSRQGVNLNSWTDQDSKDSYMS	634
Db	137	IPPPSEQLTSGGASVVCFLNNFPKIDINVWKIDGSRQGVNLNSWTDQDSKDSYMS	196

Qy	635	S	635
Db	197	S	197
RESULT 40			
S69131			
Ig heavy chain (DOT) - human (fragment)			
N:Alternate names: anti-riboflavin Igg Fd fragment			
C:Species: Homo sapiens (man)			
C:Date: 12-Feb-1998 #sequence_revision 22-May-1998 #text_change 21-Jan-2000			
A:Accession: S69131			
R:Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.			
Eur. J. Biochem. 228, 886-893, 1995			
A:Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins.			
A:Reference number: S69130; MUID:95255298; PMID:7737190			
A:Accession: S69131			
A:Molecule type: protein			
A:Residues: 1-241 <STO>			
A:Cross-references: UNIPARC:UPI0000176F40			
C:Superfamily: immunoglobulin C region; immunoglobulin homology			
C:Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglytamic acid			
F:1-241/Product: Ig heavy chain (DOT) {fragment} #status experimental <MAT>			
F:140-205/Domain: immunoglobulin homology <IMM>			
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental			
Query Match 18.8%; Score 661.5; DB 2; Length 241;			
Best Local Similarity 59.4%; Pred. No. 1e-27;			
Matches 130; Conservative 35; Mismatches 51; Indels 3; Gaps 3;			
Qy	1	EVQLQQSGDPLVKPGASVKISCKASYFTGYMHVVKQSPGKLEWIGRINPNNGVTLY	60
Db	1	QVQLVQSGVERKVPQASVRIKCKASYAFENYIHVRQAPGLGLEWMGIFNPVAG-AVS	59
Qy	61	NQKFKDKATLTVDKSTTAYMELRSLTSDSVAYYCAR-STMITNYMDYWGQGTSTVYS	119
Db	60	SEKFRDLVMSSDTSANTVSMQLRLSRDDTCRYFCARVSYDFSQGYMDVMWGQGTTVIS	119
Qy	120	SAKTPPSPVYPLAPGSAQTNSMVTLCGLVKYGFPEPTVTWNSGSLSGVHTFPVAVLS	179
Db	120	SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLOS	179
Qy	180	D-LYTLSSSVTPSPSETVTCNVAHPASSTKVDKKI	217
Db	180	SGLYSLSSVTVFPSSNFGTQYTCNVHDHKPSNTKVDKTV	218
RESULT 41			
A23746			
Ig kappa chain V-III (KAU cold agglutinin) - human			
C:Species: Homo sapiens (man)			
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000			
A:Accession: A23746			
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.			
J. Biol. Chem. 266, 2836-2842, 1991			
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglob			
A:Reference number: A23746; MUID:91131575; PMID:1993660			
A:Accession: A23746			
A:Status: preliminary			
A:Molecule type: protein			
A:Residues: 1-215 <LEO>			
A:Cross-references: UNIPARC:UPI0000176985			
C:Superfamily: immunoglobulin V region; immunoglobulin homology			
C:Keywords: heterotetramer; immunoglobulin			
F:16-91/Domain: immunoglobulin homology <IMM>			
Query Match 18.7%; Score 659.5; DB 2; Length 215;			
Best Local Similarity 62.0%; Pred. No. 1.1e-27;			
Matches 132; Conservative 31; Mismatches 49; Indels 1; Gaps 1;			
Qy	460	IWVTOPTTSLVYSGDRVTITCKASQSV-SNDVAWYQKPGQSPKLLISYTSRVA	518
Db	2	IVLTQSPATLSLSPGERATLISGASQSVSNLYAWYQKPGQAPRLIIYDASSRATGIPD	61

C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 1-70/Domain: V region (fragment) <VR>
F; 12-18/Region: complementarity-determining 1
F; 19-51/Region: framework 1
F; 52-60/Region: complementarity-determining 2
F; 61-70/Region: framework 2
F; 71-178/Domain: C region <CR>
F; 96-156/Disulfide bonds: #status predicted
F; 176/disulfide bonds: interchain #status predicted

[illegible]

RESULT 48

A20969

IG kappa chain precursor V-J-C regions - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000

C:Accession: A20969; A25448

R:McCartney-Francis, N.; Skurla Jr., R.M.; Mage, R.G.; Bernstein, K.E.
Proc. Natl. Acad. Sci. U.S.A. 81, 1794-1798, 1984

A:Title: Kappa-chain allotypes and isotypes in the rabbit: cDNA sequences of clones encoding type expression.

A:Reference number: A20969; MUID:84170389; PMID:6424124

A:Accession: A20969

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-229 <MCC>

A:Cross-references: UNIPARC:UPI00001148DA; GB:K01359; NID:G165373; PIDN:AAA31334.1; PTD:R:Akimeno, M.A.; Mariame, B.; Rougeon, P.
Proc. Natl. Acad. Sci. U.S.A. 83, 5180-5183, 1986

A:Title: Evolution of the immunoglobulin kappa light chain locus in the rabbit: evidence from cDNA clones.

A:Reference number: A94110; MUID:86259753; PMID:3088570

A:Contents: Ig kappa-1 chain, 69 allotype, J-KI.2 segment

A:Accession: A25448

A:Molecule type: DNA

A:Residues: 111-123 <AKI>

A:Cross-references: UNIPARC:UPI0000117CE8; GB:M14062; GB:M14063; GB:M14064; GB:M14065

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:143-212/Domain: immunoglobulin homology <IMM>

	Query Match	16.2%	Score 570.5;	DB 2;	Length 229;
	Best Local Similarity	53.0%;	Pred. NO. 5.3e-23;		
	Matches 114;	Conservative 35;	Mismatches 63;	Indels 3;	Gaps 3
Qy	459	SIWMTQPTSLVLSAGDRVTITTCASQSVNSDVAWYQOKPGQSPKLLISYSSRRVAGVDP	518		
Db	15	ALVMTQTPASVAAGVTITIKQSENINYSGLAWYQOKPGQPPKLLIYGASTLASGVPS	74		
Qy	519	RFGSGYGTDFTLTISVQAEADAAYVFC-QQDYNSPPTFGGGTKLEIK-RADAAPTVAISF	576		
Db	75	RFGSRSGTEYLTISGVQREDAATYICLGSDSSDTAFGGGTELEILCDPIAFTVLLF	134		
Qy	577	PPSSEQITSGGASVVCFLNNFPKIDINVWKIKDGSERQNGVLNSWTDQSKDSTYSMSGT	636		
Db	135	PPSADOLTEVTVTCVANKERPNDIITVTKVDDEIOOSGTENSTTPQSPEDCTVNLST	194		

Qy	637	LTLAKDVEYRHNSTCEATHTKSTSPVKSFNRRNE	671
		: : : : :	
Db	195	LSLTKAQINSHSVITCEVHH-NSGSAIVQSFNRGD	228
RESULT 49			
	S29594		
	Ig gamma chain (WM65) - mouse (fragment)		
	C;Species: Mus musculus (house mouse)		
	C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #t		
	C;Accession: S29594		

submitted to the EMBL Data Library, February 1991

A;Reference number: S29593

A;Accession: S29594

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-178 <SEY>

A;Cross-references: UNIPARC:UPI0000115F09; EMBL:X57857; NID:g52590; PIDN:CAA409

C;Keywords: immunoglobulin

RESULT 50

154782 gene Pvt-1a/Ig-Ck protein - mouse (fragment)

C/Species: Mus sp. (mouse)

C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Sep-2000

C/Accession: I54782

R/Huppi, K.; Siwarski, D.

Int. J. Cancer 59, 848-851, 1994

A/Title: Chimeric transcripts with an open reading frame are generated as a

A/Reference number: I54782; MUID:95080867; PMID:7989128

A/Accession: I54782

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-136 <RES>

A/Cross-references: UNIPARC:UPI0000113715; GB:S76258; NID:G913277; PIDN:AAB

C/Genetics:

A/Gene: Pvt-1a/Ig-Ck

C/Superfamily: pre-B cell omega light chain; immunoglobulin homology

	Query Match	15.98;	Score 561;	DB 2;	Length 126;	
	Best Local Similarity	93.08;	Pred. No. 7.7e-23;			
	Matches 107;	Conservative 2;	Mismatches 6;	Indels 0;	Gaps 0	
Qy	557	GGGTKELEKRAADAPT	VS	IFPPSEQITSGGASVVCFLNNFPYKDI	INVKWKIDGSRQNG	616
		::				
Db	11	GAAAKVKSIWADAAPT	VS	IFPPSEQITSGGASVVCFLNNFPYKDI	INVKWKIDGSRQNG	70
Qy	617	VLSNWTDDQSDKSTYS	MS	SLTLTKDYEHRNSYTCETHKTSPIVKSFN	RNE	671
Db	71	VLSNWTDDQSDKSTYS	MS	SLTLTKDYEHRNSYTCETHKTSPIVKSFN	RNE	125

RESULT 51
PL0011
Ig heavy chain precursor V region (4C11) - mouse (fragment)

C;Accession: B02159; A02160; B02158
R;Honjo, T.; Ohta, M.; Yamawaki-Kataoka, Y.; Kataoka, T.; Kawakami, T.; Takahashi, N.;
Cell 18, 559-568, 1979
A;Title: Cloning and complete nucleotide sequence of mouse immunoglobulin gamma1 chain c
A;Reference number: A02159; MUID:80045036; PMID:115593
A;Accession: B02159
A;Molecule type: DNA
A;Residues: 1-393 <HON>
A;Cross-references: UNIPROT:P01869; UNIPARC:UPI00000272D5; GB:J00453
A;Note: the sequence was determined from the germline gene
R;Tyler, B.M.; Cowman, A.F.; Gerondakis, S.D.; Adams, J.M.; Bernard, O.
Proc. Natl. Acad. Sci. U.S.A. 79, 2008-2012, 1982
A;Title: mRNA for surface immunoglobulin gamma chains encodes a highly conserved transme
A;Reference number: A02160; MUID:82197626; PMID:6804950
A;Accession: A02160
A;Molecule type: mRNA
A;Residues: 323-393 <TYL>
A;Cross-references: UNIPARC:UPI00001737A9
R;Rogers, J.; Choi, E.; Souza, L.; Carter, C.; Word, C.; Kuehl, M.; Eisenberg, D.; Wall,
Cell 26, 19-27, 1981
A;Title: Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma c
A;Reference number: A02158; MUID:82115295; PMID:6799207
A;Accession: B02158
A;Molecule type: DNA
A;Residues: 323-366 <ROG>
A;Cross-references: UNIPARC:UPI00001737AA
A;Note: this sequence is the translation of the first exon of the M segment
C;Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The ma
ncode membrane-bound chains in that it contains an alternative 3' end, encoded in separa
C;Genetics:
A;Introns: 1/1; 98/1; 111/1; 218/1; 323/1; 366/3
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F;131-200/Domain: immunoglobulin homology <IMM>
F;340-357/Domain: transmembrane #status predicted <TM>
F;358-393/Domain: intracellular #status predicted <INT>
F;174,278/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.88; Score 557; DB 1; Length 393;
Best Local Similarity 28.34; Pred. No. 5.2e-22;
Matches 156; Conservative 48; Mismatches 89; Indels 258; Gaps 13;

QY 121 AKTTPSVYPLAGSAAQTNSMTGLCLVKGYPPEVTVTWNSGSLSSGVHTTTPAVLQSD 180
|||||
1 AKTTPSVYPLAGSAAQTNSMTGLCLVKGYPPEVTVTWNSGSLSSGVHTTTPAVLQSD 60
|||||

QY 181 LYTLSSTVTPSSSTWPTETTCNVHPASSTKVDKIKIVPRDSGGPSEKSEINEKOLRKK 240
|||||
61 LYTLSSTVTPSSSTWPTETTCNVHPASSTKVDKIKIVPRDCG----- 103
|||||

QY 241 SELQGTALGNLKOIYYNSKATISSEKSAQDFLTNTLLFKGFTGHPYNDLLVDLGSTA 300
: : : : :
104 CKPCICTVPEVSVFIPPPK-----PKDVLTTTL----- 132
: : : : :
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPKTKCMYGGVTLTDHNNLTETKVPINLWIDGKQ 360
||| : : : : :
133 -----TP-KVTCVVVDIS-----KDDPEVQFQSFVD--- 157
: : : : :
QY 361 TTVPIDKVTSSKEV-----TVQELDLOARHYLHGK-FGL-YNSDSPFGKGVORGLIVF 411
: : : : :
158 -DVEVHTAQTPREEQPNSTFRSVELPIMHQDLWNGKEPKCRVNSAAPPAPTEK----- 211
: : : : :
QY 412 HSSEGSTVSYDLDAQCOQYPTDLLRIYRDNTTISSTLSLSLYLYTTSIYMTQPTSLIV 471
||| : : : : :
212 -----TISKT----- 216
: : : : :
QY 472 SAGDRVTTTCASQSVSNDVAVYQKPGQPKLLISYTSRYAGVDPDRFGSGVGVDFTL 531
: : : : :
217 ----- 216
: : : : :
QY 532 TISSVQAEDAAVFCQDYNSPPTFGGGTKLEIKRADAAPTIFPPSPBQLTSGGASVV 591

Db 217 -----KGRPKAPQVYTIPTPPKEQMAKDKVSLT 243
: : : : :
QY 592 CFLNNFYPKDIINVKKIDGSERON-----GVLNSWTDQDSKDYTSYNSSTLTITLKDEYER 646
: : : : :
Db 244 CMITDFPEDITVEWONGQPAENYKNTQPIMT-----NGSYFYSKLVNPKVQSNWEA 296
: : : : :
QY 647 HNSYTCEATHK 657
: : : : :
Db 297 GNTFTCSVLHE 307
: : : : :
RESULT 54
KIMS
IG kappa chain C region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1980 #sequence revision 17-Dec-1982 #text change 09-Jul-2004
C;Accession: B90262; A90778; B93736; A92322; A93748; A02119
R;Svasti, J.; Milstein, C.
Biochem. J. 128, 427-444, 1972
A;Title: The complete amino acid sequence of a mouse kappa light chain.
A;Reference number: A90262; MUID:73053310; PMID:4638343
A;Contents: myeloma protein MOPC 21
A;Accession: B90262
A;Molecule type: protein
A;Residues: 1-52, 'BSBTZWB', 60-106 <SVA>
A;Cross-references: UNIPROT:P01837; UNIPARC:UPI0000173772
R;Svasti, J.; Milstein, C.
Biochem. J. 126, 837-850, 1972
A;Title: The disulphide bridges of a mouse immunoglobulin G1 protein.
A;Reference number: A90259; MUID:73008899; PMID:5073237
A;Contents: annotation; MOPC 21, disulfide bonds
A;Note: Cys-106 is involved in a light-heavy chain bond
R;Hamlyn, P.H.; Brownlee, G.G.; Cheng, C.C.; Gait, M.J.; Milstein, C.
Cell 15, 1067-1075, 1978
A;Title: Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA
A;Reference number: A90778; MUID:79084137; PMID:103625
A;Accession: A90778
A;Molecule type: mRNA
A;Residues: 1-106 <HAM>
A;Cross-references: UNIPARC:UPI0000024D73
R;Hamlyn, P.H.; Gait, M.J.; Milstein, C.
Nucleic Acids Res. 9, 4485-4494, 1981
A;Title: Complete sequence of an immunoglobulin mRNA using specific priming and the dideo
A;Reference number: A93736; MUID:82059477; PMID:6170937
A;Contents: MOPC 21
A;Accession: B93736
A;Molecule type: mRNA
A;Residues: 1-106 <HA2>
A;Cross-references: UNIPARC:UPI0000024D73
R;Max, E.E.; Maizel Jr., J.V.; Leder, P.
J. Biol. Chem. 256, 5116-5120, 1981
A;Title: The nucleotide sequence of a 5-kilobase DNA segment containing the mouse kappa
A;Reference number: A92322; MUID:81191915; PMID:6262318
A;Accession: A92322
A;Molecule type: DNA
A;Residues: 1-106 <MAX>
A;Cross-references: UNIPARC:UPI0000024D73
A;Note: the sequence was determined from the germline gene
R;Altenburger, W.; Neumaier, P.S.; Steinmetz, M.; Zachau, H.G.
Nucleic Acids Res. 9, 971-981, 1981
A;Title: DNA sequence of the constant gene region of the mouse immunoglobulin kappa chain
A;Reference number: A93748; MUID:81198949; PMID:6785724
A;Accession: A93748
A;Molecule type: DNA
A;Residues: 1-106 <ALT>
A;Cross-references: UNIPARC:UPI0000024D73
A;Note: the sequence was determined from the germline gene
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer
F;26-86/Disulfide bonds: #status experimental

Query Match		15.8%;	Score 556;	DB 1;	Length 106;
Best Local Similarity		100.0%;	Pred. No. 1.1e-22;		
Matches 105;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	567	ADAAPTVSIFPPPSSEQLTSGGASVGVCFNNFYKPDINVKWKIDGSRQNGVLNSWTDQDS	626		
DB	1	ADAAPTVSIFPPPSSEQLTSGGASVGVCFNNFYKPDINVKWKIDGSRQNGVLNSWTDQDS	60		
QY	627	KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPVKSFNNE	671		
DB	61	KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPVKSFNNE	105		
RESULT 55					
A56446					
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)					
C:Species: Mus musculus (house mouse)					
C>Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996					
C:Accession: A56446					
R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.					
J. Biol. Chem. 270, 7829-7835, 1995					
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical					
A:Reference number: A56446; MUID:95229583; PMID:7713873					
A:Accession: A56446					
A>Status: preliminary					
A:Molecule type: mRNA					
A:Residues: 1-268 <TAN>					
A:Cross-references: UNIPARC:UPI000017C6D0; GB:U20617					
C:Keywords: heterotetramer; immunoglobulin					
Query Match		15.8%;	Score 556;	DB 2;	Length 268;
Best Local Similarity		26.7%;	Pred. No. 3.6e-22;		
Matches 152;		Conservative 36;	Mismatches 55;	Indels 326;	Gaps 9;
QY	1	EVQLQSGDPLVPGASVKISKASGVSFTGYVMHWKQSPGKLEWIGRIHPNNGVTLY	60		
DB	3	QVKLQSGAEVLKPGASVKLSCTSFNFKDTYMHVVKQRPQEGLEWIGRIAPANGITKY	62		
QY	61	NQKFKDKATLTVDKSTTAYMELRSITSEDSAVYYCARSTMINYYMDYWGQSTVTSS	120		
DB	63	DPKFGKATIAADTSNTAYQLSSLTSEDTAVYYCA-SYLLTRY-ENYWGQSTVTVS-	119		
QY	121	AKTTPSVVPLAPGSAQTNSMTLGLCLVKGYFPEPVTTWNSGSLSSGVHIFPAVLQSD	180		
DB	120	-----	119		
QY	181	LYTLSSSVTPSPSTWTPSETVTCNVAHPASSTKVDDKIIVPRDSGGPSEKSEINEKDLRKK	240		
DB	120	-----	122		
QY	241	SELQGTALGNLKOIYYNSKAITSEKSADQFLTNTLLFKGPTFGHPWYNDDLVLGSTA	300		
DB	123	-----	122		
QY	301	ATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQ	360		
DB	123	-----	127		
QY	361	TTVPIDKVTSKKEVTVQELDLQARHLHGKFLGYNDSFGGKVGQRLIVFHSSEGSTVS	420		
DB	128	-----	135		
QY	421	YDLFDAQQGVPTDLLRIYRNTTISLTSLSISLYLTTSIIVMTQTPTSLLSVAGDRVTIT	480		
DB	136	-----	157		
QY	481	CKASQSVNDVAVYQKPGSKLLSYTSRRYAGVDPDRPSGSGYCTDFTLTSSVQAE	540		
DB	158	CRASSSV-NFIYVYQKQSDASPKLWYIYTHLPFGVPARFSGSGNSYSLTSSMEGED	216		
QY	541	AAVYFCQQDYNSPPTFGGGTKLEIKRADA	569		

Db 217 AATYYCQQTSSPFTFGSGTKLEIKRSAA 245

RESULT 56

PS0017

IG gamma-1 chain C region - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004

C:Accession: PS0017; C25941

R:Brueggemann, M.

Gene 74, 473-482, 1988

A:Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.

A:Reference number: PS0017; MUID:89232738; PMID:3149946

A:Accession: PS0017

A:Molecule type: DNA

A:Residues: 1-326 <BRU>

A:Cross-references: UNIPROT:P20759; UNIPARC:UPI000012B27A

R:Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobboid, S.; Waldmann, H.

Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986

A:Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse

A:Reference number: A25941; MUID:86287397; PMID:3016742

A:Accession: C25941

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 220-326 <BR2>

A:Cross-references: UNIPARC:UPI0000176F06

C:Genetics:

A:Introns: 98/1; 113/1; 220/1

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F;20-84/Domain: immunoglobulin homology <IMW>

Query Match 15.6%; Score 550; DB 2; Length 326;

Best Local Similarity 27.7%; Pred. No. 9.5e-22;

Matches 150; Conservative 64; Mismatches 90; Indels 238; Gaps 14;

QY 121 AKTTPSVVPLAPGSAQTNSMTLGLCLVKGYFPEPVTTWNSGSLSSGVHIFPAVLQSD 180

DB 1 AEITAPSVVPLAPGTALKSNMTLGLCLVKGYFPEPVTTWNSGALSSGVHIFPAVLQSG 60

QY 181 LYTLSSSVTPSPSTWTPSETVTCNVAHPASSTKVDDKIIVPRDSGGPSEKSEINEKDLRKK 240

DB 61 LYTLTSSVTPSPSTWTPSETVTCNVAHPASSTKVDDKIIVPRNCGGCKPC----- 109

QY 241 SELQGTALGNLKOIYYNSKAITSEKSADQFLTNTLLFKGPTFGHPWYNDDLVLGSTA 300

DB 110 ----- 130

QY 301 ATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEKKVPINLWIDG-- 358

DB 131 ----- 162

QY 359 ---KQTPVIDKVTSKKEVTVQELDLQARHLHGKFLGYNDSFGGKVGQRLIVFHSSE 415

DB 163 VHTAQTRPPEEQFNSTFR--SVSELPILHQDWLNGR----- 196

QY 416 GSTVSDVLFDAQQGVPTDLLRIYRNTTISLTSLSISLYLTTSIIVMTQTPTSLLSVAGD 475

DB 197 ----- 196

QY 476 RVITITCKASQSVNDVAVYQKPGSKLLISYTSRRYAGVDPDRFSGSGYGTDTLTITISS 535

DB 197 --TFRCV----- 217

QY 536 VQAEADAVYFCQDYNSPPTFGGGTKLEIKRADAAPTIVSIFPPSSQLTSGGASVVCFLN 595

DB 218 PE----- 249

QY 596 NYPKIDINVKWKIDGSRONGVLNSMTDODSKDSTYSMSSTLTLTDKDEYERHNSYTCEAT 655

DB 250 GRYPDIYVEWQMGQPOEN-YKNTPTPTWDT-DGSYFLYSKLVNKKRQWQGNFTICSVL 307

QY 656 HK 657

Db 308 HE 309

RESULT 57
PS0019

IG gamma-2a chain C region - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: PS0019; D25941
R;Bruggemann, M.
Gene 74, 473-482, 1988
A;Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.
A;Reference number: PS0017; MUID:89232738; PMID:3149946
A;Accession: PS0019
A;Molecule type: DNA
A;Residues: 1-322 <BRU>
A;Cross-references: UNIPROT:P20760; UNIPARC:UPI000012B28D
R;Bruggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A;Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody
A;Reference number: A25941; MUID:86287397; PMID:3016742
A;Accession: D25941
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 216-322 <BR2>
A;Cross-references: UNIPARC:UPI0000176F03
C;Genetics:
A;Introns: 98/1; 109/1; 216/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-84/Domain: immunoglobulin homology <IMM>

Query Match 15.3%; Score 539; DB 2; Length 322;
Best Local Similarity 28.2%; Pred. No. 3.5e-21;
Matches 153; Conservative 55; Mismatches 92; Indels 242; Gaps 15;

Qy 121 AKTTPSVYPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTVNSGSLSSGSHVHTEFPAVLQSD 180
Db 1 AETAPSVYPLAPGTAALKSNMTVLGCLVKGYFPEPVTVTVNSGSLSSGSHVHTEFPAVLQSG 60

Qy 181 LYTLSSVTPSPSTWSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLKK 240
Db 61 LYTLSSVTPSPSTWSSQAVTCNVAHPASSTKVDKIVPREC----- 102

Qy 241 SELQGTALGNLKQIYYNSKAITSSSEKSAQDLTNTLLPKGFTGHFWYNDLLVLDGSTA 300
Db 103 -----NPGCGTGSSEVSS-----VFIFPKTKDVL----- 126

Qy 301 ATSEYEGSSVDLYGAYGYQACGTFNKTACMYGGVTLHDNNRLTEBKVPINLWIDG-- 358
Db 127 -----TITL-----TP-KVTCVVVDISQND-----PEVRFSGWFIDDVE 158

Qy 359 ---KQTVPTDKVTSKKEVTVQELDQARHYLHGKFLYNSDSFGKVGORGLIVFHSSE 415
Db 159 VHTAQTHAPEKQSNSTLR--SVSELPIVHRDLNGK-----TFKCKVN----- 199

Qy 416 GSTVSYDLFDAQGQYPTLLRIYRDNRTTISSTLSISLYLTTISIVMTQPTSLLSVAGD 475
Db 200 -----SGAFPAPI----- 207

Qy 476 RVITTCASQSVGNDVAMVYQKQFQSPKLLAIYSTSRYAGVDPDRFSGSGYGTDTLTISS 535
Db 208 -----EKSIS-----KEGTFR----- 219

Qy 536 VQAEADAAVYFQQDYNSSPPTFGGKTLEIKRADAAPTVSIFFPSSEQLTSGGASVVCFLN 595
Db 220 -----GQVYTWAPPKKEMTQSQVSITCMVK----- 245

Qy 596 NFPKQDINVKWIKDGSBRQVNLNMTDQDSKDYSSMSSTLTLTKDVEYERHNSYTCAT 655
Db 246 GFYPDPDIYEWKNGWQPOEN-YKNTPTMDT-DGSYFLYSLKLVNKKETWQOQNTFTCSVL 303

Qy 656 HK 657
Db 304 HE 305

RESULT 58
S29690

IG heavy chain VDJ region - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 20-Jun-2000
C;Accession: S29690
R;Dammers, P.M.; Bos, N.A.; Kroese, F.G.M.
submitted to the EMBL Data Library, October 1992
A;Description: Analysis of the rat B cell repertoire: cloning of rat Vh genes.
A;Reference number: S29690
A;Accession: S29690
A;Molecule type: mRNA
A;Residues: 1-288 <DAM>
A;Cross-references: UNIPARC:UPI0000176F0E; EMBL:X68782; NID:g56442; PID:g1334294
A;Experimental source: strain D2B
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;12-95/Domain: immunoglobulin homology <IMM>

Query Match 15.2%; Score 536; DB 2; Length 288;
Best Local Similarity 45.0%; Pred. No. 4.4e-21;
Matches 113; Conservative 36; Mismatches 78; Indels 24; Gaps 7;

Qy 4 LQSGPDLVKGASVKISKACGYSTGYMHVWVKSPGKLEWIGRINPNNGVTLYNQK 63
Db 1 LQESGTELVRPSSSVKISKACGYTFTDYMHVWVKRPQGLVWIGRINPANGNTEYAEK 60

Qy 64 FKDKATLTVDKSTTAYMELSLTSDSAVYVCARSTMITNTYVMDYWGQGTSTVTSASAKT 123
Db 61 FKSRATLTADKSNNTAYMQLSLTSDTATYCTINGTVVPF--DYNGQGVMTVTSSESQ 118

Qy 124 TTPSVYPLAP-GSAAQTNSMTVLGCLVKGYFPEPVTVTV---NSGSLSSGSHVHTEFPAVLQS 179
Db 119 SSPTPLVLVSCSPISDENLVAMGCLARDFLPSSISFSWNYQNTVMQGVRTFTLTGT 178

Qy 180 DLYTLSSSVTPSST---WPSETVTCNVAH-----PA---SSTKVDKIVPRDS 222
Db 179 DKYATATSVLLSAKNVLEGSDEYLVCKIHGNKNKDLHVPVAVEMNPVSVFIPRDA 238

Qy 223 -GGPSEKSEBEI 232
Db 239 FSGPAPRKSRLL 249

RESULT 59
A35944

IG gamma-2a chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1990 #sequence_revision 30-Nov-1990 #text_change 16-Jul-1999
C;Accession: A35944
R;Igarashi, T.; Sato, M.; Katsube, Y.; Takio, K.; Tanaka, T.; Nakanishi, M.; Arata, Y.
Biochemistry 29, 5727-5733, 1990
A;Title: Structure of a mouse immunoglobulin G that lacks the entire C-H1 domain: protein
A;Reference number: A35944; MUID:90344795; PMID:2116900
A;Accession: A35944
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-170 <IGA>
A;Cross-references: UNIPARC:UPI0000176F39
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;56-120/Domain: immunoglobulin homology <IMM>

Query Match 15.0%; Score 530; DB 2; Length 170;
Best Local Similarity 73.1%; Pred. No. 4.6e-21;
Matches 106; Conservative 13; Mismatches 20; Indels 6; Gaps 3;

Qy 85 SLTSDSAVYVCARSTMITNTYV-MDYWGQGTSTVTSASAKTTPSPVPLAPGSAQAQNSMV 143

Db 2 TLRAEDTGIYC--TGIYYHPWFAYMGQGLTVLTVSAAKTAPSVYPLAVCGDITGSSV 59

QY 144 TLGCLVKGYPPEVTVTWNSGSLSSGVHTFPFPAVLQSDLYTLSSSVTVPSSTWSPSETVTGN 203

Db 60 TLGCLVKGYPPEVTVTWNSGSLSSGVHTFPFPAVLQSDLYTLSSSVTVPSSTWSPQSITCN 119

QY 204 VAHPASSTKVDKIVPRDSSGSEK 228

Db 120 VAHPASSTKVDKIEPR---GPTIK 141

RESULT 60

S41374

single chain Fv antibody - mouse

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C:Accession: S41374

R:Artekenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A:Description: Construction and functional characterization of a single chain Fv antibody

A:Reference number: S41374

A:Accession: S41374

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-249 <ART>

A:Cross-references: UNIPARC:UPI000017C74A; EMBL:Z29480

Query Match 15.0%; Score 529.5; DB 2; Length 249;

Best Local Similarity 25.7%; Pred. No. 7.9e-21;

Matches 147; Conservative 41; Mismatches 54; Indels 331; Gaps 9;

QY 1 EVLOQSGDPLVKPGASVKISKASGYSTGYMHVWVKSPGKLEWIGRINPNNGVTLY 60

Db 1 QVLOQSGAELVRPGASVKLSCTASGTFKDDYIHVWVKRPEKLEWIAPIASGVNKY 60

QY 61 NQKFKDKATLVDSKSTTAYMELRLSTSDSAVYYCA-RSTMITNTVMYDYGQGTSTVTS 119

Db 61 VRFQDKAITADTSNTAYLLSSITSEDTAVYYCARRDTLYTS--LGWGGQGSIVTVS 118

QY 120 SAKTTPPSVYPLAPGSAATNSMVTLGCLVKGYFPEFVTVTWNSGSLSSGVHTFPVLOS 179

Db 119 S-----RGGG----- 123

QY 180 DLYTLSSSVTVPSSTWSETVTCNVAHPASSTKVDKKIVPRDSSGSEKSEINEKDLRK 239

Db 124 -----SGG----- 126

QY 240 KSELQGTALGNLKIYYYNKAITSSSEKSGADQFLTNTLLFKGFFTGHFWNDLLVLDGST 299

Db 127 ----- 126

QY 300 AATSEYEGSDVLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGK 359

Db 127 -----GG----- 131

QY 360 QITVPIDKVKTSKEVTVQELDLQAKHYLHGKFLGSLNSDFGKVGQGLIVFHSSEGSIV 419

Db 132 -----GG----- 133

QY 420 SYDLFDAQGYPDTLRIYRDNTTISLSISLYLTTYSIVMTQPTSLVLSAGDRVTI 479

Db 134 -----SDIELTQSPSPVWVTPGESVSI 155

QY 480 TKCASQSV-----SNDAVYQQKPGQSKLLIYSYTSRVAGVDPDRFGSGGYGTDFTLTIS 534

Db 156 SCRSSKLLYSDDSYLFWFLQRPQSGPQLLIYRMSNLASGVDPDRFGSGSGSTFTLRIS 215

QY 535 SYQAEAAVYFCOODYNSPTEFGGKLEIKRA 567

Db 216 RVEAEDVGVTYCMQHREYPLTFGAGTKLEIKRA 248

RESULT 61

PN0444

Ig heavy chain V region precursor - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PN0444

R:Kaluza, B.; Betz, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.

Gene 122, 321-328, 1992

A:Title: A general method for chimeraization of monoclonal antibodies by inverse polymerase

A:Reference number: PN0444; MUID:93138402; PMID:1339379

A:Accession: PN0444

A:Molecule type: mRNA

A:Residues: 1-150 <KAL>

A:Cross-references: UNIPARC:UPI0000176A08; GB:I02346

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-13/Domain: signal sequence #status predicted <SIG>

F:20-150/Product: Ig heavy chain V region #status predicted <MAT>

F:20-117/Domain: variable region <VRG>

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 15.0%; Score 527; DB 2; Length 150;

Best Local Similarity 79.7%; Pred. No. 5.6e-21;

Matches 106; Conservative 4; Mismatches 21; Indels 2; Gaps 1;

QY 1 EVLOQSGDPLVKPGASVKISKASGYSTGYMHVWVKSPGKLEWIGRINPNNGVTLY 60

Db 20 EVLOQFGAELVKPGTSVKISKASGYIFTDYNMDVWVKSHGKSLWIGDIDPNPSSSY 79

QY 61 NQKFKDKATLVDSKSTTAYMELRLSTSDSAVYYCARSTMITNTVMYDYGQGTSTVTS 120

Db 80 NQKFKGKATLVDSKSTTAYMELRLSTSEDTAVYYCARGGF--PYGMDYMGQGTSTVTS 137

QY 121 AKTTPPSVYPLAP 133

Db 138 AKTTPPSVYPLAP 150

RESULT 62

A46507

Ig alpha chain - chicken

C:Species: Gallus gallus (chicken)

C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999

C:Accession: A46507

R:Mansikka, A.

J:Immunol. 149, 855-861, 1992

A:Title: Chicken Iga H chains. Implications concerning the evolution of H chain genes.

A:Reference number: A46507; MUID:92340889; PMID:1634774

A:Accession: A46507

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-585 <MAN>

A:Cross-references: UNIPARC:UPI0000176F32; GB:S40610; NID:g251907; PID:g251908

A>Note: sequence inconsistent with the nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:109906, NCBIIP:109907)

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 14.7%; Score 516.5; DB 2; Length 585;

Best Local Similarity 24.4%; Pred. No. 1.1e-19;

Matches 174; Conservative 99; Mismatches 228; Indels 211; Gaps 25;

QY 2 VOLQSGDPLVKPGASVKISKASGYSTGYMHVWVKSPGKLEWIGRINPNNGVTLYN 61

Db 21 VTLDSGGGLQTPGGALSLVCKASGFTFSYSGWNRQAPGKLEWVAGIDDDGSGTGYG 80

QY 62 QKFQDKATLVDSKSTTAYMELRLSTSDSAVYYCARSTMITNTVY---MDYWGQGTSTVTV 118

Db 81 PAVQGRATISRDNGQSTVRLQLNNLRAEDTATYCYAKGASGGCAGCAGSIDAWHGTEVIV 140

QY 119 SSKATTPPSVYPLAPGSAATNSMVTLGCLVKGYFPEFVTVTWNSGSL--SSGVHFFPAV 176

Db 141 SSASASRPTLYQLLPLFSDCPDPNVITGLVTSFLPPPTVTVTTGGAADATATVSLPVA 200

Db	93	KENFKGRATVTVDKSSSTVYMQLSLTSSEDSAVYYCAREGGFGRN-SLDYWGQGTSVNVSS	151
QY	121	AKTTPPSVYPLAPG	134
Db	152	AKTTPPSVYPLAPG	165
RESULT 66			
A27609			
Ig heavy chain precursor V region (I29) - mouse			
C:Species: Mus musculus (house mouse)			
C>Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999			
C:Accession: A27609			
R:Klein, D.; Nieuwkoop, J.; Sirlin, S.; Stavnezer, J.			
J. Immunol. 140, 1676-1684, 1988			
A:Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain switch			
A:Reference number: A27609; MUID:88154467; PMID:3126234			
A:Accession: A27609			
A:Molecule type: DNA			
A:Residues: 1-139 <KLE>			
A:Cross-references: UNIPARC:UPI0000114D5D; EMBL:M19401; NID:9195441; PIDN:AAA38303.1; PID:9195441			
C:Genetics: 16/1			
C:Superfamily: immunoglobulin V region; immunoglobulin homology			
C:Keywords: heterotetramer; immunoglobulin			
F:1-19/Domain: signal sequence #status predicted <SIG>			
F:20-139/Product: Ig heavy chain V region I29 #status predicted <VAR>			
F:34-117/Domain: immunoglobulin homology <IMM>			
Query Match 14.4%; Score 506; DB 2; Length 139;			
Best Local Similarity 80.8%; Pred. No. 6.3e-20;			
Matches 97; Conservative 7; Mismatches 16; Indels 0; Gaps 0;			
QY	1	EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWVKSPGKLEWIGRINPNNGVTLY	60
Db	20	EVLOQSGPELVKPGASVKISCKASGYSTGYMHVWVKSPGKLEWIGRINPNNGVTLY	79
QY	61	NQKFKDKATLVDKSSTAYMELRLSLTSDSAVYYCARSTMITNYMDYWGQGTSTVTS	120
Db	80	NQKFKGKATLVDKSSSTAYMQLSLTSDSAVYYCARYSYAYMDYWGQGTSTVTS	139
RESULT 67			
I37267			
Ig heavy chain V region (I29) - mouse			
C:Species: Mus musculus (house mouse)			
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996			
C:Accession: I37267			
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.			
J. Biol. Chem. 266, 6607-6613, 1991			
A:Title: Heavy and light chain variable region sequences and antibody properties of anti			
A:Reference number: A38740; MUID:91177923; PMID:1706720			
A:Accession: I37267			
A:Molecule type: mRNA			
A:Residues: 1-128 <RUF>			
A:Cross-references: UNIPARC:UPI0000176C52			
C:Superfamily: immunoglobulin V region; immunoglobulin homology			
C:Keywords: heterotetramer; immunoglobulin			
F:19-102/Domain: immunoglobulin homology <IMM>			
Query Match 14.3%; Score 503; DB 2; Length 128;			
Best Local Similarity 79.7%; Pred. No. 8.2e-20;			
Matches 98; Conservative 7; Mismatches 14; Indels 4; Gaps 1;			
QY	2	VOLQSGPDLVKPGASVKISCKASGYSTGYMHVWVKSPGKLEWIGRINPNNGVTLYN	61
Db	6	VOLQSGPELVKPGASVKISCKSGTFTFYTHVWVKQSHGKSLWIGINPNNGTSTN	65
QY	62	QKFKDKATLVDKSSTAYMELRLSLTSDSAVYYCARSTMITNYMDYWGQGTSTV	117
Db	66	QKFKGKATLVDKSSSTAYMELRLSLTSDSAVYYCARRGLITVWAKSYFYDYGQGTTLT	125

QY	118	VSS	120
Db	126	VSS	128
RESULT 68			
PS0057			
Ig heavy chain precursor V region (PAR) - mouse			
C:Species: Mus musculus (house mouse)			
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000			
C:Accession: PS0057			
R:Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.			
J. Biochem. 104, 337-343, 1988			
A:Title: Biased expression of variable region gene families of the immunoglobulin heavy			
A:Reference number: PS0057; MUID:89197817; PMID:2467902			
A:Accession: PS0057			
A:Molecule type: DNA			
A:Residues: 1-135 <YAO>			
A:Cross-references: UNIPARC:UPI000011B257; GB:D00307; NID:9220448; PIDN:BAA00213.1; PID:9220448			
A:Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly			
C:Comment: The gene encoding this protein was isolated from a hybridoma that produces an			
C:Superfamily: immunoglobulin V region; immunoglobulin homology			
C:Keywords: heterotetramer; immunoglobulin			
F:1-19/Domain: signal sequence #status predicted <SIG>			
F:20-135/Product: Ig heavy chain V region PAR #status predicted <MAT>			
F:34-117/Domain: immunoglobulin homology <IMM>			
Query Match 14.3%; Score 502; DB 2; Length 135;			
Best Local Similarity 82.5%; Pred. No. 9.8e-20;			
Matches 99; Conservative 6; Mismatches 11; Indels 4; Gaps 1;			
QY	1	EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWVKSPGKLEWIGRINPNNGVTLY	60
Db	20	EVLOQSGPELVKPGASVKISCKASGYSTGYMHVWVKQSHGKSLWIGRINPNNGDTFY	79
QY	61	NQKFKDKATLVDKSSTAYMELRLSLTSDSAVYYCARSTMITNYMDYWGQGTSTVTS	120
Db	80	NQKFKGKATLVDKSSSTAHMELRLSLTSDSAVYYCAR----LNYRGAYWGQGTTLTVSA	135
RESULT 69			
A34891			
Ig heavy chain precursor V region - ladyfish			
C:Species: Ellops saurus (ladyfish)			
C>Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 21-Jul-2000			
C:Accession: A34891			
R:Ameniya, C.T.; Litman, G.W.			
Proc. Natl. Acad. Sci. U.S.A. 87, 811-815, 1990			
A:Title: Complete nucleotide sequence of an immunoglobulin heavy-chain gene and analysis			
A:Reference number: A34891; MUID:90138916; PMID:2105490			
A:Accession: A34891			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-568 <AME>			
A:Cross-references: UNIPARC:UPI0000114B5D; GB:M26182; NID:9213134; PIDN:AAA49238.1; PID:9213134			
C:Superfamily: immunoglobulin C region; immunoglobulin homology			
C:Keywords: heterotetramer; immunoglobulin			
F:33-116/Domain: immunoglobulin homology <IMM>			
Query Match 14.1%; Score 495.5; DB 2; Length 568;			
Best Local Similarity 22.8%; Pred. No. 1.3e-18;			
Matches 159; Conservative 109; Mismatches 225; Indels 203; Gaps 24;			
QY	4	LQOSGPDLVKPGASVKISCKASGYSTGYMHVWVKSPGKLEWIGRINPNNGVTLYNQK	63
Db	22	LTSEBPAVKKPGSEKHLCTASGFTFSNYMGWIRQAPGKLEWLTATLKYSABEYYS	81
QY	64	FKDKATLVDKSSTAYMELRLSLTSDSAVYYCARSTMITNYMDYWGQGTSTVTS	123
Db	82	VGRFTTIRSDNSKNQIYQMNLSRAEDTAVYYCAR--VYGYWAFDWGRTWVTVTGEQ	139
QY	124	TPPSVYPLAPGSAATNSMVTGLCLVKGYFPEPVTVTVNSGSL--SGVHTFPFVAVLQSDLY	182

Db 140 ASPTVPFLV--SCGATSGYVTMGICGKYLPLDLSLTFWSKSDTLDLTDYLYQVSVLGGKY 197
QY 183 TLSSSVTPSSTWPESTVTTCNVAHPASSTKVDKKI VPRDSGPGSEKSEENEDLRKKE 242
Db 198 D-----RVSH-----ARTEGDFKSAE 215
QY 243 LQ-GTALGNLQIYYNSKAITSE--KSADQFLTNLLPKGFPTGHPWYNDLLVDLGST 299
Db 216 FKCTTELGGKK-----TPVVIKPEPKPPRPQVLSIMT-----PSQEELTLN--- 258
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMGVGTLLHNNRLTEKKVPINLMI-DG 358
Db 259 -KTATFACLAATDFPKGHSFK-----MURDG 283
QY 359 KQTVTPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKQVQRGLIVFHSSEGST 418
Db 284 KEVTDGIATITECQK-----GDKSFTASSFLQASESOW 317
QY 419 VSYD-----LFDAGQYQVPTLLRIYRDNNTTISSTLSISLYLVTTSIVMTQTPTSLLSVA 473
Db 318 KRLDGTFTCFIQEGETE-----QTVKYSSAECSPQAQIDAKISPTPEELFLQ- 367
QY 474 GDRVTITCKASQSVS--NDVAM--YQKPKQ-----SPKLISYTSRRYAGVDPDRFG 522
Db 368 -QRTLTCTKITGVDGVRNVTVWEGSEVRVQDFDEQRMISKLLIDYE----- 413
QY 523 SGYGTDTTLTIISSVOAEDAAVYFCQDYNPSPT-----FGGQTKLEIKRADAAPTV 573
Db 414 -----EWKRTYCTCKVEHSDLPRLTSYRRCGKQW-----SPTV 451
QY 574 SIPTPSEQITSGASVVCFLNFPKIDINVKWIDGSEKQNGVNSWTDQDSKDSYSYM 633
Db 452 FILAP-AEQRNLSVTLLICVAKDFYEQVLISMLVDDQPVETDV--PTTEWVKTEGTSYV 508
QY 634 SSTLTITKBEYERHNSYTCATHKTSPIVKSFN 669
Db 509 FSQITIPASDWDGSGVYSCAVHHTVMSVVKTVR 544

RESULT 70
C37267
Ig heavy chain V region (Py69) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C:Accession: C37267
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991.
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: C37267
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-128 <RUF>
A:Cross-references: UNIPARC:UPI0000176B3A
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 14.1%; Score 495; DB 2; Length 128;
Best Local Similarity 77.2%; Pred. No. 2.1e-19;
Matches 95; Conservative 9; Mismatches 15; Indels 4; Gaps 1;
QY 2 VQLQQSGPDLVKPGASVKISCKASGYSTFYGMHWVKQSPGKLEWIGRINPNNGVTLYN 61
Db 6 VQLQQSGPELVKPGASVKISCKTSGYTFYTHWVKQSHGKLEWIGRINPNNGGSTYN 65
QY 62 QKFKDKATLTVDKSSSTAYMELSLTSDSAVYICAR-----STMITNYMDYWGQGSTV 117
Db 66 QKFKGKATLTVDKSSSTAYMELSLTSDSAVYICARPGYGNVYTSYYPDYWGQGTTLT 125
QY 118 VSS 120
Db 126 VSS 128

RESULT 71

PS0024
Ig heavy chain precursor V region (6A4) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996
C:Accession: PS0024
R:Marget, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
Gene 74, 335-345, 1988
A:Title: Cloning and characterization of cDNAs coding for the heavy and light chains of
A:Reference number: PS0023; MUID:89232725; PMID:3149944
A:Accession: PS0024
A:Molecule type: mRNA
A:Residues: 1-139 <MAR>
A:Cross-references: UNIPARC:UPI0000176D41
A:Experimental source: strain BALB/c
C:Comment: This chain is obtained from an IgG2a monoclonal antibody against Pseudomonas
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin; pyroglytamic acid
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-139/Domain: Ig heavy chain V region #status predicted <IGV>
F:34-117/Domain: immunoglobulin homology <IMM>
F:20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

Query Match 14.0%; Score 492; DB 2; Length 139;
Best Local Similarity 77.5%; Pred. No. 3.4e-19;
Matches 93; Conservative 8; Mismatches 19; Indels 0; Gaps 0;
QY 1 EVLQQSGPDLVKPGASVKISCKASGYSTFYGMHWVKQSPGKLEWIGRINPNNGVTLY 60
Db 20 QVQLQQSGAELAKPGASVKMSCKASGYTFYTHWVKQSPGQGLEWIGVINPTGYTEY 79
QY 61 NQKFKDKATLTVDKSSSTAYMELSLTSDSAVYICARSTMITNYMDYWGQGSTVTVSS 120
Db 80 NQKFKDKATLTADKSSSTAYMQLSLTSDSAVYICARSTYINNEGAMDYWGQGSTVTVSS 139

RESULT 72
G2MSA
Ig gamma-2a chain C region, secreted form (allele a) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1980 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C:Accession: A02152; A32657; A32658
R:Sikorav, J.L.; Aufray, C.; Rougeon, F.
Nucleic Acids Res. 8, 3143-3155, 1980
A:Title: Structure of the constant and 3' untranslated regions of the murine Balb/C gamma
A:Reference number: A02152; MUID:81076554; PMID:6777755
A:Accession: A02152
A:Molecule type: mRNA
A:Residues: 1-330 <SIK>
A:Cross-references: UNIPROT:P01863; UNIPARC:UPI00000272CF; GB:V00798; MID:g51835; PIDN:CJ
R:Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.
Nucleic Acids Res. 9, 1365-1381, 1981
A:Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and evol
A:Reference number: A32657; MUID:81198976; PMID:6262729
A:Accession: A32657
A:Molecule type: DNA
A:Residues: 1-330 <YAM>
A:Cross-references: UNIPARC:UPI00000272CF; GB:J00470
A:Note: the sequence was determined from the germline gene
R:Ollo, R.; Auffray, C.; Mochamps, C.; Rougeon, F.
Proc. Natl. Acad. Sci. U.S.A. 78, 2442-2446, 1981
A:Title: Comparison of mouse immunoglobulin gamma-2A and gamma-2B chain genes suggests t
A:Reference number: A32658; MUID:81223894; PMID:6787604
A:Accession: A32658
A:Molecule type: DNA
A:Residues: 1-330 <OLL>
A:Cross-references: UNIPARC:UPI00000272CF
A:Note: the sequence was determined from the germline gene
R:Bourgois, A.; Fougereau, M.; Rocca-Serra, J.
Eur. J. Biochem. 43, 423-435, 1974

A:Title: Determination of the primary structure of a mouse IgG2a immunoglobulin: amino-a
A:Reference number: A32659; MUID:74175517; PMID:4831970
A:Contents: annotation; myeloma protein MOPC 173
A:Note: this is one paper in a series reporting the sequence; for additional references,
A:Note: this sequence differs from that shown at a number of positions
R:de Preval, C.; Fougereau, M.
Eur. J. Biochem. 30, 452-462, 1972
A:Title: Determination of the primary structure of a mouse gammaG2a immunoglobulin. Ident
A:Reference number: A32660; MUID:73056887; PMID:4565406
A:Contents: annotation; MOPC 173, disulfide bonds
C:Genetics:
A:Introns: 1/1; 98/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F:20-84/Domain: immunoglobulin homology <IM1>
F:98-113/Region: hinge
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:15/Disulfide Bonds: interchain (to light chain) #status experimental
F:27-82,144-204,250-308/Disulfide bonds: #status experimental
F:107,110,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 14.0%; Score 491.5; DB 1; Length 330;
Best Local Similarity 26.4%; Pred. No. 1.1e-18;
Matches 151; Conservative 43; Mismatches 110; Indels 267; Gaps 13;
QY 121 AKTTSPSVYPLAPGSAQAOTNSMTLGLVKGYFPEPTVTCNVAHPASSTKVKKIIVPRDSGGPSEKEEINEKDLRKK 240
DB 1 AKTTASVYPLAPVCGDITGSSVTLGLVKGYFPEPTVTLTNWSGSLSSGVHTFPVQLQSD 60
QY 181 LYTLSSTVTPSPSTWSPSETVTCNVAHPASSTKVKKIIVPRDSGGPSEKEEINEKDLRKK 240
DB 61 LYTLSSTVTPSTWSPSQSITCNVAHPASSTKVKKIEPR---GPTIKPCP----- 108
QY 241 SELQGTALGNLQKIYYNNSKAITSSSEKSDQFLTNTLLFKGPTGHPWYNLLVDLGSTA 300
DB 109 ----- 108
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTBEKKVPINLWIDGKQ 360
DB 109 -----PCKCPAPN-----LLGGPSVF----- 124
QY 361 TTVPIDKVTSKKEVTVQELDLOARHYLHGKFLGYNDSFGGKVQGLIVFHSSEGSTVS 420
DB 125 -----IPPPKIKDVLMI---SLSPIVT 143
QY 421 YDLFDAQGOYPTDLLRIYRDNTTISSTLSISLYLTTISIVMTQTPTSLLSVAGDRVIT 480
DB 144 CVVDVSEDDPD-----VOISWFVNNVEVHTAQTOT----- 174
QY 481 CKASQSVSNDVAWYQOKPGSQPKLLISYTSRRYAGVDRFSGSGYGTDFTLTSSVQAE 540
DB 175 -----HREDYNSILRVV---- 186
QY 541 AAVYFCQDYNPPTFGGKTLEIKRAD-----AAPTYSIFPPSSEQIT 584
DB 187 SALPIQHODWMSGEF---KCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPEEEMT 242
QY 585 SGGASVVCFLNFPKIDNVKKIDGSERON-----GVLSNWTDDQSKDSTYSMSSTLT 639
DB 243 KQVTLTVMTDMPEDIIVETWNNKGTLEYNKNTPEVLDS-----DGSYFMYSKLRV 295
QY 640 TKDEYERHNSYTCEATHK-TSTSPIVKSFRN 669
DB 296 EKKWVERNSYCSVVHEGLNHHHTTKFSR 326
RESULT 73
G2MSAM
Ig gamma-2a chain C region, membrane-bound form - mouse

C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1984 #sequence revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: A02154; B32657; I57809
R:Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T.
Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982
A:Title: Nucleotide sequences of gene segments encoding membrane domains of immunoglobuli
A:Reference number: A02154; MUID:82222190; PMID:6283537
A:Accession: A02154
A:Molecule type: DNA
A:Residues: 329-399 <YAM>
A:Cross-references: UNIPROT:P01865; UNIPARC:UPI00001737A4; GB:J00471
A:Note: the sequence was determined from the germline gene
R:Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.
Nucleic Acids Res. 9, 1365-1381, 1981
A:Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and evol
A:Reference number: A32657; MUID:81198976; PMID:6262729
A:Accession: B32657
A:Molecule type: DNA
A:Residues: 1-329, 'K' <YA2>
A:Cross-references: UNIPARC:UPI00000272CF
R:Hall, B.; Milcarek, C.
Mol. Immunol. 26, 819-826, 1989
A:Title: Sequence and polyadenylation site determination of the murine immunoglobulin gan
A:Reference number: I57809; MUID:90097953; PMID:2513486
A:Accession: I57809
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 373-399 <RES>
A:Cross-references: UNIPARC:UPI000011508C; GB:M35032; NID:gl94478; PIDN:AAA37919.1; PID:5
C:Comment: The sequence of residues 1-328 was assumed to be identical with the correspond
C:Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The ma
hat it contains an alternative 3' end, encoded in separate exons, that is homologous wit
C:Genetics:
A:Introns: 1/1; 98/1; 114/1; 224/1; 329/1; 372/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobul
F:137-206/Domain: immunoglobulin homology <IM1>
F:346-363/Domain: transmembrane #status predicted <TM>
F:364-399/Domain: intracellular #status predicted <INT>
F:180/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 14.0%; Score 491.5; DB 1; Length 399;
Best Local Similarity 26.4%; Pred. No. 1.3e-18;
Matches 151; Conservative 43; Mismatches 110; Indels 267; Gaps 13;
QY 121 AKTTSPSVYPLAPGSAQAOTNSMTLGLVKGYFPEPTVTCNVAHPASSTKVKKIIVPRDSGGPSEKEEINEKDLRKK 240
DB 1 AKTTASVYPLAPVCGDITGSSVTLGLVKGYFPEPTVTLTNWSGSLSSGVHTFPVQLQSD 60
QY 181 LYTLSSTVTPSPSTWSPSETVTCNVAHPASSTKVKKIIVPRDSGGPSEKEEINEKDLRKK 240
DB 61 LYTLSSTVTPSTWSPSQSITCNVAHPASSTKVKKIEPR---GPTIKPCP----- 108
QY 241 SELQGTALGNLQKIYYNNSKAITSSSEKSDQFLTNTLLFKGPTGHPWYNLLVDLGSTA 300
DB 109 ----- 108
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTBEKKVPINLWIDGKQ 360
DB 109 -----PCKCPAPN-----LLGGPSVF----- 124
QY 361 TTVPIDKVTSKKEVTVQELDLOARHYLHGKFLGYNDSFGGKVQGLIVFHSSEGSTVS 420
DB 125 -----IPPPKIKDVLMI---SLSPIVT 143
QY 421 YDLFDAQGOYPTDLLRIYRDNTTISSTLSISLYLTTISIVMTQTPTSLLSVAGDRVIT 480
DB 144 CVVDVSEDDPD-----VOISWFVNNVEVHTAQTOT----- 174
QY 481 CKASQSVSNDVAWYQOKPGSQPKLLISYTSRRYAGVDRFSGSGYGTDFTLTSSVQAE 540

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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:08:30 ; Search time 221.277 Seconds
(without alignments)
2142.628 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522

Sequence: 1 EVLOQSGPDLVKPGASVKI.....EATHKTSPIVKSFNRNES 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1107	31.4	257	1	ETXE_STAAU	P12993 staphylococ
2	1010	28.7	463	2	Q99LC4_MOUSE	Q99LC4 mus musculus
3	983.5	27.9	458	2	Q5BJZ2_RAT	Q5BJZ2 rattus norv
4	975	27.7	472	2	Q6PUJ7_MOUSE	Q6PUJ7 mus musculus
5	951	27.0	261	2	Q5PSP6_STAAU	Q5PSP6 staphylococ
6	948	26.9	257	1	ETXA_STAAU	P0A012 staphylococ
7	948	26.9	257	1	ETXA_STAAU	P0A011 staphylococ
8	948	26.9	257	2	Q6GY77_STAAS	Q6GY77 staphylococ
9	948	26.9	260	2	Q931M4_STAAM	Q931M4 staphylococ
10	945.5	26.8	465	2	Q6PJB2_MOUSE	Q6PJB2 mus musculus
11	945	26.8	468	2	Q569W9_MOUSE	Q569W9 mus musculus
12	944.5	26.8	458	2	Q5BK05_RAT	Q5BK05 rattus norv
13	941	26.7	240	2	Q521L6_MOUSE	Q521L6 mus musculus
14	938	26.6	238	2	Q58EU4_MOUSE	Q58EU4 mus musculus
15	935	26.5	257	2	Q6GFA8_STAAR	Q6GFA8 staphylococ
16	929.5	26.4	477	2	Q58E56_MOUSE	Q58E56 mus musculus
17	924.5	26.2	473	2	Q9D814_MOUSE	Q9D814 mus musculus
18	918	26.1	260	2	Q99SU3_STAAN	Q99SU3 staphylococ
19	910	25.8	238	2	Q6EUS7_MOUSE	Q6EUS7 mus musculus
20	904	25.7	241	2	Q63ZX4_MOUSE	Q63ZX4 mus musculus
21	901.5	25.6	219	2	Q65ZC0_MOUSE	Q65ZC0 mus musculus
22	900.5	25.6	464	2	Q6PF95_MOUSE	Q6PF95 mus musculus
23	899.5	25.5	470	2	Q7TMK1_MOUSE	Q7TMK1 mus musculus
24	898	25.5	219	2	Q6XZE9_STAAR	Q6XZE9 staphylococ
25	897	25.5	468	2	Q505N9_MOUSE	Q505N9 mus musculus
26	891	25.3	467	2	Q4VBH1_RAT	Q4VBH1 rattus norv
27	888.5	25.2	474	2	Q8R3H6_MOUSE	Q8R3H6 mus musculus
28	886	25.2	236	2	Q7TS98_MOUSE	Q7TS98 mus musculus
29	880.5	25.0	237	2	Q569Y8_MOUSE	Q569Y8 mus musculus
30	879.5	25.0	239	2	Q58EU8_MOUSE	Q58EU8 mus musculus
31	871	24.7	236	2	Q52L95_MOUSE	Q52L95 mus musculus

32	870.5	24.7	235	2	Q5XEY8_MOUSE	Q5XEY8 mus musculus
33	867.5	24.6	235	2	Q58EV6_MOUSE	Q58EV6 mus musculus
34	867.5	24.6	458	2	Q65ZQ1_HUMAN	Q65ZQ1 homo sapien
35	858.5	24.4	234	2	Q5XKG4_MOUSE	Q5XKG4 mus musculus
36	858.5	24.4	468	2	Q569B4_RAT	Q569B4 rattus norv
37	852	24.2	461	2	Q5M7V3_RAT	Q5M7V3 rattus norv
38	851	24.2	465	2	Q510J0_RAT	Q510J0 rattus norv
39	836.5	23.8	476	2	Q569X1_MOUSE	Q569X1 mus musculus
40	832.5	23.6	458	2	Q5M842_RAT	Q5M842 rattus norv
41	815.5	23.2	471	2	Q66K04_MOUSE	Q66K04 mus musculus
42	803	22.8	464	2	Q6PIP8_MOUSE	Q6PIP8 mus musculus
43	803	22.8	473	2	Q91Z05_MOUSE	Q91Z05 mus musculus
44	791	22.5	234	2	Q4KM66_RAT	Q4KM66 rattus norv
45	787	22.3	234	2	Q5M838_RAT	Q5M838 rattus norv
46	775	22.0	268	2	Q76LS7_STAAR	Q76LS7 staphylococ
47	768	21.8	268	2	Q85217_STAAR	Q85217 staphylococ
48	765	21.7	154	2	Q6R2G0_STAAR	Q6R2G0 staphylococ
49	755.5	21.5	518	2	Q6N030_HUMAN	Q6N030 homo sapien
50	750	21.3	469	2	Q7Z7P5_HUMAN	Q7Z7P5 homo sapien
51	747.5	21.2	469	2	Q5M839_RAT	Q5M839 rattus norv
52	741.5	21.1	470	2	Q4G060_RAT	Q4G060 rattus norv
53	741.5	21.1	480	2	Q6PJF1_HUMAN	Q6PJF1 homo sapien
54	741	21.0	519	2	Q5EBM2_HUMAN	Q5EBM2 homo sapien
55	734	20.8	236	2	Q6GMW1_HUMAN	Q6GMW1 homo sapien
56	733	20.8	475	2	Q6N095_HUMAN	Q6N095 homo sapien
57	721.5	20.5	472	2	Q6N089_HUMAN	Q6N089 homo sapien
58	719	20.4	469	2	Q569F4_HUMAN	Q569F4 homo sapien
59	717.5	20.4	478	2	Q6PI81_HUMAN	Q6PI81 homo sapien
60	715	20.3	465	2	Q6GMX6_HUMAN	Q6GMX6 homo sapien
61	714	20.3	475	2	Q5RE17_PONPY	Q5RE17 pongo pygma
62	712	20.2	234	2	Q5EFE6_HUMAN	Q5EFE6 homo sapien
63	710	20.2	236	2	Q6PIH7_HUMAN	Q6PIH7 homo sapien
64	707.5	20.1	235	2	Q6GMW0_HUMAN	Q6GMW0 homo sapien
65	706	20.0	236	2	Q6GMX0_HUMAN	Q6GMX0 homo sapien
66	705	20.0	236	2	Q6GMX8_HUMAN	Q6GMX8 homo sapien
67	703.5	20.0	470	2	Q68CN4_HUMAN	Q68CN4 homo sapien
68	699	19.8	236	2	Q6GMX9_HUMAN	Q6GMX9 homo sapien
69	698.5	19.8	470	2	Q6PUA4_HUMAN	Q6PUA4 homo sapien
70	697.5	19.8	466	2	Q6IN78_HUMAN	Q6IN78 homo sapien
71	696	19.8	235	2	Q502W4_HUMAN	Q502W4 homo sapien
72	694.5	19.7	235	2	Q6GMV9_HUMAN	Q6GMV9 homo sapien
73	694	19.7	475	2	Q6MZQ6_HUMAN	Q6MZQ6 homo sapien
74	691	19.6	234	2	Q7Z473_HUMAN	Q7Z473 homo sapien
75	689	19.6	236	2	Q6P5S8_HUMAN	Q6P5S8 homo sapien
76	689	19.6	236	2	Q7Z3Y4_HUMAN	Q7Z3Y4 homo sapien
77	689	19.6	465	2	Q6P6C4_HUMAN	Q6P6C4 homo sapien
78	689	19.6	475	2	Q6GMW7_HUMAN	Q6GMW7 homo sapien
79	687.5	19.5	617	2	Q4KML5_MOUSE	Q4KML5 mus musculus
80	687	19.5	473	2	Q6MZV7_HUMAN	Q6MZV7 homo sapien
81	687	19.5	475	2	Q5EFE5_HUMAN	Q5EFE5 homo sapien
82	686.5	19.5	482	2	Q7Z3J51_HUMAN	Q7Z3J51 homo sapien
83	686	19.5	544	2	Q6PJ95_HUMAN	Q6PJ95 homo sapien
84	684.5	19.4	235	2	Q6PUF2_HUMAN	Q6PUF2 homo sapien
85	684	19.4	236	2	Q6PIT5_HUMAN	Q6PIT5 homo sapien
86	683.5	19.4	480	2	Q6N094_HUMAN	Q6N094 homo sapien
87	682	19.4	473	2	Q6P055_HUMAN	Q6P055 homo sapien
88	681.5	19.3	464	2	Q6MZU6_HUMAN	Q6MZU6 homo sapien
89	681.5	19.3	466	2	Q6N096_HUMAN	Q6N096 homo sapien
90	679	19.3	236	2	Q6PIL8_HUMAN	Q6PIL8 homo sapien
91	678.5	19.3	476	2	Q6GMX1_HUMAN	Q6GMX1 homo sapien
92	669.5	19.0	239	2	Q8NEK0_HUMAN	Q8NEK0 homo sapien
93	667	18.9	236	2	Q6PIH4_HUMAN	Q6PIH4 homo sapien
94	666.5	18.9	470	2	Q7Z5W1_HUMAN	Q7Z5W1 homo sapien
95	666	18.9	240	2	Q6PIH6_HUMAN	Q6PIH6 homo sapien
96	665	18.9	481	2	Q6N097_HUMAN	Q6N097 homo sapien
97	662.5	18.8	473	2	Q8TC63_HUMAN	Q8TC63 homo sapien
98	654.5	18.6	239	2	Q8TCDD_HUMAN	Q8TCDD homo sapien
99	652	18.5	234	2	Q6G919_HUMAN	Q6G919 homo sapien
100	651.5	18.5	590	2	Q4V9V8_MOUSE	Q4V9V8 mus musculus
101	648	18.4	487	2	Q65ZL2_MOUSE	Q65ZL2 mus sp. fv/
102	648	18.4	614	2	Q7TWT6_MOUSE	Q7TWT6 mus musculus
103	646.5	18.4	239	2	Q6P491_HUMAN	Q6P491 homo sapien
104	643.5	18.3	560	2	Q4V801_XENLA	Q4V801 xenopus lae

105	641	18.2	521	2	Q8N4Y9_HUMAN	Q8N4Y9 homo sapien	178	505	14.3	240	2	Q65ZC9_HUMAN	Q65ZC9 homo sapien
106	640	18.2	476	2	Q6MXZ7_HUMAN	Q6mxz7 homo sapien	179	504.5	14.3	496	2	Q96DK0_HUMAN	Q96dk0 homo sapien
107	639	18.1	616	2	Q504M7_MOUSE	Q504m7 mus musculus	180	504	14.3	615	2	Q569B6_RAT	Q569b6 rattus norv
108	631	17.9	483	2	Q4VAB6_MOUSE	Q4vab6 mus musculus	181	502.5	14.3	168	2	Q8VDC9_MOUSE	Q8vdc9 mus musculus
109	619.5	17.6	488	2	Q8K0F2_MOUSE	Q8kof2 mus musculus	182	502.5	14.3	591	2	Q5I0L9_RAT	Q5iol9 rattus norv
110	619	17.6	598	2	Q568Y0_RAT	Q568y0 rattus norv	183	501	14.2	493	2	Q6GMX2_HUMAN	Q6gmx2 homo sapien
111	618.5	17.6	482	2	Q8K172_MOUSE	Q8k172 mus musculus	184	500	14.2	145	2	Q924Q7_MOUSE	Q924q7 mus musculus
112	618.5	17.6	613	2	Q8VCX7_MOUSE	Q8vcx7 mus musculus	185	500	14.2	145	2	Q924R3_MOUSE	Q924r3 mus musculus
113	612.5	17.4	591	2	Q4QQM0_RAT	Q4qqm0 rattus norv	186	498.5	14.2	117	2	Q9QXF0_MOUSE	Q9qxf0 mus musculus
114	611	17.3	258	1	ETXD_STAAU	Q20723 staphylococ	187	498.5	14.2	146	2	Q924Q8_HUMAN	Q924q8 mus musculus
115	609	17.3	584	2	Q6INK3_XENLA	Q6ink3 xenopus lae	188	497	14.1	576	2	Q6P4I8_HUMAN	Q6p4i8 homo sapien
116	606	17.2	243	2	Q7TQM2_MOUSE	Q7tqm2 mus musculus	189	496	14.1	137	2	Q924R6_MOUSE	Q924r6 mus musculus
117	602.5	17.1	488	2	Q91WR1_MOUSE	Q91wr1 mus musculus	190	493	14.0	241	2	Q921A6_MOUSE	Q921a6 mus musculus
118	598.5	17.0	417	2	Q6N093_HUMAN	Q6n093 homo sapien	191	492	14.0	141	2	Q924Q4_MOUSE	Q924q4 mus musculus
119	589.5	16.7	585	2	Q6GXP4_XENLA	Q6gxp4 xenopus lae	192	492	14.0	575	2	Q5FQS1_RAT	Q5fpq1 rattus norv
120	587	16.7	244	2	Q65ZC8_HUMAN	Q65zc8 homo sapien	193	492	14.0	480	2	Q7T0R1_XENLA	Q7t0r1 xenopus lae
121	585	16.6	485	2	Q58E61_MOUSE	Q58e61 mus musculus	194	491.5	14.0	140	2	Q924P8_MOUSE	Q924p8 mus musculus
122	584	16.6	593	2	Q61NM5_XENLA	Q61nm5 xenopus lae	195	491.5	14.0	330	1	GCAA_MOUSE	P01863 mus musculus
123	583	16.6	481	2	Q91WT1_MOUSE	Q91wt1 mus musculus	196	491	13.9	590	2	Q569B8_RAT	Q569b8 rattus norv
124	576.5	16.4	243	2	Q6NTU5_XENLA	Q6ntu5 xenopus lae	197	490.5	13.9	588	2	Q61R66_XENLA	Q61r66 xenopus lae
125	575	16.3	589	2	Q5XHD5_XENLA	Q5xhd5 xenopus lae	198	488	13.9	143	2	Q924R7_MOUSE	Q924r7 mus musculus
126	573	16.3	481	2	Q8VCV5_MOUSE	Q8vcv5 mus musculus	199	487.5	13.8	398	1	GCM_MOUSE	P01865 mus musculus
127	572.5	16.3	555	2	Q5FW04_XENTR	Q5fw04 xenopus tro	200	487.5	13.8	605	2	Q6GN83_XENLA	Q6gn83 xenopus lae
128	570	16.2	498	2	Q6N041_HUMAN	Q6n041 homo sapien	201	484	13.7	493	2	Q8NCL6_HUMAN	Q8ncl6 homo sapien
129	566.5	16.1	480	2	Q8K0Z4_MOUSE	Q8k0z4 mus musculus	202	483	13.7	143	2	Q91VA2_MOUSE	Q91va2 mus musculus
130	565.5	16.1	239	2	Q5HZC6_XENTR	Q5hzc6 xenopus tro	203	483	13.7	143	2	Q924Q5_MOUSE	Q924q5 mus musculus
131	565	16.0	489	2	Q8VCX4_MOUSE	Q8vcx4 mus musculus	204	481.5	13.7	117	1	HV12_MOUSE	P01756 mus musculus
132	563.5	16.0	486	2	Q5ZYI6_MOUSE	Q5zyi6 mus musculus	205	481.5	13.7	144	2	Q924P5_MOUSE	Q924p5 mus musculus
133	561	15.9	597	2	Q96BB9_HUMAN	Q96bb9 homo sapien	206	481	13.7	139	1	HV07_MOUSE	P01751 mus musculus
134	560	15.9	475	2	Q5FVP3_RAT	Q5fvp3 rattus norv	207	480.5	13.6	117	1	HV13_MOUSE	P01757 mus musculus
135	559	15.9	483	2	Q52L51_MOUSE	Q52l51 mus musculus	208	480	13.6	118	1	HV51_MOUSE	P06330 mus musculus
136	557	15.8	324	1	IGHI1_MOUSE	P01868 mus musculus	209	480	13.6	477	2	Q6GMX7_HUMAN	Q6gmx7 homo sapien
137	557	15.8	393	1	IGHM_MOUSE	P01869 mus musculus	210	479.5	13.6	570	2	Q5BJ31_BRARE	Q5bj31 brachydanio
138	556	15.8	106	1	KAC_MOUSE	P01837 mus musculus	211	479	13.6	336	1	GCB_MOUSE	P01866 mus musculus
139	554	15.7	255	2	Q6KE05_MOUSE	Q6kb05 mus musculus	212	477	13.5	487	2	Q6ZVX0_HUMAN	Q6zvx0 homo sapien
140	553	15.7	367	2	Q5MBX4_XENTR	Q5mbx4 xenopus tro	213	475	13.5	404	1	GCBM_MOUSE	P01967 mus musculus
141	550.5	15.6	606	2	Q6GMY2_HUMAN	Q6gmy2 homo sapien	214	474.5	13.5	506	2	Q6N090_HUMAN	Q6n090 homo sapien
142	550	15.6	326	1	GCI_RAT	P20759 rattus norv	215	474	13.5	139	2	Q924R5_MOUSE	Q924r5 mus musculus
143	548	15.5	237	2	Q7S236_XENLA	Q7s236 xenopus lae	216	474	13.5	479	2	Q5PQK9_RAT	Q5pqk9 rattus norv
144	546.5	15.5	614	2	Q6DDQ7_XENLA	Q6ddq7 xenopus lae	217	472.5	13.4	225	2	Q6PAF5_XENLA	Q6paf5 xenopus lae
145	545.5	15.5	480	2	Q6P089_HUMAN	Q6p089 homo sapien	218	472	13.4	106	1	KACA_RAT	P01836 rattus norv
146	545	15.5	597	2	Q9BQB8_HUMAN	Q9bqb8 homo sapien	219	471	13.4	506	2	Q6MZW0_HUMAN	Q6mzw0 homo sapien
147	542.5	15.4	500	2	Q6N091_HUMAN	Q6n091 homo sapien	220	469	13.3	485	2	Q6PDB8_MOUSE	Q6pdb8 mus musculus
148	540	15.3	208	2	Q6ZP87_HUMAN	Q6zpb7 homo sapien	221	468.5	13.3	483	2	Q5U413_MOUSE	Q5u413 mus musculus
149	540	15.3	595	2	Q8WUX4_HUMAN	Q8wux4 homo sapien	222	468	13.3	499	2	Q8N5K4_HUMAN	Q8nsk4 homo sapien
150	540	15.3	597	2	Q9BU10_HUMAN	Q9bu10 homo sapien	223	467.5	13.3	494	2	Q96K68_HUMAN	Q96k68 homo sapien
151	540	15.3	597	2	Q6GMX5_HUMAN	Q6gmx5 homo sapien	224	467	13.3	335	1	GCA_MOUSE	P01864 mus musculus
152	540	15.3	625	2	Q96AA6_HUMAN	Q96aa6 homo sapien	225	465.5	13.2	123	2	Q8VIJ1_MOUSE	Q8vij1 mus musculus
153	539	15.3	322	1	GCA_RAT	P20760 rattus norv	226	465	13.2	143	2	Q924P9_MOUSE	Q924p9 mus musculus
154	537.5	15.3	613	2	Q8WTK1_HUMAN	Q8wtk1 homo sapien	227	464	13.2	348	2	Q6PVX1_HUMAN	Q6pvx1 homo sapien
155	535	15.2	145	2	Q924Q9_MOUSE	Q924q9 mus musculus	228	462	13.1	143	2	Q91V67_MOUSE	Q91v67 mus musculus
156	535	15.2	481	2	Q91WT3_MOUSE	Q91wt3 mus musculus	229	462	13.1	152	2	Q6R2F9_STAAU	Q6r2f9 staphylococ
157	534	15.2	145	2	Q924Q6_MOUSE	Q924q6 mus musculus	230	461	13.1	143	2	Q924Q0_MOUSE	Q924q0 mus musculus
158	533	15.1	136	2	Q7TPE3_MOUSE	Q7tpe3 mus musculus	231	461	13.1	476	2	Q4V9Z4_MOUSE	Q4v9z4 mus musculus
159	527.5	15.0	484	2	Q91LA6_MOUSE	Q91la6 mus musculus	232	461	13.1	479	2	Q6MZV6_HUMAN	Q6mzv6 homo sapien
160	527	15.0	145	2	Q924R4_MOUSE	Q924r4 mus musculus	233	460.5	13.1	142	2	Q924Q2_MOUSE	Q924q2 mus musculus
161	525.5	14.9	620	2	Q96EY0_HUMAN	Q96ey0 homo sapien	234	458.5	13.0	120	1	HV03_MOUSE	P01747 mus musculus
162	523.5	14.9	500	2	Q9BRV0_HUMAN	Q9brv0 homo sapien	235	458.5	13.0	482	2	Q91X92_MOUSE	Q91x92 mus musculus
163	519	14.7	145	2	Q924R1_MOUSE	Q924r1 mus musculus	236	458.5	13.0	572	2	Q66IQ7_XENLA	Q66iq7 xenopus lae
164	518.5	14.7	146	2	Q924Q3_MOUSE	Q924q3 mus musculus	237	458	13.0	99	2	Q9JL74_MOUSE	Q9jl74 mus musculus
165	515	14.6	145	2	Q924P7_MOUSE	Q924p7 mus musculus	238	457	13.0	106	1	KACB_RAT	P01835 rattus norv
166	514	14.6	143	2	Q924R0_MOUSE	Q924r0 mus musculus	239	456.5	13.0	248	2	Q65ZQ7_9MURI	Q65zq7 mus sp. b3 (
167	514	14.6	573	2	Q8WJ38_HUMAN	Q8wj38 homo sapien	240	454	12.9	137	1	HV11_MOUSE	P01755 mus musculus
168	512.5	14.6	477	2	Q659B1_RAT	Q659b1 rattus norv	241	454	12.9	477	2	Q510J1_RAT	Q510j1 rattus norv
169	511.5	14.5	134	2	Q65ZR6_MOUSE	Q65zr6 mus musculus	242	454	12.9	479	2	Q91WP5_MOUSE	Q91wp5 mus musculus
170	509	14.5	189	2	Q56917_HUMAN	Q56917 homo sapien	243	453.5	12.9	478	2	Q5FPQ3_RAT	Q5fpq3 rattus norv
171	508.5	14.4	117	2	Q9QXE9_MOUSE	Q9qxe9 mus musculus	244	451.5	12.8	478	2	Q6NVH3_HUMAN	Q6nvh3 homo sapien
172	507.5	14.4	142	2	Q924Q1_MOUSE	Q924q1 mus musculus	245	451.5	12.8	494	2	Q6ZW64_HUMAN	Q6zw64 homo sapien
173	507	14.4	143	2	Q924P6_MOUSE	Q924p6 mus musculus	246	450.5	12.8	140	1	HV02_MOUSE	P01746 mus musculus
174	507	14.4	594	2	Q5FW13_XENTR	Q5fw13 xenopus tro	247	450.5	12.8	496	2	Q96KX8_HUMAN	Q96kx8 homo sapien
175	506.5	14.4	140	2	Q924R2_MOUSE	Q924r2 mus musculus	248	449.5	12.8	119	2	Q9GYZ2_MOUSE	Q9gyz2 mus musculus
176	506	14.4	497	2	Q8WY24_HUMAN	Q8wy24 homo sapien	249	449.5	12.8	120	2	Q920E8_MOUSE	Q920e8 mus musculus
177	505.5	14.4	146	2	Q924R8_MOUSE	Q924r8 mus musculus	250	448	12.7	483	2	Q6MZX9_HUMAN	Q6mzx9 homo sapien

251	448	12.7	487	2	Q99KA4_MOUSE	Q99ka4 mus musculus	RT
252	447	12.7	479	2	Q5BK12_RAT	Q5bk12 rattus norv	RL
253	446	12.7	114	2	Q9JL81_MOUSE	Q9jl81 mus musculus	RN
254	446	12.7	333	1	QCB_RAT	R20761 rattus norv	RP
255	446	12.7	487	2	Q80Z17_MOUSE	Q80z17 mus musculus	RX
256	445	12.6	234	2	Q8N355_HUMAN	Q8n355 homo sapien	RA
257	444.5	12.6	484	2	Q8V8A0_MOUSE	Q8v8a0 mus musculus	RD
258	444	12.6	479	2	Q7TMK4_MOUSE	Q7tmk4 mus musculus	RE
259	443	12.6	236	2	Q6GMX4_HUMAN	Q6gmx4 homo sapien	RF
260	443	12.6	478	2	Q7Z379_HUMAN	Q7z379 homo sapien	RG
261	442	12.5	487	2	Q5BK15_RAT	Q5bk15 rattus norv	RH
262	441	12.5	110	2	Q9JL77_MOUSE	Q9jl77 mus musculus	RI
263	440.5	12.5	234	2	Q5HFG0_STAAC	Q5hfg0 staphylococ	RJ
264	440.5	12.5	492	2	Q7Z374_HUMAN	Q7z374 homo sapien	RK
265	439.5	12.5	233	2	Q8TBC9_HUMAN	Q8tbc9 homo sapien	RL
266	439	12.5	234	2	Q6GMW3_HUMAN	Q6gmw3 homo sapien	RM
267	439	12.5	234	2	Q6NS95_HUMAN	Q6ns95 homo sapien	RN
268	438.5	12.5	229	2	Q6G8W7_STAAS	Q6g8w7 staphylococ	RO
269	438.5	12.5	229	2	Q8NW97_STAAM	Q8nw97 staphylococ	RP
270	438	12.4	236	2	Q6GMX3_HUMAN	Q6gmx3 homo sapien	RQ
271	437.5	12.4	138	1	HV48_MOUSE	P03980 mus musculus	RR
272	437.5	12.4	329	1	GCC_RAT	P20762 rattus norv	RS
273	437.5	12.4	479	2	Q9RM22_MOUSE	Q9rm22 mus musculus	RT
274	437	12.4	236	2	Q6GMV7_HUMAN	Q6gmv7 homo sapien	RU
275	434.5	12.3	235	2	Q567P1_HUMAN	Q567p1 homo sapien	RV
276	434.5	12.3	617	2	Q569B3_RAT	Q569b3 rattus norv	RW
277	434	12.3	236	2	Q8NEJ1_HUMAN	Q8nej1 homo sapien	RX
278	433.5	12.3	486	2	Q91207_MOUSE	Q91207 mus musculus	RY
279	433	12.3	96	2	Q5R3X6_MOUSE	Q5r3x6 mus musculus	RZ
280	433	12.3	120	1	HV50_MOUSE	P06329 mus musculus	SA
281	432	12.3	109	2	Q9JL75_MOUSE	Q9jl75 mus musculus	SB
282	432	12.3	118	2	Q5R3X0_MOUSE	Q5r3x0 mus musculus	SC
283	432	12.3	483	2	Q566J7_MOUSE	Q566j7 mus musculus	SD
284	431	12.2	97	2	Q5R3Y0_MOUSE	Q5r3y0 mus musculus	SE
285	430.5	12.2	235	2	Q6GMW6_HUMAN	Q6gmw6 homo sapien	SF
286	428.5	12.2	235	2	Q6IN99_HUMAN	Q6in99 homo sapien	SG
287	428	12.2	118	2	Q9Z1C4_MOUSE	Q9z1c4 mus musculus	SH
288	427	12.1	519	2	Q6N092_HUMAN	Q6n092 homo sapien	SI
289	426.5	12.1	233	2	Q6NS96_HUMAN	Q6ns96 homo sapien	SJ
290	426	12.1	236	2	Q6IPQ0_HUMAN	Q6ipq0 homo sapien	SK
291	426	12.1	262	2	Q65Z11_MOUSE	Q65z11 mus musculus	SL
292	425	12.1	117	1	HV05_MOUSE	P01753 mus musculus	SM
293	425	12.1	232	2	Q5FWF9_HUMAN	Q5fwf9 homo sapien	SN
294	424.5	12.1	147	2	Q9Z5S3_MOUSE	Q9z5s3 mus musculus	SO
295	424.5	12.1	231	2	Q6GNB8_XENLA	Q6gnb8 xenopus lae	SP
296	424.5	12.1	237	2	Q6DHW4_HUMAN	Q6dhw4 homo sapien	SQ
297	424	12.0	234	2	Q6GMV8_HUMAN	Q6gmv8 homo sapien	SR
298	423	12.0	149	1	KV5A_MOUSE	P01633 mus musculus	SS
299	422	12.0	117	1	HV14_MOUSE	P01758 mus musculus	ST
300	422	12.0	233	2	Q6GMW4_HUMAN	Q6gmw4 homo sapien	SV

ALIGNMENTS

RESULT 1

ETXE_STAAM STANDARD; PRT; 257 AA.

AC P12933;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Enterotoxin type E precursor (SBE).

GN Name=entE;

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=1280;

RN [1]

RC NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 28-74.

RP STRAIN=MJB265;

RX MEDLINE=88257005; PubMed=3384800;

RA Couch J.D., Soltis M.T., Betley M.J.;

RT "Cloning and nucleotide sequence of the type E staphylococcal

enterotoxin gene.";

J. Bacteriol. 170:2954-2960 (1988).

[2]

3D-STRUCTURE MODELING.

MEDLINE=96022987; PubMed=7552730;

Swaminathan S., Porey W.F. Jr., Fletcher J., Sax M.;

"Residues defining V beta specificity in staphylococcal enterotoxins.";

Nat. Struct. Biol. 2:680-686 (1995).

-I- FUNCTION: Staphylococcal enterotoxins cause the intoxication by high fever, hypotension, diarrhea, shock, and in some cases death.

-I- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary for the toxin interaction with MHC class II (By similarity).

-I- SUBCELLULAR LOCATION: Secreted.

-I- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.

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EMBL; M21319; AAA26617.1; -; Genomic_DNA.

PIR; A28179; A28179.

PDB; 1SBE; Model; @=28-257.

InterPro; IPR006177; Bctrl_tox.

InterPro; IPR006123; Staph/Strep_toxin.

InterPro; IPR006126; Staph/Strep_tox.

Pfam; PF02876; Staph_Strep_tox_C; 1.

Pfam; PF01123; Staph_Strep_toxin; 1.

PRINTS; PR00279; BACTRTOXIN

PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.

PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

3D-structure; Antigen; Direct protein sequencing; Enterotoxin; Metal-binding; Signal; Superantigen; Toxin; Zinc.

SIGNAL 1 27

CHAIN 28 257 Enterotoxin type E.

METAL 211 211 Zinc (By similarity).

METAL 249 249 Zinc (By similarity).

METAL 251 251 Zinc (By similarity).

HELIX 33 35

HELIX 39 41

STRAND 42 42

TURN 46 47

HELIX 48 51

HELIX 52 54

STRAND 59 64

TURN 66 67

STRAND 69 69

TURN 73 74

STRAND 75 79

TURN 83 84

STRAND 90 94

HELIX 98 104

TURN 105 106

STRAND 109 113

STRAND 115 116

TURN 118 119

STRAND 128 132

STRAND 135 137

TURN 139 140

STRAND 142 142

STRAND 152 152

STRAND 154 155

TURN 156 157

STRAND 163 163

STRAND 171 171

STRAND 173 175

HELIX 176 190

Db 356 -----KGRPKAPQVVTIPPPKEQMAKDKVSLT 382

QY 592 CFLNNFYPKIDINVKWIKDSERQNGVLNSWTDODSKDSTYSMSSTLTLDKDEYERHNSVT 651

Db 383 CMITDFPEPDIYEWQWNGQPAEN-YKNTOPIMDT-DGSFYISKLVNQSKEAGNTFT 440

QY 652 CEATHK 657

Db 441 CSQLHE 446

RESULT 3

Q5BUZ2_RAT PRELIMINARY; PRT; 458 AA.

AC Q5BJZ2; 30, Created

DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)

DE LOC367586 protein.

GN Names=LOC367586;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Thymus;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalski U., Smallos D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RL and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Thymus;

RG NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

CC -I- FUNCTION: Beta-2-microglobulin is the beta-chain of major

CC histocompatibility complex class I molecules (By similarity).

CC -I- SUBCELLULAR LOCATION: Secreted (By similarity).

DR EMBL; BC091272; AAH91272.1; -, mRNA.

DR SNR; Q5BUZ2; 21-454.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig cl.

DR InterPro; IPR003596; Ig v.

DR Pfam; PF07654; Cl-set; 3.

DR SMART; SM00409; IG; 3.

DR SMART; SM00407; IGC1; 2.

DR SMART; SM00406; IG; 1.

DR PROSITE; PS50835; IG LIKE; 4.

KW Immunoglobulin domain; Repeat.

SQ SEQUENCE 458 AA; 50161 MW; A0A61DCDD2CA433E CRC64;

Query Match 27.9%; Score 983.5; DB 2; Length 458;

Best Local Similarity 36.3%; Pred. No. 9.8e-53;

Matches 240; Conservative 64; Mismatches 113; Indels 245; Gaps 17;

QY 1 EVLOQSGDPLVKPGASVKISKASGVSYFYGMHWKQSPGKGLWIGRINPNNGVTLY 60

Db 20 QVLOQSGELVKPGSVKISKASGYTFNYDIHWIKQOPGNGLEWIGHYFCNGNTKY 79

QY 61 NQKFKDKATLVDSSTTAYMELRLSTSEDSAVYYCARSTMTIYNYMVDYNGQGTSTVSS 120

Db 80 NQKFNKGATLTADKSSSTAYMQLSSTSEDSAVYFCARD-YFDGY--DYMGQGVMTVSS 136

QY 121 AKTTTPSVVPLAPGSAQTNSMTVLGLVKGYPEPVVTWNSGSLSSGVHTTFAVLQSD 180

Db 137 AETTAPSVVPLAPGTALKNSMTVLGLVKGYPEPVVTWNSGSLSSGVHTTFAVLQSG 196

QY 181 LYTSSSVTVPSSTWSPSETVTCNVAPASSTKVDKIVPRDSDGSPSEKSEINEKDLRKK 240

Db 197 LYTSSSVTVPSSTWSSQAVTCNVAPASSTKVDKIVPREC----- 238

QY 241 SELQGTALGNLKOIYYYNKAITSSSEKSAQDFLTNTLLFKGFTGHPWYNDLLVDLGSTA 300

Db 239 -----NPCGCTGSEVSS-----VFIFPPKTKDVL----- 262

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEKKYPINLWIDG-- 358

Db 263 -----TITL-----TP-KVTCVVVDISQND-----PEVRFSEFIDVVE 294

QY 359 ---KQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGGKVGRLIVPHSSE 415

Db 295 VHTAQTAAHEKQSNSTLR--SVSELPVHRDLNGK-----TFKCKVN----- 335

QY 416 GSTVSYDLFDAQGYPTLRIYRDNTTISSTLSISLYLYTTSIVMTQPTSLLSVAGD 475

Db 336 -----SGAPPAPI----- 343

QY 476 RVITTCASQSVNDVANYQKPGQSPKLLISYTSRYAGVPDRFSSGSGYGTDFTLISS 535

Db 344 -----EKST-----KPEGTPR----- 355

QY 536 VQAEADAAYVFCQDYNSPPTFFGGGTLEIKRADAAPTYSIFPPSSSEQLTSGGSAVWCFLN 595

Db 356 -----GQVYTWAPPKEMTQSVSITCMVK 381

QY 596 NFVPKIDINVKWIKDSERQNGVLNSWTDQSKDSTYSMSSTLTLDKDEYERHNSYTCEAT 655

Db 382 GFYPDPDIYEWKMGQPOEN-YKNTPTTMDT-DGSFYISKLVNKKETWQGTTCVSVL 439

656 HK 657

Db 440 HE 441

RESULT 4

Q6PJAT_MOUSE PRELIMINARY; PRT; 472 AA.

AC Q6PJAT; 27, Created

DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)

DE Hypothetical protein.

GN Name=Igh-1a;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Czech II;

RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.

RC Expression driven by an MMTV-LTR enhancer.;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,


```
DB      208 RGLVHTSTEPSVNYDLFGAQGYGNTLLRIYDRNKTISSENMHIDLYLTS 260
|||||:| :|:|||| |||| :||||||| |||| :| :|||:
|||||:| :|:|||| |||| :||||||| |||| :| :|||:
208 RGLVHTSTEPSVNYDLFGAQGYGNTLLRIYDRNKTISSENMHIDLYLTS 260

RESULT 6
ETXA_STRAU
ID      ETXA_STRAU      STANDARD;      PRT;      257 AA.
AC      POA0L2; P13163;
DT      01-JAN-1990 (Rel. 13, Created)
DT      01-JAN-1990 (Rel. 13, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      Enterotoxin type A precursor (SEA).
GN      Name=entA;
OS      Staphylococcus aureus.
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=1280;
ON      [1]_
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=PRI337;
RX      MEDLINE=8722293; PubMed=3335483;
RA      Betley M.J., Mekalanos J.J.;
RT      "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
RL      J. Bacteriol. 170:34-41 (1988).
RN      [2]
RP      PROTEIN SEQUENCE OF 25-257.
RX      MEDLINE=8722293; PubMed=3584106;
RA      Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
RT      "Complete amino acid sequence of staphylococcal enterotoxin A.";
RL      J. Biol. Chem. 262:7006-7013 (1987).
RN      [3]
RP      X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX      MEDLINE=95354648; PubMed=7628431;
RA      Schae E.M., Zaitseva I., Zaitsev V.N., Dohlsten M., Kalland T.,
RT      Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
RT      "Crystal structure of the superantigen staphylococcal enterotoxin type
RL      A.";
RL      EMBO J. 14:3292-3301 (1995).
RN      [4]
RP      X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX      MEDLINE=97113025; PubMed=8943278; DOI=10.1074/jbc.271.50.32212;
RA      Sundstroom M., Hallen D., Svensson A., Schae E., Dohlsten M.,
RA      Abrahamson L.;
RT      "The Co-crystal structure of staphylococcal enterotoxin type A with
RT      Zn2+ at 2.7-A resolution. Implications for major histocompatibility
RT      complex class II binding.";
RL      J. Biol. Chem. 271:32212-32216 (1996).
RN      [5]
RP      3D-STRUCTURE MODELING.
RX      MEDLINE=96022987; PubMed=7552730;
RA      Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
RT      "Residues defining V beta specificity in staphylococcal
RT      enterotoxins.";
RL      Nat. Struct. Biol. 2:680-686 (1995).
RN      [6]
RP      COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX      MEDLINE=97334373; PubMed=9191070; DOI=10.1006/jmbi.1997.1023;
RA      Schae E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT      "A structural and functional comparison of staphylococcal enterotoxins
RT      A and C2 reveals remarkable similarity and dissimilarity.";
RL      J. Mol. Biol. 269:270-280 (1997).
CC      -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC      staphylococcal food poisoning syndrome. The illness characterized
CC      by high fever, hypotension, diarrhea, shock, and in some cases
CC      death.
CC      -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC      for the toxin interaction with MHC class II.
CC      -1- SUBUNIT: Monomer.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- MISCELLANEOUS: This toxin seems to be coded by a bacteriophage.
CC      -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC      family.
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CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
-----
DR      EMBL; M18970; AAA26681.1; -; Genomic_DNA.
DR      PIR; A28664; A28664.
DR      PDB; 1DQ; X-ray; A=25-257.
DR      PDB; 1ESF; X-ray; A/B=25-257.
DR      PDB; 1I4G; X-ray; A/B=25-257.
DR      PDB; 1I4H; X-ray; A/B=25-257.
DR      PDB; 1LOS; X-ray; D=25-257.
DR      PDB; 1SEA; Model; @=25-257.
DR      PDB; 1SXT; X-ray; A/B=25-257.
DR      SMR; POA0L2; 25-257.
DR      InterPro; IPR006177; Bcrl tox.
DR      InterPro; IPR006123; Staph/Strep toxin.
DR      InterPro; IPR006126; Staph/Strep tox.
DR      InterPro; IPR006173; Staph_tox_OB.
DR      Pfam; PF02876; Staph_Strep_toxin; 1.
DR      PRINTS; PR00279; BACTRLTOXIN.
DR      PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR      PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW      3D-structure; Antigen; Direct protein sequencing; Enterotoxin;
KW      Metal-binding; Signal; Superantigen; Toxin; Zinc.
FT      SIGNAL      1..24
FT      CHAIN       25..257      Enterotoxin type A.
FT      METAL       211..211      Zinc.
FT      METAL       249..249      Zinc.
FT      METAL       251..251      Zinc.
FT      DISULFID    120..130
FT      CONFLICT    242..242
FT      HELIX       33..35
FT      HELIX       39..41
FT      TURN        44..45
FT      HELIX       46..55
FT      STRAND      59..65
FT      STRAND      75..78
FT      TURN        79..80
FT      STRAND      90..94
FT      HELIX       98..104
FT      TURN        105..106
FT      STRAND      109..114
FT      STRAND      116..116
FT      HELIX       117..119
FT      TURN        122..123
FT      TURN        126..127
FT      STRAND      128..132
FT      STRAND      135..137
FT      TURN        139..140
FT      STRAND      142..148
FT      STRAND      151..155
FT      TURN        156..157
FT      STRAND      158..160
FT      TURN        164..165
FT      STRAND      168..171
FT      STRAND      173..175
FT      HELIX       176..191
FT      TURN        193..194
FT      HELIX       197..199
FT      TURN        200..200
FT      STRAND      205..211
FT      STRAND      218..221
FT      TURN        222..223
FT      TURN        227..228
FT      TURN        230..232
FT      HELIX       233..237
FT      TURN        238..239
FT      STRAND      242..244
FT      TURN        245..247
FT      STRAND      249..255
SQ      SEQUENCE      257 AA; 29669 MW; ADEBF5BCAIF14677 CRC64;
```

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Query Match          26.9%; Score 948; DB 1; Length 257;
Best Local Similarity 76.4%; Pred. No. 7e-51;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDKRKSELOQTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDKRKSELOQTALGNLKOIYYNEKAKTENKESHDOFLOHTILFKGFFTD 84
QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTAQCMYGGVTLHDNNRLT 345
DB 85 HSWYNDLLVDFPDSKDIDVKYKGKVDLYGAYGYQCAGGTPNKTAQCMYGGVTLHDNNRLT 144
QY 346 EKKVPINLWIDGKQTTVPIDKVTSKKEVTYVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EKKVPINLWIDGKQTTVPIDKVTSKKEVTYVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNTTISSTSLSLSLYLYTT 458
DB 205 RGLIVFHTSTEPSVNYDLFGAQGYVNTLLRIYRDNTTINSENHMDIYLYTS 257

RESULT 7
ETXA STAAW
ID ETXA STAAW STANDARD; PRT; 257 AA.
AC POA011; P13163;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Enterotoxin type A precursor (SEA).
GN Name=entA; OrderedLocusNames=MW1889;
OS Staphylococcus aureus (strain MW2)
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC Staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death (By similarity).
CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BA000033; BAB95754.1; -; Genomic_DNA.
CC SMR; POA011; 25-257.
CC InterPro; IPR006177; Bcrl tox.
CC InterPro; IPR006123; Staph/Strep toxin.
CC InterPro; IPR006126; Staph/Strep tox.
CC InterPro; IPR006173; Staph tox OB.
CC Pfam; PF02876; Staph_Strep_tox_C; 1.
CC Pfam; PF01123; Staph_Strep_toxin; 1.
CC PRINTS; PR00279; BACTRLTOXIN.
CC PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
CC PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
CC Antigen; Complete proteome; Enterotoxin; Metal-binding; Signal;
CC Superantigen; Toxin; Zinc.

```

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FT SIGNAL          1 24
FT CHAIN          25 257
FT METAL          211 211
FT METAL          249 249
FT METAL          251 251
FT DISULFID       120 130
SQ SEQUENCE       257 AA; 29669 MW; ADBF5BCAIF14677 CRC64;

Query Match          26.9%; Score 948; DB 1; Length 257;
Best Local Similarity 76.4%; Pred. No. 7e-51;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDKRKSELOQTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDKRKSELOQTALGNLKOIYYNEKAKTENKESHDOFLOHTILFKGFFTD 84
QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTAQCMYGGVTLHDNNRLT 345
DB 85 HSWYNDLLVDFPDSKDIDVKYKGKVDLYGAYGYQCAGGTPNKTAQCMYGGVTLHDNNRLT 144
QY 346 EKKVPINLWIDGKQTTVPIDKVTSKKEVTYVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EKKVPINLWIDGKQTTVPIDKVTSKKEVTYVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNTTISSTSLSLSLYLYTT 458
DB 205 RGLIVFHTSTEPSVNYDLFGAQGYVNTLLRIYRDNTTINSENHMDIYLYTS 257

RESULT 8
G6GY7 STAAW
ID G6GY7 STAAW PRELIMINARY; PRT; 257 AA.
AC G6GY7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enterotoxin type A.
GN OrderedLocusNames=SAS1872;
OS Staphylococcus aureus (strain MSSA476)
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; EX571857; CA943678.1; -; Genomic_DNA.
DR SMR; Q6GY7; 25-257.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
SQ SEQUENCE       257 AA; 29669 MW; ADBF5BCAIF14677 CRC64;

Query Match          26.9%; Score 948; DB 2; Length 257;

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Best Local Similarity 76.4%; Pred. No. 7e-51;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSLQGTALGNLKOIYYNSKAITSEKSGADQPLTNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSLQGTALGNLKOIYYNEKAKTENKSHDQPLQHTILFKGFFTD 84
QY 286 HPWYNLLVLDLGGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HSWYNLLVDFDSKDIIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDFGKQV 405
Db 145 EEKVPINLWDGKQNTVPLETVKTKNKVNTVQELDLQARRYLQEKYLNYSVDFGKQV 204
QY 406 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYTT 458
Db 205 RGLIVFTSTEPSVNYDLFGAQOQYNTLLRIYRDNTKNTINSENHDIYLYTS 257

RESULT 9
Q931M4 STAA
ID Q931M4 STAA PRELIMINARY; PRT; 260 AA.
AC Q931M4;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DE Enterotoxin P.
GN Names=sep; OrderedLocuNames=SAV1948;
OS Staphylococcus aureus (strain Mu50 / ATCC 706699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=2131192; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Iwazawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekinizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshino K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; BA000017; BAB58110.1; -; Genomic_DNA.
DR HSSP; P13163; ILO5.
DR SMR; Q931M4; 28-260.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Stap Strp toxin; 1.
DR Pfam; PF02876; Stap Strp tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00217; STAPH STREP TOXIN 1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
KW SEQUENCE 260 AA; 30016 MW; 15C2D36270FA8241 CRC64;

Query Match 26.9%; Score 948; DB 2; Length 260;
Best Local Similarity 76.4%; Pred. No. 7.1e-51;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSLQGTALGNLKOIYYNSKAITSEKSGADQPLTNTLLFKGFFTG 285
Db 28 SEKSEINEKDLRKSLQGTALGNLKOIYYNEKAKTENKSHDQPLQHTILFKGFFTD 87
QY 286 HPWYNLLVLDLGGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 88 HSWYNLLVDFDSKDIIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 147

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QY 346 EEKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDFGKQV 405
Db 148 EEKVPINLWDGKQNTVPLETVKTKNKVNTVQELDLQARRYLQEKYLNYSVDFGKQV 207
QY 406 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYTT 458
Db 208 RGLIVFTSTEPSVNYDLFGAQOQYNTLLRIYRDNTKNTINSENHDIYLYTS 260

RESULT 10
Q6FUB2 MOUSE
ID Q6FUB2 MOUSE PRELIMINARY; PRT; 465 AA.
AC Q6FUB2;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN Name=Igh-la;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.; DOI=10.1073/pnas.2426038999;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018280; AAH18280.1; -; mRNA.
DR HSSP; P01865; 1KB5.
DR SMR; Q6FUB2; 20-461.
DR MGI; MGI:96443; Igh-la.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

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QY 361 TTVPIDKVKTSKEVTVOELDLQARHYLHGKGLYNSDSFGKVGQRLIVFHSSEGSTVS 420
Db 263 -----IFPPKIKDVLMI---SLSPWMT 281
QY 421 YDLFDAQGYPDILLRIYRDNNTISSTLSLSLYLTTISVMTQPTSLLSVSGADRVIT 480
Db 282 CVVVDVSEDDPD-----VQISFVNVNEVLTAQTQT----- 312
QY 481 CKASQSVNDVAVYQKQPGSKLLISYTSRVAGVDPDFSGSGYGTDFTLTISVQA-- 538
Db 313 -----HREDYNSLTRVVSALP 328
QY 539 -----EDAAVYFCQDYNPPTFGGTGKLEIKRADAAPTIVSIFPPSSEQLTSGGASVVC 592
Db 329 IQHDMWSGKEFKCKVNNKALPAPIERTISKPGSVRAPQVYVLPPEPEMTKKQVTLTC 388
QY 593 FLNNFPYKDNVKKWDIGSERON-----GVLYNSWTDDSKDSTYSMSSTLTTLTKDYERH 647
Db 389 MVYDFMPEDIYVETWNTNGKTELNYKNTPEVLDs-----DGSYFMYSKLRVEKKNVVER 441
QY 648 NSYTCBATHK-TGTSPIVKSFR 669
Db 442 NSYSCSVVHEGLNHNHTTKSFR 464

RESULT 12
Q5BK05_RAT PRELIMINARY; PRT; 458 AA.
AC Q5BK05;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DE LOC367586 protein.
GN Name=LOC367586;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC -!- histocompatibility complex class I molecules (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC091257; AAH91257.1; -; mRNA.
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DR SMR; Q5BK05; 21-454.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS0835; IG LIKE; 4.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 458 AA; 49943 MW; 74D964EC1DFCD12F CRC64;

Query Match 26.8%; Score 944.5; DB 2; Length 458;
Best Local Similarity 35.0%; Pred. No. 2.6e-50;
Matches 232; Conservative 71; Mismatches 114; Indels 245; Gaps 16;

QY 1 EYVLOQSGDPLVKPGASVKISKASQSYSTGYMHVVKSPGKLEWIGRINPNNGVTLY 60
Db 20 QVLOQSGAELAKPGSSVKISKASGYTFTSDVSVIKQTQGLLEYIYINTGSGGIY 79
QY 61 NOKFKDKATLTVDKSTTAYMELRSLTSDSAVYVCARSTMITNYVMDVYMGQSTSVTVSS 120
Db 80 TEKFKGKATLTVDKSSSTAFMQLSLTPEDTAVYYCTRD---GTRINDANGQSTSVTVSS 136
QY 121 AKTTTPSVYPLAPGSAQTNSMVTGLCLVKGYFPEPTVTWNSGSLSSSGVHTFPAVLQSD 180
Db 137 AETTAPSVYPLAPGTALKSNMVTGLCLVKGYFPEPTVTWNSGALSSSGVHTFPAVLQSG 196
QY 181 LYTLSSTVTPSTWSPSETVTCNVAHPASSTKVDKIKIVPRDGGPSEKSEINEKDLRKK 240
Db 197 LYTLSSTVTPSTWSSQAVTCNVAHPASSTKVDKIKIVPREC----- 238
QY 241 SELQGTALGNLQIYYVNSKATISSEKSAQDLTNTLLFKGPTGHPWYNDLVLGSTA 300
Db 239 -----NPGCGTGSVSS-----VPFPKTKDVL----- 262
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEKKVPINLWDIG-- 358
Db 263 -----TITL-----TP-KVTCVVVDISQND-----PEVRFSEWIDDE 294
QY 359 ---KQTTVIDKVKTSKEVTVOELDLQARHYLHGKGLYNSDSFGKVGQRLIVPHSSE 415
Db 295 VHTAQTHAPEKQSNSTLR--SVSELPVHRDMLNGK-----TPKCKVN----- 335
QY 416 GSTVSVDLFDAGQYDPTLLRIYRDNNTISSTLSLSLYLTTISVMTQPTSLLSVAGD 475
Db 336 -----SGAFPAP----- 343
QY 476 RVTTTCASQSVNDVAVYQKQPGSKLLISYTSRVAGVDPDFSGSGYGTDFTLTIS 535
Db 344 -----EKSIS-----KPEGTFR----- 355
QY 536 VQAEADNAVFCQDYNPPTFGGTGKLEIKRADAAPTIVSIFPPSSSEQLTSGGASVVCFLN 595
Db 356 -----GFQVYTMAPPKEEMTQSQVSITCMVK 381
QY 596 NFYPKDNVKKWDIGSERONGVLYNSWTDDSKDSTYSMSSTLTTLTKDEYERHNSYTCAT 655
Db 382 GFYPDPDIYETWRKMGQPOEN-YKNTPTPTWDT-DGSYFLYSKLVNKKETWQGGNTFTCSVL 439
QY 656 HK 657
Db 440 HE 441

RESULT 13
Q52L64_MOUSE PRELIMINARY; PRT; 240 AA.
ID Q52L64_MOUSE
AC Q52L64;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
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Db 146 SEQLTSGASVWFLNNFYPKDINVKWKIDGSRQVNLNSWTDQDSKDSYMSSTLTL 205
QY 640 TKDEYERHNSYTCATHTKTSTPIVKSFNRE 671
Db 206 TKDEYERHNSYTCATHTKTSTPIVKSFNRE 237

RESULT 15
Q6GFA8 STAAAR PRELIMINARY; PRT; 257 AA.
AC Q6GFA8 STAAAR PRELIMINARY; PRT; 257 AA.
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Enterotoxin type A.
GN OrderedLocusNames=SAR2043;
OS Staphylococcus aureus (strain MSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitz E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
DR ENBL; BX571856; CAG41028.1; -; Genomic_DNA.
DR SNR; Q6GFA8; 25-257.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 257 AA; 29674 MW; 56B0A6D952EDFED4 CRC64;

Query Match 26.5%; Score 935; DB 2; Length 257;
Best Local Similarity 75.5%; Pred. No. 4, 5e-50;
Matches 176; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKKSELOQTALGNLKQIYYNKAITSSEKADQFLTNLLFKGFFTG 285
Db 25 SEKSEINEKDLRKKSELOQTALGNLKQIYYNKAITENKESHDQFLQHTILFKGFFTN 84

QY 286 HPWYNLLVDLGSTAATSEYEGSSVDLYGAYGVCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HSWYNLLVDVDFDSKQIDVKYKGGKVDLYGAYGVCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWDGKQTTPIDKVKTSKKEVTQVLELDLQARHYLHGKFGLYNSDSFGKVKQ 405
Db 145 EEKVPINLWDGKQNTVPLETVTKNKQNTVQVLELDLQARHYLQEKYNSVDFGKVKQ 204

QY 406 RGLIVFHSSRGSTVSYDLFPAQGGYQPTLLRIYRDNRTTSSLSLSLYLT 458
Db 205 RGLIVFHTSTSPSYVDLFGAQGQNSNTLLRIYRDNKNTINSNNHIDIYLYTS 257

RESULT 16
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Q58E56_MOUSE
ID Q58E56_MOUSE PRELIMINARY; PRT; 477 AA.
AC Q58E56;
DT 10-MAY-2005 (T-EMBLrel. 30, Created)
DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)
DE Igh-1a protein.
GN Name=Igh-1a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenker C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Spletten L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedtin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC092061; AAH92061.1; -; mRNA.
DR MGI; MGI:96443; Igh-1a.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IEA.
DR GO; GO:0005771; C:multivesicular body; IEA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IEA.
DR GO; GO:0003033; P:antigen processing; IEA.
DR GO; GO:0008958; P:complement activation, classical pathway; IEA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IEA.
DR GO; GO:0008333; P:endosome to lysosome transport; IEA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IEA.
DR GO; GO:0006910; P:phagocytosis, recognition; IEA.
DR GO; GO:0050871; P:positive regulation of B cell activation; IEA.
DR GO; GO:0050778; P:positive regulation of immune response; IEA.
DR GO; GO:0050766; P:positive regulation of phagocytosis; IEA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IEA.
DR GO; GO:0001798; P:positive regulation of type I hypersensitivity; IEA.
DR GO; GO:0030162; P:regulation of proteolysis and peptidolysis; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IG1; 1.
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DR	PROSITE; PS50835; IG_LIKE; 4;	
DR	PROSITE; PS00290; IG_MHC; UNKNOWN 1.	
SQ	SEQUENCE 477 AA; 52222 MW; 519211BE5EA12364 CRC64;	
	Query Match 26.4%; Score 929.5; DB 2; Length 477;	
	Best Local Similarity 33.9%; Pred. No. 2.3e-49;	
	Matches 240; Conservative 51; Mismatches 128; Indels 289; Gaps 14;	
Qy	1	EVQLQSGPDLVKPGASVKISKASGYSTGYMHVVKSPGKGLRWIGRIINPNNGVTLY 60
Db	20	EVQLHQSGPELVEAGASVKLSKASGYTFGDIYVHVVKSHGSKSLDWIGNIYPNNGNDY 79
Qy	61	NQKFKDKATLVTDKSTTAYMELRSITSDSAVYICARSTMI---TNYMDYVKGQGTSTV 117
Db	80	NQKFKGKATLVTDKASSTAYMELRSITSDSAVYICARGNVYIYSDQYFDNMGQGTIT 139
Qy	118	VSSAKTTPSPVPLAPGSAQAQNSMTVLGCLVKGYPEPPTVWNSGSLSSGVHTFPAPVL 177
Db	140	VSSAKTAPSPVPLAPVCGGTGSSVTLGCLVKGYPEPPTLVWNSGSLSSGVHTFPALL 199
Qy	178	QSDLYTLSSSVTPSPSTWPTVTCNVAPASSTKVDKIVPRDSGGPSEKSEINEKDL 237
Db	200	QSGLYTLSSSVTTSNTPSQITTCNVAPASSTKVDKIEPR----- 242
Qy	238	RKSELSQGTALGNLKIYYNSKAITSSSEKSDQFLTNLLPKGPTGHPWYNDLLVDLG 297
Db	243	----- 242
Qy	298	STAATSEYEGSSVDLYGAYYQCAGGTPNKTACMYGGVTLHDNNRLTBKKVPINLWID 357
Db	243	-----VPI----- 245
Qy	358	GKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLGYNDSFGGKVGQLIVFHSSEG 417
Db	246	---TQNPCLPKCEPCAA-----PDLLGGP----- 268
Qy	418	TVSYDLFDAQQYPPDPLLRIYRDNVTISSTLSLSILYLTSTVMTQTTPTSLLSVAGDRV 477
Db	269	----SVFIFFPKIKQVLM-----ISLPMVTCVV----- 294
Qy	478	TITCKASQSVNDVAWYQKPGSPKLLISYTSRYAGVPDRFSGSGYGTDFTLTISVQ 537
Db	295	-----DVSED-----DPDVQISW-----FVNVE 313
Qy	538	AEDAAYVFCQDDYNSPPTGGGKLEIKRAD----- 568
Db	314	VHTAQQTTHREDYNS--TLRVVSALPIQHDWMSGKEFKCKVNNRALPSPIETISKPRG 371
Qy	569	--AAPTVISIIPPSSEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQGVLSNWDQDS 626
Db	372	PVRAPQVYVLPPEAEEMTKKEFSLTTCMTGFLPAEIAVDWTSNGRTEQN--YKNTATVLD 430
Qy	627	KDSTYSMSSTLTLDKDEYERHNSYTCETHK-----TSTSPIVKSFNR 669
Db	431	-DGSFYFMYSKLRVQKQSWERGSIFACSVVHEGLHNLTKTISRSLSGK 477
RESULT 17		
Q9DBL4 MOUSE		
ID	Q9DBL4_MOUSE PRELIMINARY; PRT; 473 AA.	
AC	Q9DBL4_MOUSE PRELIMINARY; PRT; 473 AA.	
DT	01-JUN-2001 (TrEMBLrel. 17, Created)	
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:181006009 product:Immunoglobulin heavy chain 6 (heavy chain of IgM), full insert sequence.	
DE	Name:Igh-1a;	
GN	Mus musculus (Mouse).	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;	
OC	Muridae; Murinae; Mus.	
NCBI_TaxID=10090;		

RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=C57BL/6J; TISSUE=Pancreas;	
RX	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;	
RA	Carninci P., Hayashizaki Y.;	
RT	"High-efficiency full-length cDNA cloning.";	
RL	Meth. Enzymol. 303:19-44(1999).	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=C57BL/6J; TISSUE=Pancreas;	
RX	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;	
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,	
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,	
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,	
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,	
RA	Kado T., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,	
RA	Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,	
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,	
RA	Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,	
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,	
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,	
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,	
RA	Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,	
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,	
RA	Nordone P., Ringwald M., Rodriguez I., Sakamoto N.,	
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,	
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,	
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohseki S.,	
RA	Hayashizaki Y.;	
RT	"Functional annotation of a full-length mouse cDNA collection.";	
RL	Nature 409:685-690(2001).	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=C57BL/6J; TISSUE=Pancreas;	
RA	The FANTOM Consortium,	
RT	"The RIKEN Genome Exploration Research Group Phase I & II Team;	
RT	"Analysis of the mouse transcriptome based on functional annotation of	
RT	60,770 full-length cDNAs.";	
RL	Nature 420:563-573(2002).	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=C57BL/6J; TISSUE=Pancreas;	
RX	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;	
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,	
RA	Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;	
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to	
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";	
RL	Genome Res. 10:1617-1630(2000).	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=C57BL/6J; TISSUE=Pancreas;	
RX	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;	
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,	
RA	Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,	
RA	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,	
RA	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,	
RA	Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,	
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,	
RA	Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;	
RT	"RIKEN integrated sequence analysis (RISA) system-384-format	
RT	sequencing pipeline with 384 multicapillary sequencer.";	
RL	Genome Res. 10:1757-1771(2000).	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=C57BL/6J; TISSUE=Pancreas;	
RX	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;	
RA	Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,	
RA	Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,	
RA	Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,	
RA	Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,	
RA	Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,	
RA	Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,	
RA	Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K., Sakai T.,	
RA	Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,	

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RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK007918; BAB25349.1; -, mRNA.
DR PIR; PH1165; PH1165.
DR PIR; S19966; S19966.
DR PIR; S26746; S26746.
DR HSSP; P01864; IBOG.
DR SMR; Q9D8L4; 20-469.
DR Ensemble; ENSMUSG00000054328; Mus musculus.
DR MGI; MGI:96443; Igh-1a.
DR GO; GO:0042543; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0005771; C:multivesicular body; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0030333; P:antigen processing; IDA.
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0008333; P:endosome to lysosome transport; IDA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0050871; P:positive regulation of B cell activation; IDA.
DR GO; GO:0050778; P:positive regulation of immune response; IDA.
DR GO; GO:0005766; P:positive regulation of phagocytosis; IDA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001798; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0030162; P:regulation of proteolysis and peptidolysis; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 26.2%; Score 924.5; DB 2; Length 473;
Best Local Similarity 33.8%; Pred. No. 4.7e-49;
Matches 239; Conservative 53; Mismatches 123; Indels 293; Gaps 15;

QY 1 EVQLQSGDPLVPGASVKISKASGYFTGYMHVWYKQSPKGLWIGRIINPNNGVTLY 60
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLKQSGAELVPGASVKISKASGYFTDYVINWVKQRPQGLWIGKIGPGSGSTY 79
QY 61 NQPKFKATLTVDKSSSTATWELRLTSSEDSAVYFCARSTWITNYVMD----YNGQGTSTV 117
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 NEKFKGKATLTADKSSSTATWELRLTSSEDSAVYFCARS----GYDYDFWYNGQGTSTV 135
QY 118 VSSAKTTPPSVPLAPGSAQTSMVTLGCLVKGYPPEVTVTWNSGSLSSGVHTTPAVL 177
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
136 VSAKATTPSVPLAPVCGGTTGSSVTLGCLVKGYPPEVTVTWNSGSLSSGVHTFPALL 195
QY 178 QSDLYTLSSSVTPSPSTWSETVCNVAHPASSTKVDKIVPRDSGGSPKSEINEKOL 237
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
196 QSGLYTLSSSVTVTSNTWPSQTICNVAHPASSTKVDKIEPR----- 238
QY 238 RKKSELGQTALGNLKOIYYNSKAITSSEKSAQDFLNTLLFKGFTGHPWYNDLLVDLG 297
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
239 ----- 238
QY 298 STAATSEYSGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNRLTEKKYPIINLWID 357
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
239 -----VPI----- 241
QY 358 GKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGLVIFHSSEGS 417
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
242 ---TQNPCLKECPCAA-----PDLLGGP----- 264
QY 418 TVSYDLFDAQGVDPDILLRIYRNTTISSTLSISLYLTTSIVMTQPTSTLLVSAGDRV 477
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

265 ----SVIFPPPKIKOVLV-----ISLSPWTCVVV----- 290
478 TITCKASQSVNDVAVYQQKQSPKLLISYTSRYAGVDPDRFSGGYGDTFLTITSSVQ 537
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
291 -----DVSED-----DPDVQISW-----FVNVE 309
QY 538 AEDAIVFOODVNSPPTFGGTYKLEIKRAD----- 568
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
310 VHTAQQTQTHREDYNS--TLRVVSALPIQHDWMMSGKEFKCKVNNRALLPSPIETISKPRG 367
QY 569 --AAPTIVSIPPSSEQLTSGASVVCFLNNFYPKDINVKWKIDGSESRQNGVLSWTDODS 626
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
368 PVRAPQVYVLPPEAEWTKKPELSLTGFLPAETAVDWTSGRTQN--YKNTATVLDS 426
QY 627 KDSTYSMSSTLTITKDEYERHNSYTCETHK-----TSTSPIVKSNFR 669
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
427 -DGSYFMYSKLRVQKSTWERSLFACSVHVEGLHNLHTTKTISRSLGK 473

RESULT 18
Q99SU3 STAAH
ID Q99SU3 STAAH PRELIMINARY; PRT; 260 AA.
AC Q99SU3; 2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Enterotoxin P.
GN Names-sep; OrderedLocusNames=SA1761;
OS Staphylococcus aureus (strain N315);
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshino A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
RA Katsuhisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240 (2001).
DR EMBL; BA000018; BAB43036.1; -, Genomic_DNA.
DR PIR; C89984; C89984.
DR HSSP; P13163; 1SXT.
DR SMR; Q99SU3; 28-260.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH STREP TOXIN 1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 260 AA; 29708 MW; 087C5B4EC028CFDB CRC64;

Query Match 26.1%; Score 918; DB 2; Length 260;
Best Local Similarity 73.0%; Pred. No. 5.2e-49;
Matches 170; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLKKSELOQTALGNLKOIYYNSKAITSSEKSAQDFLNTLLFKGFTG 285
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
28 SEKSEINEKDLKKSELOQTALGNLKOIYYNSKAITSSEKSAQDFLNTLLFKGFTG 87
QY 286 HPWYNDLLVDLGSSTAATSEYSGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNRLT 345
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
88 HPWYNDLLVDLGSSTAATSEYSGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNRLT 147
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Qy	515	GVPDRFGSGYGTDFTLTITISVQAEADAAVFCQDYNSPPPTFGGTTKLEIKRADAAPTVS	574
Dd			
Dd	62	GVPDRFGSGSGTDFTLKISRVEAEDLGIVFCSQSTHVPGTGGTGKLEIKRADAAPTVS	121
Qy	575	IFPSSSEQLTSGGASVVCFLNFPKDINVKWKIDGSRONGVLNWSWTDQDSKOSTYSMS	634
Dd	122	IFPSSSEQLTSGGASVVCFLNFPKDINVKWKIDGSRONGVLNWSWTDQDSKOSTYSMS	181
Qy	635	STLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRRNE	671
Dd	182	STLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRRGE	218

RESULT 22

Q6PF95_MOUSE
ID Q6PF95_MOUSE PRELIMINARY; PRT; 464 AA.

AC Q6PF95

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBurel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBurel. 27, Last annotation update)

DE Hypothetical protein.

GN Name=Igh-1a;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.

RX NCBI_TaxId=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=CZECH II;

RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
Expression driven by an MMTV-LTR enhancer.;
MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg B.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickens M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=CZECH II;

RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
Expression driven by an MMTV-LTR enhancer.;

RC Strausberg R.;

RL Submitted (SEP-2003) to the ENBL/GenBank/DBJ databases.
ENBL; BC057672; AAHS7672.1; -; mRNA.

DR HGSP; P01865; 1KB5.

DR MGI; MGI:96443; Igh-1a.

DR GO; GO:0003823; P; antigen binding; IEA.

DR InterPro; IPRO03599; Ig.

DR InterPro; IPRO07110; Ig-like.

DR InterPro; IPRO03597; Ig cl.

DR InterPro; IPRO03006; Ig_MHC.

DR InterPro; IPRO03596; Ig_v.

DR Pfam; PF07654; Cl-set; 3.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 3.

Query Match		25.5%;	Score 897;	DB 2;	Length 468;
Best Local Similarity		32.9%;	Pred. No. 2.4e-47;		
Matches		225;	Conservative	63;	Mismatches 143; Indels 252; Gaps 12;
QY	1	EVOLQSGDPLVKPGASVKISCKASGYFTGYMHVVKQSPGKLEWIGRINPNNGVTLY	60		
Db	20	EVOLQSGAELVRPGASVKLSCTASGPNIKDSLHWVKQRPQGLWIGWIDPEGETKY	79		
QY	61	NOKFKDKATLVDKSGSTTAYMELRSITSDSAVYYCARSTMINTNYVMDYWGQTSVTVSS	120		
Db	80	APKFDQKATITADTSNTAYLQLSLTSDTAIYYCARNLLYGGY-YDYWGQGTITIVSS	138		
QY	121	AKTTSPSVYPLAPGSAQAQNSMTYGLVKGYPEPVTVTWNSGSLSSGVHFPFPAVLQSD	180		
Db	139	AKTTAPSVYPLAPVCGDGTGSSVTGLVKGYPEPVTVTWNSGSLSSGVHFPFPAVLQSD	198		
QY	181	LYTLSSSVTPSPSTWSPSETVTCNVHPASSTKVKKIVPRDSGPGSEKEEINEKDLRKK	240		
Db	199	LYTLSSSVTVTSSTWSPSQSITCNVHPASSTKVKKIEPR---GPTIKPCP-----	246		
QY	241	SELQGTALGNLKOIYYNSKAITSSSEKSADQFLNTLLFKGFTGHPWNTDLLVDLGSTA	300		
Db	247	-----	246		
QY	301	ATSEYEGSSVDLYGAYGYQCAGGTGNKTAQMYGVTLHDNNRLTEKKVPINLWIDGKQ	360		
Db	247	-----PCKCPAPN-----LLGGPSVF-----	262		
QY	361	TTVPIDKVKTSKEVTYVQBELDQARHYLHGKFGLYNSDSFGGKVQRLIVFHSSEGSTVS	420		
Db	263	-----IPPKIKDVLMI---SLSPMT	281		
QY	421	YDLFDAQQYVPTLLRIYRDNNTTISSTLSISLYLTYTIVMTQTPTSLLSAGDRVTIT	480		
Db	282	CVVDVDSDDPD-----VQISWFFNVNVEVLTAQTQT-----	312		
QY	481	CRASQSVSDNVAWYQQKPGSKLLISYTSRYAGVDPDRFSGSGYGTDFTLTISSVQA--	538		
Db	313	-----HREDYNSTLRVVSALP	328		
QY	539	-----EAAVYFCQDYNSPPTFGGTTKLEIKRADAAPTIVSIFPPSSBQLTSGGASVVC	592		
Db	329	IQHQDMSGKFKPKVNNKALPAPIERTISKPKGSVRAPQVYVLPPEPEEMTKKQVTLTC	388		
QY	593	FLNNFPKDKINVKWIDGSEKQY-----GVLSNWTQDQSKDSTYSMSSTLTITKDYERH	647		
Db	389	MVTDMPEDYVETWNTNGKTELNYKNTEPVLDSE-----DGSYFMYSKLRVEKKWVER	441		
QY	648	NSYTCEATHK-TSTSPIVKSFNR	669		
Db	442	NSYSCSVVHEGLNHHHTTKSFSR	464		
RESULT 26					
ID	Q4VBH1_RAT	PRELIMINARY;	PRT;	467	AA.
AC	Q4VBH1;				
DT	13-SEP-2005 (TrEMBLrel. 31, Created)				
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)				
DE	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)				
DE	LOC299354 protein.				
GN	Name=LOC299354;				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;				
OC	Muroidea; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Thymus;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				

Query Match		25.3%;	Score 891;	DB 2;	Length 467;
Best Local Similarity		31.8%;	Pred. No. 5.6e-47;		
Matches		211;	Conservative	88;	Mismatches 125; Indels 240; Gaps 15;
QY	1	EVOLQSGDPLVKPGASVKISCKASGYFTGYMHVVKQSPGKLEWIGRINPNNGVTLY	60		
Db	20	EVOLVETGGLVQGRSLKSLVASGFTFSSTWMIWIRQAPGKLEWVSSINTDGGSTYY	79		
QY	61	NOKFKDKATLVDKSSTTAYMELRSITSDSAVYYCARSTMI--TNYVMDYWGQTSVTV	118		
Db	80	PSVKGRTISRDAENAVTYLQWNSLRSEDATYYCAKGEYYGYNYPFYWGQGVMTV	139		
QY	119	SSAKTTPPSVYPLAPGSAQAQNSMTYGLVKGYFPPEPVTVTWNSGSLSSGVHFTFPAVLQ	178		
Db	140	SSAETTPASVYPLAPGTALKNSMTYGLVKGYFPPEPVTVTWNSGALSSGVHFTFPAVLQ	199		
QY	179	SDLYTLSSSVTPSPSTWSPSETVTCNVHPASSTKVKKIVPRDSGPGSEKEEINEKDLR	238		
Db	200	SGLYTLTSSVTVPSTWSPSQSITCNVHPASSTKVKKIVPRNCGGDKPC	250		
QY	239	KKSELQGTALGNLKOIYYNSKAITSSSEKSADQFLNTLLFKGFTTGHHPWNTDLLVDLGS	298		
Db	251	-----ICTGSEVSS-----VFIFPPKPKDVL-----	271		
QY	299	TAATSEYEGSSVDLYGAYGYQCAGGTGNKTAQMYGVTLHDNNRLTEKKVPINLWIDG	358		
Db	272	-----TITL-----TP-KVTCVVVDIS-----QDDPEVHFMSFVDD	301		
QY	359	-----KQTVPIIDKVKTSKEVTQBELDQARHYLHGKFGLYNSDSFGGKVQRLIVFHS	413		
Db	302	VEVHTAQTTPPEEQNFSTFR--SVSELPTLHQDWLNGR-----	337		
QY	414	SEGSTVSYDLFDAQQYVPTLLRIYRDNNTTISSTLSISLYLTYTIVMTQTPTSLLVSA	473		


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Db 338 -----337
QY 474 GDRVTITCKASVSNDVANYQQKPGSPKLLISYTSRRYAGVDPDRFSGSGYGTDFTLTI 533
Db 338 -----TFCKV-----TSAPFSPPEKTI 356
QY 534 SSVOAEDAAYFCQDYNPSPTFGGKGLIKRADAAPTVSIFFPSSEQLTSGGASVVCF 593
Db 357 SKPE-----GRQV-----PHYVTMSPTKEEMTQNEVSITCM 388
QY 594 LNNFYPKDINVKWIKDGSERQNGVLNSWTQDQSKDSTYSMSSTLTTLTKDEYERHNSVTC 653
Db 389 VKGFPPDIIVEMQNMGPQOEN-YKNTPTPTMDT-DGSYFLYSLKLVNKKERKQNGTFTCS 446
QY 654 ATHK 657
Db 447 VLHE 450

RESULT 27
Q8R3H6_MOUSE PRELIMINARY; PRT; 474 AA.
AC Q8R3H6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ighg protein.
GN Name=Ighg; Synonyms=AU044919;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH 11;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH 11;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RA Director MGC Project;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AAH25447.1; -, mRNA.
DR HSSP; P01869; ICL7.
DR SMR; Q8R3H6; 20-470.
DR MGI; MGI:2144967; AU044919.
DR MGI; MGI:2144967; Ighg.
DR GO; GO:0003823; F-antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 474 AA; 51749 MW; 8608B57C6CD2874A CRC64;

Query Match 25.2%; Score 888.5; DB 2; Length 474;
Best Local Similarity 35.0%; Pred. No. 8.1e-47;
Matches 234; Conservative 69; Mismatches 124; Indels 241; Gaps 18;

QY 1 EVLOQSGDPLVKPGASVKISKASGYSTFTGYMHVYKQSPGKGLEWIGRINPNNGVTLY 60
Db 20 QVLOQSGDPLVKPGASVKISKASGYSTFTGYMHVYKQSPGKGLEWIGRIFPGDGDTHY 79
QY 61 NQKFKDKATLTVDKSSSTAYMELSLTSDSANYCYCARSTMTITNYVMYDYGQGTSTVSS 120
Db 80 SGKFGQKAKLTADKSSVTAPLQLTSLTSDSANYCYCARSTMTITNYVMYDYGQGTSTVSS 138
QY 121 AKTTTPSVVPLAPGSAQAQNSMVTGLCLVKGYFPEPVPTVTNWSGSLSSGKVHTTTPAVLQSD 180
Db 139 AKTTTPSVVPLAPGCGDGTTCSSVTGLCLVKGYFPEPVPTVTNWSGSLSSGKVHTTTPAVLQSG 198
QY 181 LYTLSSTVTPGSTWSPSETVTCNVAHPASSTKYDKKIVPRDSCGSPSEKSEINE----KD 236
Db 199 LYTMSSSVTPGSTWSPSETVTCNVAHPASSTKYDKKIVPRDSCGSPSEKSEINE----SGP---ISTINPCPCKE 252
QY 237 LRK--KSEIQGTALGNLKOIYYNYSKAITSSSEKSAQDLTNTLLFKGFTFGHFWYNDLLV 294
Db 253 CHKCPAPNLEG---GPSVFIFPPENIKDV-----LMI 280
QY 295 DLGSTAATSEYEGSSVDLYGAYVGYQCAGGTPTNKTACMYGGVTLHDNNRLTEKKVPINL 354
Db 281 SL-----TP-----284
QY 355 WIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLGSLYNSDSFGKQVQGLIIVPHSS 414
Db 285 ----KVTGVVD-----VSEDDPDVQISWPNV-----VEVHTA 314
QY 415 EGSSTVSYDLFDAQGYPTDLLRIYRNTTISSTLSLSLYLYTTSIVMTQPTPTSLLYSAG 474
Db 315 QTQTHREDY-----NSTIR-----VWSA- 332
QY 475 DRVTITCKASQSVNDVANYQQKPGSPKLLISYTSRRYAGVDPDRFSGSGYGTDFTLTI 534
Db 333 -----LPIQHDWMSGKEFKCKVN 351
QY 535 SVOAEDAAYFCQDYNPSPTFGGKGLIKRADAAPTVSIFFPSSEQLTSGGASVVCFL 594
Db 352 N-----KDLPSPIE---RTISKIKGLVRAPQVIVLPAPAEQLSRKDVSLTCLV 396
QY 595 NNFYPKDINVKWIKDGSERQNGVLNSWTQDQSKDSTYSMSSTLTTLTKDEYERHNS 649
Db 397 VGFNPGDISVEMTSNGHTENYKDTAPVLDS-----DGSYFIYSLDKDITKSKWEKTD 449
QY 650 YTCEATHK 657
Db 450 FSCNVRHE 457

RESULT 28
Q7TS98_MOUSE PRELIMINARY; PRT; 236 AA.
AC Q7TS98;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-colorectal carcinoma light chain.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
```


RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091750; AAH91750.1; -; mRNA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 239 AA; 26302 MW; 98FC4BA8EB404215 CRC64;
Query Match 25.0%; Score 879.5; DB 2; Length 239;
Best Local Similarity 76.8%; Pred. No. 1.1e-46;
Matches 175; Conservative 15; Mismatches 33; Indels 5; Gaps 2;
QY 449 LSLISLYLTTISVMTQPTSLLSAGDRVTITCKASQSV--SND---VAVYQKPGQSPK 503
DB 11 LVLSIQETNGDVMTQPTLTLVITGPASISCKSSQSLHNSGKYLVNLLQRPQSPK 70
QY 504 LLISYTSRRYAGVDPDFSGSGYGTDFLTITSSVQAEADAAYFCQDYNPPTFGGGTKLE 563
DB 71 LLILVYSKLSGVPDFSGSGSGTDFTLKISRVEAEDLVYVYCLQATHPRPTFGGGTKLE 130
QY 564 IKRAADAAPTYSIPPPSEQLTSGGASVYVCFNNFYPKDINVKWKIDGSRQNGVLNSWTD 623
DB 131 IKRAADAAPTYSIPPPSEQLTSGGASVYVCFNNFYPKDINVKWKIDGSRQNGVLNSWTD 190
QY 624 QDSKDSYSSMSSTLTLLTKDEYRHNSYTCETHTKTSTSPIVKSFNRNE 671
DB 191 QDSKDSYSSMSSTLTLLTKDEYRHNSYTCETHTKTSTSPIVKSFNRNE 238
RESULT 31
Q52L95_MOUSE PRELIMINARY; PRT; 236 AA.
AC Q52L95_MOUSE PRELIMINARY; PRT; 236 AA.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426030899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC094013; AAH94013.1; -; mRNA.
DR SMR; Q52L95; 23-236.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 26446 MW; 570453C3B97CD655 CRC64;
Query Match 24.7%; Score 871; DB 2; Length 236;
Best Local Similarity 77.4%; Pred. No. 3.8e-46;
Matches 164; Conservative 20; Mismatches 28; Indels 0; Gaps 0;
QY 460 IVMTQPTSLLSAGDRVTITCKASQSVSNDVAVYQKPGQSPKLLISYTSRRYAGVDPDR 519
DB 24 IKMTQSPSMYSVLSGSAVTITCKASQDIYSFLKWKFOKKPKPTLIYHTRDMDGVPSR 83
QY 520 FSGSGYGTDFLTITSSVQAEADAAYFCQDYNPPTFGGGTKLEIKRADAAPTVSIFPPS 579
DB 84 FSGSGSGYSLTINSLECEDMGIIYVYCLQYDEPPLTFGGGKLELRADAAPTVSIFPPS 143
QY 580 SEQLTSGGASVYVCFNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYSSMSSTLTLL 639
DB 144 SEQLTSGGASVYVCFNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYSSMSSTLTLL 203
TQDEYRHNSYTCETHTKTSTSPIVKSFNRNE 671
204 TQDEYRHNSYTCETHTKTSTSPIVKSFNRNE 235
RESULT 32
Q5XFY8_MOUSE PRELIMINARY; PRT; 235 AA.
ID Q5XFY8_MOUSE PRELIMINARY; PRT; 235 AA.
AC Q5XFY8_MOUSE PRELIMINARY; PRT; 235 AA.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)

```

25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC084683; AA084683.1; -; mRNA.
DR SMR; Q5XPy8; 23-235.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25835 MW; 82859ED277PDC667 CRC64;

Query Match 24.7%; Score 870.5; DB 2; Length 235;
Best Local Similarity 76.2%; Pred. No. 4e-46;
Matches 170; Conservative 20; Mismatches 32; Indels 1; Gaps 1;

QY 449 LSISLYLTYTSIVMTPTSLIVSAGDRTITCKASQSVNDVAVYQKPGSPKLLISY 508
Db 13 ISASVIIRSGQIVLTSQSPAILSGFPGKEKVTMTCRASSV-NYMHYQKPGSPKPWIA 71

QY 509 TSSRYAGVDRFSGSGYGTFTLTSSVQAEADAAYVFCQDYNSTPTFGGTGKLEIKRAD 568
Db 72 TSKLASGVPARFSGSGSGTSYSLTIRVEADAATYCCQWSSNPLTFGAGTGLEIKRAD 131

QY 569 AAPTIVIFPPSSQLTSGGASVCFVFNPKDINVKWKIDGSRQGVNSNTDQDSKD 628
Db 132 AAPTIVIFPPSSQLTSGGASVCFVFNPKDINVKWKIDGSRQGVNSNTDQDSKD 191

QY 629 STYSMSSTLTLTQDEYERHNSYTCEATHKSTSTSPVKSFNRNE 671
Db 192 STYSMSSTLTLTQDEYERHNSYTCEATHKSTSTSPVKSFNRNE 234
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RESULT 33

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Q58EV6_MOUSE PRELIMINARY; PRT; 235 AA.
ID Q58EV6;
AC Q58EV6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091736; AA091736.1; -; mRNA.
DR SMR; Q58EV6; 23-235.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 235 AA; 25719 MW; BE4E4ABDD2578252 CRC64;

Query Match 24.6%; Score 867.5; DB 2; Length 235;
Best Local Similarity 75.8%; Pred. No. 6.2e-46;
Matches 169; Conservative 20; Mismatches 33; Indels 1; Gaps 1;

QY 449 LSISLYLTYTSIVMTPTSLIVSAGDRTITCKASQSVNDVAVYQKPGSPKLLISY 508
Db 13 ISASVIIRSGQIVLTSQSPAILSGFPGKEKVTMTCRASSV-NYMHYQKPGSPKPWID 71

QY 509 TSSRYAGVDRFSGSGYGTFTLTSSVQAEADAAYVFCQDYNSTPTFGGTGKLEIKRAD 568
Db 72 TSKLASGVPARFSGSGSGTSYSLTSSMEADAATYCCQWSSNPLTFGAGTGLEIKRAD 131
```

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QY 569 AAPTVPISPPSSSEQLTSGGASVVCFLNNFPKQINVKWKIDGSRQGVLSNWTDDQSKD 628
Db 132 AAPTVPISPPSSSEQLTSGGASVVCFLNNFPKQINVKWKIDGSRQGVLSNWTDDQSKD 191
QY 629 STYSMSSTLTITKDEYERHNSYTCETHKSTSPVKSPNRNE 671
Db 192 STYSMSSTLTITKDEYERHNSYTCETHKSTSPVKSPNRNE 234

RESULT 34
Q65ZQ1_HUMAN
ID Q65ZQ1_HUMAN PRELIMINARY; PRT; 458 AA.
AC Q65ZQ1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Anti-colorectal carcinoma heavy chain.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93383497; PubMed=8372513;
RA Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
RT "Cloning and characterization of 1116NS19.9 heavy and light chain
RT cDNAs and expression of antibody fragments in Escherichia coli.";
RL Year Immunol. 7:56-62(1993).
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; S65761; AAB28159.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR PFam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 4.
KW Immunoglobulin domain.
SQ SEQUENCE 458 AA; 50602 MW; 4AEA29F9981D8DFF CRC64;

Query Match 24.6%; Score 867.5; DB 2; Length 458;
Best Local Similarity 22.3%; Pred. No. 1.6e-45;
Matches 216; Conservative 69; Mismatches 126; Indels 257; Gaps 16;

QY 1 EVLQOQSGPDLVRFGASVKISKASGYSTGYTMHWYKQSPGRGLEWIGRI--NPNNGV 58
Db 20 EVKLESGGGVLQPGGSMKLSKAASGFTFSDANMDWVRQSPKGLWVAEIGNKNNHAT 79
QY 59 LYNQKFKDATLTVDKSSYATYAMELRLTSEDAVYICARSTWITVYMDYWGCGSTVT 118
Db 80 YYAESVKGRTFVRDSDSKRSVRLQMSLRVEDTGYTCT----TRFA--YMGQGLTVT 132
QY 119 SSAKTPPSVYPLAPGAAQTNSMTVLGCLVKGVFPPEPTVTWNSSGSLSGVHTFPVLQ 178
Db 133 SAAKTPPSVYPLAPGAAQTNSMTVLGCLVKGVFPPEPTVTWNSSGSLSGVHTFPVLQ 192
QY 179 SLDYTLSSSVTPSSWSPSTVTCNVAHPASSTKVDKKIYVPRDSGGPSEKSEINEKDLR 238
Db 193 SLDYTLSSSVTPSSWSPSTVTCNVAHPASSTKVDKKIYVPRDCG-----237
QY 239 KKSLEQGTALCNLKQIYYNYSKAITSSEKSAQDFLTWTLFKGFFTHGHPYNDLLVDLGS 298
Db 238 --CKPCICTVPEVSSVFIPPK-----PKDVLATLT-----266
QY 299 TAATSEYEGSSVDLYGYGVQCAGGTPTNCTACMYGGVTLHDNNRLTEKKVPLNWLIDG 358
Db 267 -----TP-KVTCVVVDIS-----KDPFVQSFVFD- 291
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QY 359 KQTTVIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGCKVQVRLI 409
Db 292 ---DVEVHTAQTPRBEQFNSTFRSVSELP:IMHQDMLNGKEFKCRVNSAAPPAPIEK--- 345
QY 410 VFHSSSGSTVSVDLPDAQGYPDTLRIYRDNTTISTSTLSISLYLTVTIVMTQTPTSL 469
Db 346 -----TISKT-----350
QY 470 LVSAGDRVTITCKASQSVSNDAVYQQKQKQPKLLISYTSRYAGVDPDRFSGSGYCTDF 529
Db 351 -----350
QY 530 TLTISVQAEADAAYFCQDYNSPPTFGGKTLEIKRADAAPTVSPSPSEQLTSGGAS 589
Db 351 -----KGRKPAQVYTIPTPPKEQMAKDKVS 375
QY 590 VVCFLNNFPKQINVKWKIDGSRQGVLSNWTDDQSKDSTYSMSSTLTITKDEYERHNS 649
Db 376 LTCWITDFPEDITVQWNGQPAEN-YKNTQIPMDT-DGSYFYSKLVKSNWNEAGNT 433
QY 650 YTCETHK 657
Db 434 FTCSVLHE 441

RESULT 35
Q5XKG4_MOUSE
ID Q5XKG4_MOUSE PRELIMINARY; PRT; 234 AA.
AC Q5XKG4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RA Director MGC Project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031349; AAH31349.1; -; mRNA.
DR SNR; Q5XKG4; 16-234.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
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ID	QSM7V3_RAT	PRELIMINARY;	PRT;	461 AA.
AC	QSM7V3;			
DT	01-FEB-2005 (TrEMBLrel. 29, Created)			
DT	01-FEB-2005 (TrEMBLrel. 29, Last sequence update)			
DT	01-FEB-2005 (TrEMBLrel. 29, Last annotation update)			
DE	LOC367586 protein.			
GN	Names=LOC367586;			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muroidea; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Lung;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Lung;			
RG	NIH MGC Project;			
RG	Submitted (DEC-2004) to the EMBL/GenBank/DBSJ databases.			
CC	-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major			
CC	histocompatibility complex class I molecules (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Secreted (By similarity).			
DE	EMBL: BC088423; AAH88423.1; -; mRNA.			
DR	InterPro: IPR003599; Ig.			
DR	InterPro: IPR007110; Ig-like.			
DR	InterPro: IPR003597; Ig.C1.			
DR	InterPro: IPR003596; Ig.V.			
DR	Pfam: PF07654; C1-set; 3.			
DR	SMART: SM00409; IG; 3.			
DR	SMART: SM00407; IGc1; 2.			
DR	SMART: SM00406; IG; 1.			
DR	PROSITE: PS50835; IG_LIKE; 4.			
KW	Immunoglobulin domain; Repeat.			
SQ	SEQUENCE 461 AA; 50949 MW; 25EA4ECE6FE0F5A9 CRC64;			
Query Match	24.2%; Score 852; DB 2; Length 461;			
Best Local Similarity	31.9%; Pred. No. 1.4e-44;			
Matches 211; Conservative 78; Mismatches 131; Indels 242; Gaps 15;				
Qy	1 EVQLQSGDPLVKGASVKISCKASGYSTGYTHHWKQSPGKLEWIGRINPNNGVTLY 60			
Db	20 EVQLVESGGGLVQPGHSLKSLCAASGFTPSDYNMAVRQAPKKGLEWVATIIYDGSRTYY 79			
Qy	61 NQKFKDKATLTVDKSTTAYMELRSITSDSAVYTCARSTMITNYVMYDYGQGTSTVSS 120			
Db	80 RDSVKGRFTISRDNKASTLYLQWDSLRSDTATYYCATNRWLLHYFDYQGQVWTVSS 139			
Qy	121 AKTTPSPVPLAPGSAQNTSNMVTGLCLVKGYFPPVPTVWNSGSLSSGVHTFPFVQLQSD 180			
Db	140 AETTAPSVVPLAPGTALKNSMVTGLCLVKGYFPEFPTVWNSGSLSSGVHTFPFVQLQSG 199			


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Qy 61 NQPKDKATLTVKSGSTTAYMELSLTSDSAVYCARSTMTNY-----VMDYWGQGT 115
Db 80 VPKFQDKATLTAATSSNTAYLQSLTSGDTATYC-----LFYGDGRDYFDYWGQGT 135
Qy 116 VYSSAKTTPSPVPLAPGSAQAQNSMTVGLGVKGYFPEPVTVWNSGSLSSGVHTFPA 175
Db 136 ITVSSAKTTPSPVPLAPGCGDTTGGSTVGLGVKGYFPEPVTVWNSGSLSSGVHTFPA 195
Qy 176 VLQSDLYTLSSVTPSPSTWSETVTCNVAHPASSTKVDDKIVPRDGGGSPSEKSEINE- 234
Db 196 LLQSLGYTMSSVTPSPSTWSETVTCNVAHPASSTKVDDKIVPRDGGGSPSEKSEINE- 249
Qy 235 ---KDLRK--KSELOGTALGNLKOIYYNYSKAITSEKSAQDFLTNTLLFKGFTGHPWY 289
Db 250 PPKCKECHKCAPNLEG---GPSVFIFPPNIKDV-----TP----- 279
Qy 290 NDLLVDLGSATAATSEYEGSSVDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLTEKK 349
Db 280 --LMISL-----TP----- 286
Qy 350 VPINLWIDGKQTTVPIDKVKTSKEVTVOBLDLOARHYLHGKFGLYNSDSFGGKVORGLI 409
Db 287 -----KVCVVVD-----VSEDDPDQISWFVN-----V 311
Qy 410 VFHSSEGSTVSYDLFDAQGYQDPDLLRIYRDNTTISSTLSISLYLTTIVMTQPTSL 469
Db 312 EVHTAQOTQTHREDY-----NSTIR----- 330
Qy 470 LVNAGDRTVITCKASQSVNDVAWYQKQKPGQSKLLISYTSRYAGVDPDFSGSGYGTDF 529
Db 331 VVSA-----LPIQHQMWSGKEF 348
Qy 530 TLTSSVQAEADAAVFCQODYNGPPTFGGQTKLEIKRADAAPTIVSIPPPSEQLTSGGAS 589
Db 349 KCKVNN-----KDLPEPIE---RTISKIKGLVAPQVYILPPAEQLSREDVS 393
Qy 590 VVCFNNFYPKDINVKWIDGSEKQ-----GVNLSTWDQDSKDYSTYSMSSTLTLTKEY 644
Db 394 LTLGVGFNPGDISVETWSNGHTEENYKDTAPVLDSE-----DGSFYIYKLDIKTSKW 446
Qy 645 ERHNSYTCETHK 657
Db 447 EKTDSPSCNVRHE 459

RESULT 40
Q5M842_RAT PRELIMINARY; PRT; 458 AA.
AC Q5M842;
DT 01-FEB-2005 (T-EMBLrel. 29, Created)
DT 01-FEB-2005 (T-EMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (T-EMBLrel. 29, Last annotation update)
DE Gamma-2a immunoglobulin heavy chain.
GN Name=IGG-2a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -i- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -i- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC088240; AAH88240.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IG1; 2.
DR PROSITE; PS50835; IG LIKE; 4.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 458 AA; 50268 MW; 0CB5AA613DD9439 CRC64;

Query Match 23.6%; Score 832.5; DB 2; Length 458;
Best Local Similarity 31.4%; Pred. No. 2,3e-43;
Matches 208; Conservative .77; Mismatches 132; Indels 245; Gaps 17;

Qy 1 EVOLQSGDPLVKPGASVKISKASGYSTGYMHWVKQSPGKLEWIGRINPNNGVTLY 60
Db 20 QVOLMESGDLVQPSSETLSLICITVSGFSLTSYNVHWVROPKGLWMMG-VMMSGGNTDY 78
Qy 61 NQPKDKATLTVDKSSTTAYMELSLTSDSAVYCARSTMTITNYMDYWGQGTSTVSS 120
Db 79 NSALKSRLSISRDTSKNQVFLKMSLQSEDAITTYCAREGY--PYFNYGQGVMTVSS 136
Qy 121 AKTTTPSPVPLAPGSAQAQNSMTVGLGVKGYFPEPVTVWNSGSLSSGVHTTFAVLQSD 180
Db 137 AETTAPSVPLAPGTALKNSMTVGLGVKGYFPEPVTVWNSGALSGVHTTFAVLQSG 196
Qy 181 LYTSSSVTPSPSTWSETVTCNVAHPASSTKVDDKIVPRDGGGSPSEKSEINEKDLRKK 240
Db 197 LYTSSSVTPSPSTWSSQAVTCNVAHPASSTKVDDKIVPRE- 238
Qy 241 SELOGTALGNLKOIYYNYSKAITSEKSAQDFLTNTLLFKGFTGHPWYNDLVDLGSTA 300
Db 239 -----NPGCTGSEVSS-----VFIFPKTKDVL----- 262
Qy 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLTEKKVPINLWIDG-- 358
Db 263 -----ITL-----TP-KVTCVVVDISQND-----PEVRFSEWFDIDVE 294
Qy 359 ---KQTTVPIDKVKTSKEVTVOBLDLOARHYLHGKFGLYNSDSFGGKVORGLIVFHSSE 415
Db 295 VHTAQTHAPEKQSNSTLR--SVSELPVHRDNLNGK-----TFCKVNN----- 335
Qy 416 GSTVSYDLFDAQGYQDPDLLRIYRDNTTISSTLSISLYLTTIVMTQPTSLLSVAGD 475
Db 336 -----SGAFPAI----- 343
Qy 476 RVITITCKASQSVNDVAWYQKQKPGQSKLLISYTSRYAGVDPDFSGSGYGTDFTLTIS 535
Db 344 -----EKSIS-----KEGTIPR----- 355
Qy 536 VQAEADAIVFCQODYNSPPTFGGQTKLEIKRADAAPTIVSIPPPSEQLTSGGASVVCFLN 595
```


[3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=7498516; DOI=10.1016/0014-5793(95)01224-3;
RA Takagi M., Kohda K., Hamuro T., Harada A., Yamaguchi H., Kamachi M.,
RT Imanaka T.;
RT "Thermostable peroxidase activity with a recombinant antibody L chain-
RL porphyrin Fe(III) complex";
RL FEBS Lett. 375:273-276(1995).
DR EMBL; BC010327; AAH10327.1; -; mRNA.
DR FIR; S68213; S68213.
DR HSSP; P01783; 1IGC.
DR SMR; Q91205; 20-469.
DR MGI; MGI:2144967; AU044919.
DR MGI; MGI:2144967; I9hg.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-aet; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 22.8%; Score 803; DB 2; Length 473;
Best Local Similarity 32.0%; Pred. No. 1.7e-41;
Matches 214; Conservative 74; Mismatches 138; Indels 242; Gaps 18;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYVMHWKSPGKGLSWIGRIIPNNQVTL 60
DB 20 EVQLVSGGGLVPGGSRKLSKAASGTFSDYGMHWQRAPEKGLWVAYINSGSTIIY 79

QY 61 NQKFKDKATLTVDKSTTAYMELRSITSDSAVYICARSTMTINMYDMYGQTSITVSS 120
DB 80 ADTVKGRFTISRDNAKNTLFLQMTLSRSEDTAMYICARELWLR--IDYWGQGTITVSS 137

QY 121 AKTTPSPVPLAPGSAQAQNSMTGLCLVKGYFPEPVPTVWNSGSLSSGVHFPVAVLQSD 180
DB 138 AKTTPSPVPLAPGCGDITGSSVTLGLVKGYFPESVTVTWNSGSLSSVHTFPALLQSG 197

QY 181 LYTLSSTVTPSTWPTSETVTCNVAHPASSTKVYKIVPRDSGPGPEKSEELNE---KD 236
DB 198 LVTMSSTVTPSTWPTSETVTCNVAHPASSTKVYKIVPRDSGPGPEKSEELNE---SGP---ISTINCPCKE 251

QY 237 LRK--KSELQGTALGNLKOIYYNSKAITSSSEKSAQDLTNTLLFKGFTGHPWYNDLIV 294
DB 252 CHKCPAPNLEG---GPSVFIFPPNIKDV-----LMI 279

QY 295 DLGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINL 354
DB 280 SL-----TP----- 283

QY 355 WIDGKOTTPIDKVKTSKKEVTVQELDLQARHVLHGKFGLYNSDSFGKVGQRLIVFHSS 414
DB 284 ----KVTGVVD-----VSDDDPDVQLSWFVN-----VEVHTA 313

QY 415 EGSVSYDLFDAQGOVPTLLRIYRNTTISSTLSLSLYLVTTSIWMTPQTPTSLVSVAG 474
DB 314 QTOTHREDY-----NSTIR-----VVS-A- 331

QY 475 DRVTITCKASQSVSNDAVYQKPGQSKLLISYTSRYAGVDPDRPSGGYGTDFTLTIS 534
DB 332 -----LPIQHQMWSGKEFKCKYN 350

QY 535 SVQAEDAAVVFCODYNSPPTFGGKLETKRADAAPTYSIPPPSEQLTSGGASVVCFL 594
DB 351 N-----KDLPSPIE---RTISKIKGLVRAPOVYILPPPAEQLSRKDVSLTCLV 395

QY 595 NNFPYKPDINVKWKIDGSRQN-----GVLSNMTDQDSKDSYMSSTLTLTKDYEYRHS 649
DB 396 VGFNPGDISVEMTSNGHTEENYKDTAPVLDS-----DGSYFIYSKLDIKTSKWEKTD 448

QY 650 YTCETHK 657
DB 449 FSCNVRHE 456

RESULT 44
Q4KM66 RAT PRELIMINARY; PRT; 234 AA.
AC Q4KM66;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH MGC Project;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC098746; AAH98746.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25692 MW; DPA12A3F8801666D CRC64;

Query Match 22.5%; Score 791; DB 2; Length 234;
Best Local Similarity 68.2%; Pred. No. 3.4e-41;
Matches 152; Conservative 29; Mismatches 38; Indels 4; Gaps 1;

QY 453 LVLYTT----SIVMTQTPTSLVSGADRVITICKASQSVSNDAVYQKPGQSKLLISY 508
DB 11 LLLWTHAICIDRMQTQSPASLSASLGVTNIECLASDIYSLAWYQQKPGSPQLLIYN 70

QY 509 TSSRYAGVDPDRPSGGYGTDFTLTISVQAEDAAYVFCODYNSPPTFGGKLEIKRAD 568
DB 71 ANSLQNGVPSRSGSGSGTQYSLKINSLOSEDAVTFCCQYNNYPWTFGGTKLEIKRAD 130

QY 569 AAPTYSIPPPSEQLTSGGASVVCFLNNFPYKPDINVKWKIDGSRONGVLSNMTDQSD 628
DB 131 AAPTYSIPPPSEQLTSGGASVVCFLNNFPYKPDINVKWKIDGSRONGVLSNMTDQSD 628

QY 629 STYSSSTLTLTCKDEYERHNSYTCETHKTSSTPIVKSFNRE 671
DB 191 STYSSSTLTSLTKRADYESHNLTYCEVVHKTSSPPVVKSFNRE 233

Matches 202; Conservative 73; Mismatches 202; Indels 185; Gaps 13;	
Qy	1 EVOLQSGDPLVKGASVKISCKASGYSTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60
Db	20 QVHLVQSGAEVKKGASVKYCTASGYPTNFHFINWVRQAPGQSGLEWGWINTGNGTKY 79
Qy	61 NQPKDKATLTVDKSSTAYMELASLTSSESAVYICARSTM--ITNVYMDYWGQGTSTV 118
Db	80 SOKPQGVVITRDTWTMTTAYMDLSLSEDAVWVCARDAPQGVTTTTFYFYWGQGTLT 139
Qy	119 SSATTPPSVYPLAPGSAQTNSMVTGLCLVKGYFPEPVTVTVWNSGSLSGVHTFPAVLQ 178
Db	140 SSASTKGPSVFPPLAPSRSTSGGTAALGCLVKDTFPEPVTVWNSGALTSGVHTFPAVLQ 199
Qy	179 SD-LYTLSSSVTVPSSTWPTSETVCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKOL 237
Db	200 SSGLYSLSSVTVPSSSLGTQTYTCNVNHPKSNTKVDKRV----- 239
Qy	238 RKXSELQGTALGNLQIYYNSKAITSSSEKADQFLNTLLFKGFTTGHFWYNDLLVDLG 297
Db	240 -----ELKTPLG 246
Qy	298 STAATSEYEGSSVDLYGAYGYCAGGTPNKT--ACMYGGVTLHDNNRLTEEKVPIPLW 355
Db	247 DTHHTCP-----RCPEPKPCDTPPPC-----PRCEPKSC----- 276
Qy	356 IDGKQTTVPIDKVKTSKEVTVQBLDQARHYLHGKFGLYNSDSFGGKVORGLIVPHSSE 415
Db	277 -----DTPPCPCPEPKSCDTPPPCPCPAPPELLGGPSVF---LFPKPKDMLISHTPE 329
Qy	416 GSTVSVDLPAQGYDPTLRIYRDNNTTISSTLSISLYLYTTSIVMTQTPTSLLSAGD 475
Db	330 VTCV---VVDVSHEDPEVQFKWYDGVGVHNAKTPREEQVNSTFRVSVLTVLHQDMLN 386
Qy	476 RVITCKASQSVNDVAVYQOKPCQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTLTSS 535
Db	387 GKYEKKVCS-----NKALPAP---IEKTIKTKGP----- 414
Qy	536 VQAEADAIVYFQQDYNPSPTFGGKTKLEIKRADAAPTVISFPPSSQLTSGGASVVCFLN 595
Db	415 -----REPOVYTLPSREEMTKNOVSLTCLVK 441
Qy	596 NFTPDKINVKWKIDGSRQNGVLSWTDQDSKOSTYSMSSTLTLDKDEYERHNSYTCBAT 655
Db	442 GFYPSDIAVWESSGQENN--YNTTPMLDSDGSPFLYSKLTVDKSRWQQGNIFSCVM 499
Qy	656 HK 657
Db	500 HE 501
RESULT 50	
Q727P5_HUMAN PRELIMINARY; PRT; 469 AA.	
ID	Q727P5_HUMAN PRELIMINARY; PRT; 469 AA.
AC	Q727P5;
DT	01-OCT-2003 (TrEMBLrel. 25, Created)
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	IGH1 protein.
GN	Name=IGH1;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC	Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Spleen;
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
Basak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;	
"Generation and initial analysis of more than 15,000 full-length human	
RT and mouse cDNA sequences.";	
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
[2]	
NUCLEOTIDE SEQUENCE.	
TISSUE=Spleen;	
NIH MGC Project;	
Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.	
EMBL; BC051328; AAH51328.1; -; mRNA.	
HSSP; P01857; 1HZH.	
SMR; Q7Z7P5; 20-469.	
InterPro; IPR007110; Ig-like.	
InterPro; IPR003597; Ig cl.	
InterPro; IPR0031006; Ig_MHC.	
InterPro; IPR003596; Ig_v.	
Pfam; PF07654; Cl-set; 3.	
SMART; SM00406; IGV; 1.	
PROSITE; PS00835; IG LIKE; 4.	
PROSITE; PS00290; IG_MHC; UNKNOWN_2.	
KW Immunoglobulin domain.	
SQ SEQUENCE 469 AA; 51395 MW; C8DSBE12BAAF795C CRC64;	
Query Match 21.3%; Score 750; DB 2; Length 469;	
Best Local Similarity 30.3%; Pred. No. 3.2e-38;	
Matches 201; Conservative 70; Mismatches 156; Indels 236; Gaps 16;	
Qy	1 EVOLQSGDPLVKGASVKISCKASGYSTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60
Db	20 QVHLVQSGAEVKKGASVKYCTASGYPTNFHFINWVRQAPGQSGLEWGWINTGNGTKY 79
Qy	61 NQPKDKATLTVDKSSTAYMELASLTSSESAVYICARSTM--ITNVYMDYWGQGTSTV 120
Db	80 ARKFGQVMTTDTSTATTSMYFSLRSDDTALFYCATKSRGQGVDFDSWGQGTLT 139
Qy	121 AKTTPPSVYPLAPGSAQTNSMVTGLCLVKGYFPEPVTVTVWNSGSLSGVHTFPAVLQSD 180
Db	140 ASTKGPSVFPPLAPSRSTSGGTAALGCLVKDTFPEPVTVWNSGALTSGVHTFPAVLQSS 199
Qy	181 -LYTLSSSVTVPSSTWPTSETVCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLRK 239
Db	200 GLYSLSVTVPSSSLGTQTYTCNVNHPKSNTKVDKKEVPSK----- 242
Qy	240 KSELQGTALGNLQIYYNSKAITSSSEKADQFLNTLLFKGFTTGHFWYNDLLVDLST 299
Db	243 -----DKTHTCCPCPAPPELLGGPSVF--LFPKPK--KDTLM----- 274
Qy	300 AATSEYEGSSVDLYGAYGYCAGGTPNKTACMYGGVTLHDNNRLTEEKVPIPLWTDGK 359
Db	275 -----ISRTPEVT--CVVDVS-----HEDPEVKFNWYVDG-- 303
Qy	360 QTTVPIDKVKTSKEVTVQBLDQARHYLHGKFGLYNSDSFGGKVORGLIVFHSSESTV 419
Db	304 ---VEVHNAKTPREEQ-----YNSTY---KVSVLTVLHQDWLNGK 339
Qy	420 SYDLFDAQGYDPTLRIYRDNNTTISSTLSISLYLYTTSIVMTQTPTSLLSAGDRVTI 479
Db	340 EY----- 341
Qy	480 TCKASQSVNDVAVYQOKPCQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTLTSSVQAE 539


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Db 140 WGGTFTVTVSSASTKGPSFPLAPSKSTSGGTAALGCLVKDYFPPEVTVTWSNGALTS 199
QY 170 VHTFPAVLQSD-LYTLSSSVTVSPSTWPTVCNVAHPASSTKVDKIVPRDSGGPSK 228
Db 200 VHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHRPSNTKDKRVEPKSC----- 253
QY 229 SBEINEKDLRKXSELQGTALGNLKOIYYNKAITSSEKSAQDFLNTLLFKGFFTHGPW 288
Db 254 -----DKHTCTPCPAPPELLGGPSVF--LFPKP- 280
QY 289 YNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTGNKTAQMGVGVTLHDNNRLTEBK 348
Db 281 -KDTLM-----ISRTPEVT-CVVVDVS-----HEDP 304
QY 349 KVPINWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGGKVQGL 408
Db 305 EVKFNWYVDG---VEVHNAKTKPREQ-----YNSTY---RVVSVL 339
QY 409 IYFHSSEGTSVVDLFDAGQGPDTLLRIYRDNTTISSTLSLSLYTTSIVMTQPTS 468
Db 340 TVLHDPWLNKGEY----- 352
QY 469 LLVSAGDRVTITCKAQSVSNDAVWYQQKPGSPKLLISYTSRYAGVDPDRFSGGYGTD 528
Db 353 -----KCKVS-----NKALPAP---IEKTSKAGQP----- 376
QY 529 FTLTSSVOAEDAAYFCQDYNPSPTFGGTTKLEIKRADAAPTYSIFPPSSEQLTSGGA 588
Db 377 -----REPQVYTLPPSREEMTKNOV 396
QY 589 SVVCFPLNYPKQDINVKWKIDGSERON-----GVLSNWDQDSKSTYSMSSTLTITKDE 643
Db 397 STCLYKGYPSDIAVWESSNGQPNKYKTPPVLDSE-----DGSFFLYSKLTVDKSR 449
QY 644 YERHNSYTCETHK 657
Db 450 WQGNVFCVSMHE 463

RESULT 54
Q5EBM2_HUMAN PRELIMINARY; PRT; 519 AA.
AC Q5EBM2_1
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
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RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RA Director MGC Project;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC089421, RAH89421.1; -, mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 519 AA; 56813 MW; 988C5C2F9289E34C CRC64;

Query Match 21.0%; Score 741; DB 2; Length 519;
Best Local Similarity 30.1%; Pred No. 1.3e-37;
Matches 199; Conservative 76; Mismatches 204; Indels 182; Gaps 14;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHVVKSPGKGLWIGRIINPNNGVTLY 60
Db 20 QVQLVQSGAEVKKPGASVKVSCEVSGHTLTSLSRHWVRQAPGKGLWVGDFDGEDTVY 79
QY 61 NQKPKDKATLTVDKSSSTAYMELRLSLTSDSAVYYCARST--MITNYV-MDYWGQSTSVT 117
Db 80 AQTFQGRVTMTEDTSTDATYMDLSNLSRSDTAVYYCATGYDVLITGSRFDYWGQGTQVT 139
QY 118 VSSAKTTPPSVPLAPGSAATNSMVTGLGVKGFPEPVTVTWNSGSLSSGGVHTFPAVL 177
Db 140 VSSASTKGPSVFLAPCSRSTSGGTAALGCLVKDYFPPEVTVTWSNGALTS 199
QY 178 QSD-LYTLSSSVTVSPSTWPTVCNVAHPASSTKVDKIVPRDSGGPSKSEINEKD 236
Db 200 QSSGLYSLSVTVTPSSSLGTQTYICNVNHRPSNTKDKRVE----- 240
QY 237 LRKSELOQTALGNLKOIYYNKAITSSEKSAQDFLNTLLFKGFFTHGPWYNDLLVDL 296
Db 241 -----ELKTP 246
QY 297 GSTAATSEYEGSSVDLYGAYGYQCAGGTGNKTAQMGVGVTLHDNNRLTEKKVPINLWI 356
Db 247 GDTHTCP-----RC-----PEPKSC---DTPPCPCPEPKSC----- 277
QY 357 DGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGGKVQGLVHFSSEG 416
Db 278 ---DTPPCPCPEPKSCDTPPCPCPAPPELLGGPSVF--LFPKPXDTLMISRTPEV 331
QY 417 STVSVDLFDAGQGPDTLLRIYRDNTTISSTLSLSLYTTSIVMTQPTSLVLSAGDR 476
Db 332 TCV---VVDVSHEDPEVQPKWYVDGVGVHNAKTKPREEQYNSTFRVSVVLTVLHQDWLNG 388
QY 477 VIITCKASQSVNDVAWYQQKPGSPKLLISYTSRYAGVDPDRFSGGYGTDFTLTISV 536
Db 389 KEYKCKVS-----NKALPAP---IEKTSKTKGP----- 415
QY 537 QAEDAAYFCQDYNPSPTFGGTTKLEIKRADAAPTYSIFPPSSEQLTSGGASVWVFLNN 596
Db 416 -----REPQVYTLPPSREEMTKNOVSLTCLVKG 443
QY 597 FYPKQINVKWKIDGSRQNGVLSNWDQDSKSTYSMSSTLTITKDEYERHNSYTCETH 656
Db 444 FYPDSIAVWESSNGQPNEN--YNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMH 501
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QY 657 K 657
Db 502 E 502

RESULT 55
Q6GMW1_HUMAN
ID Q6GMW1_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -; mRNA.
DR SNR; Q6GMW1; 24-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25751 MW; 5BF6EA087AFAC437 CRC64;

Query Match 20.8%; Score 734; DB 2; Length 236;
Best Local Similarity 65.3%; Pred. No. 1.2e-37;
Matches 139; Conservative 27; Mismatches 47; Indels 0; Gaps 0;

QY 459 SIWMTPTSLVLSAGDRVITTCASQSVSNDVAWYQOQKPGQPKLLISYTSRYAGVDP 518
Db 23 AIQMTQSPSLASVSGDRVITTCASQISNDLIGWYQOQKPGKAPKLLIYAASSLQSGVPS 82
QY 519 RFGSGYGTDFTLTISVQAEADAAYFCQDYNSPPTFGGGTKLEIKRADAPTVISIFPP 578

83 RFGSGSGTDFTLTISLQPEDFATYCYLDYNPWTFGQTKVEIKRTVAAPSVFIPPP 142
579 SSEQLTSGGASVVCFLNFPKDIINVKWKIDSGSRQNGVLNSWTDQDSKDSYSSMSSTLT 638
143 SDEQLASGTASVVCLLNFPKAYQVQKVDNALQSGNSQESVTEQDSKDSYSSLSSTLT 202
639 LTKDEYERHNSYTCATHKTSSTSPVKSPNRNE 671
203 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 235

RESULT 56
Q6N095_HUMAN
ID Q6N095_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6N095;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKF2p686K03196.
GN Name=DKF2p686K03196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640621; CAB45775.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR SNR; Q6N095; 20-475.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52360 MW; 7BA14104CD2DB8F0 CRC64;

Query Match 20.8%; Score 733; DB 2; Length 475;
Best Local Similarity 30.0%; Pred. No. 3.7e-37;
Matches 201; Conservative 65; Mismatches 161; Indels 242; Gaps 17;

QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
Db 20 QVQLVQSGAELKRPASVTSICTRASGYSTGYTHHWVROAPGQRLMMGNPRSDSKTY 79
QY 61 NOKFKDKATLTVDKSSSTTAYMELRSITSDSAVYVCARSTMITNY-----VMDYWGQGT 114
Db 80 AQTFQGRMTWTRDTSTSTVFMEINLSKSGDTAVYICTDRSGRALWFGELDAFDINGQGT 139
QY 115 SVTVSSAKTTPPSVYPLAPGSAATQNSMVTGLCVKGYFPPEVTVTNWSGSLSSGVHTFP 174
Db 140 KVTVSSAKTGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWSGALTSGVHTFP 199
QY 175 AVLQSD-LYTLSSSVTVPSSTWPSSETVTCNVAHPASTTKVDKIKIVPRDSGGPSEKSEIN 233
Db 200 AVLQSGSLYSLSVWTVPSSSLGTQTYICNVNHPKSNTKVDKKEPKSC----- 248
QY 234 EKDLRKSELSQGTALGNLKIYYNNSKATISSEKSDAQFLTNTLLFKGFTGHWPYNDLL 293
Db 249 -----DKTHTCPCPAPELGGPSVF--LFPKP--KDTL 279
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092518; AAH92518.1; -, mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;

Query Match 20.4%; Score 719; DB 2; Length 469;
Best Local Similarity 29.3%; Pred. No. 2.7e-36;
Matches 194; Conservative 70; Mismatches 163; Indels 236; Gaps 16;

QY 1 EVLOQSGDPLVKPGASVKISKASGVSFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
DB 20 EVLVESGGVVPGGSLRLSCAASGFTFDYAHMWVRQAPGKLEWVLSISWDGGSTY 79

QY 61 NQFKDKATLVDSKSTTAYMELRSLTSDSAVYCARSTMTINMYMDYMGQSTVTSV 120
DB 80 ADSVKGRFTISRDNKNSLYLQWNSLRAEDTALYYCATRGYTAGDYWGQGTTLVTSV 139

QY 121 AKTTPSPVYPLAPGSAQTNSMTVLGLVKGYPEPVTWNSGSLSSGGVHTTTPAVLQSD 180
DB 140 ASTKGSPVPLAPSSKTSKTSGLTALGCLVKDYEPPEPVTWNSGALTSVHTTTPAVLQSS 199

QY 181 -LYTLSSVTPSTWPSSTVTCNVAPASSTKVDKIVPRDSGGPSEKSEENKDLRK 239
DB 200 GLYSLSSVTPSSSLGTQYICNVNKPSTVDKVKPKSC----- 242

QY 240 KSELOGTALGNLQIYYNSKATTSSEKSAQDFLTNTLLFKGFTGHPWYNDLLVLDGST 299
DB 243 -----DKTHTCPCPAPPELLGGPSVF--LFPKPK--KDTLM----- 274

QY 300 AATSEYEGSSVDLYGAYGYQCAGGTENKTACMGVYTLHDNNRLTEKKVPINLWIDGK 359
DB 275 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVDG- 303

QY 360 QTTVPIDKVKTSKEVTVBQLDQARHYLHKFGLYNSDSFGGKQVQGLIVFHSSEGSTV 419
DB 304 --VEVHNATKPREEQ-----YNSTY--RVVSVLTVLHQDWLNGK 339

QY 420 SYDLFDAQGQYPTLLRIYRDNTTISSTLSISLYLTTTSIVMTQPTSLLSVAGDVTI 479
DB 340 EY----- 341

QY 480 TKCASQSVSNDAVYQKPGQSKLLTSYTSRYAGVDPDRFGSGYGTDTLTATSSVQAE 539
DB 342 KCKVS-----NKALPAP--LEKTSIKAKGP----- 365

QY 540 DAAVYFCQDYNPPTFGGKTKLEIKRADAAPTVISIPPPSSQLTSGGASVWVCLNNFYP 599
DB 366 -----REPOVYTLPPSRDELTKNQVSLTCLVKGFYF 396

QY 600 KDINVKKIDGSRQN-----GVLSNWTQDSKDSKTSYSMSSTLTTLTKDEYERHNSYCEA 654
DB 397 SDIAVESNGQPENNYKTTTPPVLDSD-----DGSFFLYSKLTVDKSRWQQGNVFSV 449

QY 655 THK 657
DB 450 MHE 452

RESULT 59
Q6PI81 HUMAN
ID Q6PI81 HUMAN PRELIMINARY; PRT; 478 AA.
AC Q6PI81;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -, mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGL1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 478 AA; 52667 MW; 17BED38D917970D6 CRC64;

Query Match 20.4%; Score 717.5; DB 2; Length 478;
Best Local Similarity 29.0%; Pred. No. 3.4e-36;
Matches 195; Conservative 73; Mismatches 159; Indels 245; Gaps 18;

QY 1 EVLOQSGDPLVKPGASVKISKASGVSFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
DB 20 EVLVESGGVLPGGSLRLSCAASGFTTSSYMWVRQAPGKLEWVNIKQDGSKEY 79

QY 61 NQFKDKATLVDSKSTTAYMELRSLTSDSAVYCARSTMTINMYMDYMGQSTVTSV 111
DB 80 VDSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYCARFESTMTITVADYFYFMDVWG 139

QY 112 QGTSVTVSSNAKTTTPSPVYPLAPGSAQTNSMTVLGLVKGYPEPVTWNSGSLSSGVH 171
DB 140 KGTITVTVSSASTKGPSPVPLAPSSKTSKTSGLTALGCLVKDYEPPEPVTWNSGALTSVH 199

```
QY 172 TPAVLQSD-LYTLSSSVTPSWSETVTCNVHPASSTKVDKXIVPRDSGGPSEKSE 230
DB 200 TPAVLQSGSLSSVTPSSSLGTQYICNVNHPKSNTKVDKVEPKSC----- 251
QY 231 EINEKDLRKSELQGTALGNLAKQIYYNKAITSSEKSDAQFLNTLLFKGFFTGHPWYN 290
DB 252 -----DKTHTCPCPAPPELLGGPSVF--LFPKP--K 279
QY 291 DLLVDLGGSTAATSEYEGSVLDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRLTEKKV 350
DB 280 DTLM-----ISRTPEVT-CVVVDVS-----HEDPEV 304
QY 351 PINLWDGKQTVTPIDKVTSKKEVTVOELDLQARHYLHGKFGCLYNSDFGKVGQGLIV 410
DB 305 KFNWYVDG---VEVHNAKTPREEQ-----YNSTY---RVWSVLTV 339
QY 411 FHSSEGSTVSYDLFDAQGGQVPTDLLRIYRDNTTISLSLSLYLTTISIVMTQTPTSL 470
DB 340 LHQDWLNGEY----- 350
QY 471 VSAGDRVTITCKASQSVSNDAWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDT 530
DB 351 -----KCKVS-----NKALPAP---IEKTISKAKGQP----- 374
QY 531 LTISSVQAEADAAYFCQDYNPPTFGGCTKLEIKRADAAPTIVISIPPSSEQLTSGCASV 590
DB 375 -----REPQYVTLPPSREEMTKNQVSL 396
QY 591 VCFLNFFYPKIDNVKWKIDGSRQN-----GVLSNWTDDQSKDSTYSMSSTLTLDKYE 645
DB 397 TCLVKGFSYSDIAVESNGQPNYKTPPVLDSD-----DGSFFLYSKLTVDKSRNQ 449
QY 646 RHNSYTCATHK 657
DB 450 QGNVPSVSMHE 461

RESULT 60
Q6GMX6 HUMAN
ID Q6GMX6 HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McQuellan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
```

```
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBDJ databases.
DR EMBL, BC073766; AAH73766.1; -, mRNA.
DR GO; GO:0016022; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOW_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 20.3%; Score 715; DB 2; Length 465;
Best Local Similarity 29.7%; Pred. No. 4.7e-36;
Matches 197; Conservative 64; Mismatches 162; Indels 240; Gaps 18;

QY 1 EVOLQSGDPLVKPGASVKISKASGYSTGYMHVVKSPGKLEWIGRINPNNGVTLY 60
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSGYWMIQIPAGKLEWIGRIY-TSGSTNY 78
QY 61 NQKPKDKATLTVDKSSTAYMELSLTSDSAVYVCARSTMITNYVMYDYGQGSTVTVSS 120
DB 79 NPSLSRVTVMSVDTSKNQPSLKVSVTAADTAVIYCARGFT---YDFWQGQTLTVSS 135
QY 121 AKTTPPSVYPLAPGSAATQNSMVTLCGLVKGYFPPEVTVTNWNSGSLSSGVHTFPVQLSD 180
DB 136 ASTKGPSVFPPLAPSSKSTSGGTAALGLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 195
QY 181 -LYTLSSSVTPSSWTPSETVTCNVHPASSTKVDKXIVPRDSGGPSEKSEINEKDLRK 239
DB 196 GLYSLSVVTVTPSSSLGTQYICNVNHPKSNTKVDKVEPKSC----- 238
QY 240 KSELQGTALGNLAKQIYYNKAITSSEKSDAQFLNTLLFKGFFTGHPWYNLDLVDLST 299
DB 239 -----DKTHTCPCPAPPELLGGPSVF--LFPKP--KDTLM----- 270
QY 300 AATSEYEGSVLDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRLTEKKVPIINLWDGK 359
DB 271 -----ISRTPEVT-CVVVDVS-----HEDPEVKNWYVDG- 299
QY 360 QTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGCLYNSDFGKVGQGLIVFHSSEGSTV 419
DB 300 ---VEVHNAKTPREEQ-----YNSTY---RVWSVLTVLHQDWLNGK 335
QY 420 SYDLFDAQGGQVPTDLLRIYRDNTTISLSLSLYLTTISIVMTQTPTSLVLSAGDRVTI 479
DB 336 EV----- 337
QY 480 TCKASQSVSNDAWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTSSVQAE 539
DB 338 KCKVS-----NKALPAP---IEKTISKAKGQP----- 361
QY 540 DAAYVFCQDYNPPTFGGCTKLEIKRADAAPTIVISIPPSSEQLTSGGASVVCFLNNFYP 599
DB 362 -----REPQYVTLPPSREEMTKNQVSLTCLVKGFY 392
QY 600 KDINKVKKIDGSRQN-----GVLSNWTDDQSKDSTYSMSSTLTLDKDEYERHNSYTCFA 654
DB 393 SDIAVESNGQPNYKTPPVLDSD-----DGSFFLYSKLTVDKSRWQQGNVPSVCSV 445
QY 655 THK 657
:
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Db 446 MHE 448

RESULT 61

Q5RE17_PONPY PRELIMINARY; PRT; 475 AA.

AC Q5RE17_PONPY PRELIMINARY; PRT; 475 AA.

DT 01-FEB-2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE Hypothetical protein DKFZp469C2335.

GN Name=DKFZp469C2335;

OS Pongo pygmaeus (Orangutan).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Pongo.

OC NCBI_TaxID=9600;

OC [1]

RN NUCLEOTIDE SEQUENCE.

RP TISSUE=Kidney;

RG The German cDNA Consortium;

RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,

RA Mewes H.W., Weil B., Anid C., Osanger A., Fobo G., Han M., Wiemann S.;

RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; CR857722; CAH89990.1; -; mRNA.

DR SMR; Q5RE17; 21-475.

DR GO; GO:0030106; F:MHC class I receptor activity; IEA.

DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.

DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.

DR InterPro; IPR003599; Ig-like.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig cl.

DR InterPro; IPR003006; Ig MHC.

DR InterPro; IPR003596; Ig v.

DR Pfam; PF07654; Cl-set; 3.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 3.

DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG LIKE; 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

KW Hypothetical protein_2.

SEQUENCE 475 AA; 51898 MW; 04BDBE096A2CD529 CRC64;

Query Match 20.3%; Score 714; DB 2; Length 475;

Best Local Similarity 28.1%; Pred. No. 5.6e-36;

Matches 194; Conservative 73; Mismatches 138; Indels 286; Gaps 18;

Qy 1 EVQLQSGPDLVKGASVKISKASGYSFTCYMHVWYKQSPGKLEWIGINPNNGVTLY 60

Db 20 DIQLVQSGAEVRFEGESLRISCKSGSYTFDYTWIGVWRQMPGKLEWIGIDPSNSGTY 79

Qy 61 NQKPKATLVKSSSTAYMELRSLTSEDSAVVYCARSTMI-TN-----YVMDYWGQGT 114

Db 80 NRSFEGHITADMSISITAYLQWTLKASDSAIYCARLSGTNSYHKRSYFQFWGQGT 139

Qy 115 SVTVSSAKTTPSPYPLAPGAAQTNSNVTLCGLVKGYFPPEPTVTWNSSGLSSGVHTFP 174

Db 140 LVIVSLASTKGPSVFLAPSSRSSTSGGTAALGCLVKDYFPPEPTVTWNSSGALTSGVHTFP 199

Qy 175 AVLQSD-LYTLSSSVTPSPSTWSPETVCNVAHPASSTKVDKLVPRDS-----222

Db 200 AVLQSSGLYSLSVTVTPSSSLGTQYTCNVDRKPSNTKVDKVEPKSCDTPRCPCPA 259

Qy 223 ---GGPSEKSEENEXDLRKKSELOQTALGNLQAIYYNSKAITTSSEKSAQDLFTWLL 278

Db 260 PELGGPS-----VFLFPKP-----KOTLM 280

Qy 279 FKGFPTGHPWYNLLDLGLGTAATSEYEGSSVDLYGAYGYQCAGGTPTNKTACMGVTL 338

Db 281 I-----GGPSEKSEENEXDLRKKSELOQTALGNLQAIYYNSKAITTSSEKSAQDLFTWLL 295

Qy 339 HDNRLTEKKVPINLWDGQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK 391

Db 446 MHE 448

RESULT 62

Q5FEF6_HUMAN PRELIMINARY; PRT; 234 AA.

AC Q5FEF6_HUMAN PRELIMINARY; PRT; 234 AA.

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Anti-Rhd monoclonal T125 kappa light chain precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OC NCBI_TaxID=9606;

OC [1]

RN NUCLEOTIDE SEQUENCE.

RP Gaucher C., Klein P., Beliard R.;

RT "Sequence determination of the recombinant human anti-Rhd monoclonal antibody T125.";

RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY894991; AA82027.1; -; mRNA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig v.

DR Pfam; PF07654; Cl-set; 1.

DR Pfam; PF07686; V-set; 1.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 1.

DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Signal.

FT SIGNAL 1 20 Potential.

FT CHAIN 21 234 anti-Rhd monoclonal T125 kappa light chain.

FT SEQUENCE 234 AA; 25698 MW; 866DCD1E4FD7D5EA CRC64;

Query Match 20.2%; Score 712; DB 2; Length 234;

Best Local Similarity 62.9%; Pred. No. 2.8e-36;

Matches 134; Conservative 30; Mismatches 49; Indels 0; Gaps 0;

Qy 459 SIWVTQPTSLVAGDRVTITCKASQSVNDVAVYQKQSPGKLLISVTSRYAGVDP 518

Db 21 AIRMTPSPSFSASTGDRVTITCRASQDIERNYAVYQKQSPGKLLISVTSRYAGVDP 80

Qy 519 RFSSGSGTDTLTITSSVQAEADAVYFCQDYNSPPTFGGKTKLEIKRADAAPTVSIFPP 578

Db 81 RFSSGSGTDTLTITSSVQAEADAVYFCQDYNSPPTFGGKTKLEIKRADAAPTVSIFPP 140


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QY 579 SSEQLTSGASVVCFLNNFYPKDVINVKWKIDGSRQGVNSWTDDSKDSTYSMSSTLT 638
DB 141 SDEQLKSGTASVVCLNNFYPKDVQVQKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT 200

QY 639 LTKDEYERHNSYTCEATHKTSSTPIVKSFNRRNE 671
DB 201 LSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGE 233

RESULT 63
Q6PIH7 HUMAN
ID Q6PIH7_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -; mRNA.
DR HSSP; P01607; 1AR2.
DR SMR; Q6PIH7; 23-236
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG1; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR PROSITE; 236 AA; 25603 MW; 8BC561106861213F CRC64;
SQ SEQUENCE

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Query Match      20.2%; Score 710; DB 2; Length 236;
Best Local Similarity 63.2%; Pred. No. 3.7e-36;
Matches 134; Conservative 31; Mismatches 47; Indels 0; Gaps 0;

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QY 460 IVMTOTPTSLVYAGDRVTITCKASQSVNSDVAVYQKQSPKLLISYTSRYAGVPDR 519
DB 24 IQLTQSPFLSASVGRVTITCRASQGISYLAWYQKQKGFAPNLLIYAASTLQSGVPSR 83

QY 520 FSGSGYGTDFTLTISSVQAEADAIVPCQDYNSPPTFGGKLEIKRAADAAPTVSIFPPS 579
DB 84 FSGSGSGTEFTLTISLQPEDFATVYCCQLNSSPPTFGGKTKVKKRTVAAPSVFIFPPS 143

QY 580 SEQLTSGASVVCFLNNFYPKDVINVKWKIDGSRQGVNSWTDDSKDSTYSMSSTLT 639
DB 144 DEQLKSGTASVVCLNNFYPKDVQVQKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT 203

QY 640 TKDEYERHNSYTCEATHKTSSTPIVKSFNRRNE 671
DB 204 SKADYEKKHKVYACEVTHQGLSSPVTKSFNRGE 235

RESULT 64
Q6GMW0 HUMAN
ID Q6GMW0_HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6GMW0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGKV1-5 protein.
GN Name=IGKV1-5;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG Director MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073792; AAH73792.1; -; mRNA.
DR SMR; Q6GMW0; 21-233.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 2.

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DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 20.1%; Score 707.5; DB 2; Length 235;
Best Local Similarity 63.1%; Pred. No. 5.3e-36;
Matches 137; Conservative 33; Mismatches 45; Indels 3; Gaps 2;

457 TTIVMTQPTSLVLSAGDRVTITCKASQSVNDVAWYQQKPGQSPKLLISYSSRYAGV 516
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
19 TGEIVMTQSPATLSVSPGERATLSCRASQSIISNNLAWYQQRPGQAPRLLIYGASRRVTGI 78

517 PDRFSGSGYGTDTFTLTISISSVQAEADAAVYFCQDYNS--PPTFGGTYKLEIKRADAPTVS 574
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
79 PGRFSGSGSGTEFTLTISLSQSDFAVYFCQ-QYNDWLLYTFGGGTGLEIKRTVAAPSVF 137

575 IFPPSSQLTSGGASVVCFLNNFYPKDINVVKWIKDGSERQGVLSNWTDDQSKDSTYSMS 634
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
138 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYISLS 197

635 STLTLDKDEYERHNSYTCEATHKSTSTSPVKSFNRE 671
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
198 STLTLSKADYKHKVYACEVTHQGLSLSPVTKSFNRGE 234

RESULT. 65
Q6GMX0 HUMAN
ID Q6GMX0 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073775; AAH73775.1; -; mRNA.
DR SMR; Q6GMX0; 23-236.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
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DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E32BF8F CRC64;

Query Match 20.0%; Score 706; DB 2; Length 236;
Best Local Similarity 62.7%; Pred. No. 6.6e-36;
Matches 133; Conservative 30; Mismatches 49; Indels 0; Gaps 0;

460 IVMTQPTSLVLSAGDRVTITCKASQSVNDVAWYQQKPGQSPKLLISYSSRYAGVPDR 519
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
24 IQMTQSPSSLSASGVRVTITCRASQINNNLWYQLKPGKAPNLLIYAASSLSQGVPSR 83

520 FSGSGYGTDTFTLTISISSVQAEADAAVYFCQDYNSPPTFGGTYKLEIKRADAPTVSIFPPS 579
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
84 FSGSGSGTDTFTLTISLRPDDFAVYCCQSYNIPLTFGGGTNVEIKRTVAAPSVFIFPPS 143

580 SEQLTSGGASVVCFLNNFYPKDINVVKWIKDGSERQGVLSNWTDDQSKDSTYSMSSTLT 639
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
144 DEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYISLSLTLL 203

640 TKDEYERHNSYTCEATHKSTSTSPVKSFNRE 671
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
204 SKADYKHKVYACEVTHQGLSLSPVTKSFNRGE 235

NAME=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
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QY 298 STAATSEYEGSSVDLYGAYGYOCAGGTGNTKACMYGGVTLHDNNRLTEKKVPINLWID 357
Db 276 -----ISRTEVT-CVVVDVS-----HEDPEVKFNWYVD 303
QY 358 GKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGRLIVFHSSEGS 417
Db 304 G-----VEVHNAKTKPREEQ-----YNSYV---RVVSVLTVLHQDWLNL 338
QY 418 TVSYDLFDAQQGQVPTDLLRIYRDNNTTISLSISLYLTTSIVMTQTPTSLLSVAGDRV 477
Db 339 GREY----- 342
QY 478 TITCKASQSVNDVAVYQKPGQSKLLISYTSRRYAGVDPDRFSGSGYGTDFLTITSSVQ 537
Db 343 --KCKVS-----NKALPAP---TEKTSKAKGP----- 366
QY 538 AEDAAVYFCQDYNSPPTFGGTKLEIKRADAAPTVSIIPPSPSEQLTSGGASVVCFLNPF 597
Db 367 -----REPVYTLPPSRDELTKQVSLTCLVKGF 395
QY 598 YPKDINVKKIDGSRQK-----GVLSNWTQDQSKDSTYSMSSTLTLTDEYERHNSYTC 652
Db 396 YPSDIAVEWESNGQPNKYKTPPPVLDSE-----DGSFFLYSKLTVDKSRMQQGNVFSC 448
QY 653 EATHK 657
Db 449 SVMHE 453

RESULT 70
Q6IN78_HUMAN
ID Q6IN78_HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System; DOI=10.1073/pnas.242603899;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish U.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -; mRNA.
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DR HSSP; P01861; IAD0.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50854 MW; 53EB0BCED81076E CRC64;

Query Match 19.8%; Score 697.5; DB 2; Length 466;
Best Local Similarity 29.3%; Pred. No. 5.8e-35;
Matches 195; Conservative 67; Mismatches 160; Indels 243; Gaps 19;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYSFTGYVMHWVKSPGKLEWIGRINPNNGVTLY 60
Db 20 EVQLVESGGGLIQPGSLTSLCAASGLTVSSNMYHWVRQAPGKLEWVS-VLYIGATYY 78
QY 61 NQKFKDKATLTVDKSTTAYMELRLSLTSDSAVYYCARSTMITNYMDY--WGQGSSTV 118
Db 79 ADSVKGRFTISRDNKNTLYLQMSLRABDTAVYYCARG-----NYVVPAPMGQGLTV 134
QY 119 SSAKTPPSVYPLAPGSAQAQTNMTVTLGCLVKGYPEPTVTWNSGSLSSGVHTTFAVLQ 178
Db 135 SSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYPEPTVTWNSGSLTSGVHTTFAVLQ 194
QY 179 SD-LYTLSSSVTPSPSETVTCNVAPASSTKVDKKIIVPRDSGGPSEKSEEINEKDL 237
Db 195 SSGLYSLSSVTVPSSSLGTQYICNVNKKPNTKVDKEVEPKSC----- 239
QY 238 RKKSELQGTALGNLQKIYYNYSKATTSSEKSDAQFTNTLLFKGFTGHPWNTDLLVDLG 297
Db 240 -----DKTHTCCPPCAPPELLGGPSVF--LPPPKP--KDTLM--- 271
QY 298 STAATSEYEGSSVDLYGAYGYOCAGGTGNTKACMYGGVTLHDNNRLTEKKVPINLWID 357
Db 272 -----ISRTEVT-CVVVDVS-----HEDPEVKFNWYVD 299
QY 358 GKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGRLIVFHSSEGS 417
Db 300 G-----VEVHNAKTKPREEQ-----YNSYV---RVVSVLTVLHQDWLNL 334
QY 418 TVSYDLFDAQQGQVPTDLLRIYRDNNTTISLSISLYLTTSIVMTQTPTSLLSVAGDRV 477
Db 335 GREY----- 338
QY 478 TITCKASQSVNDVAVYQKPGQSKLLISYTSRRYAGVDPDRFSGSGYGTDFLTITSSVQ 537
Db 339 --KCKVS-----NKALPAP---TEKTSKAKGP----- 362
QY 538 AEDAAVYFCQDYNSPPTFGGTKLEIKRADAAPTVSIIPPSPSEQLTSGGASVVCFLNPF 597
Db 363 -----REPVYTLPPSRDELTKQVSLTCLVKGF 391
QY 598 YPKDINVKKIDGSRQK-----GVLSNWTQDQSKDSTYSMSSTLTLTDEYERHNSYTC 652
Db 392 YPSDIAVEWESNGQPNKYKTPPPVLDSE-----DGSFFLYSKLTVDKSRMQQGNVFSC 444
QY 653 EATHK 657
Db 445 SVMHE 449

RESULT 71
Q502W4_HUMAN
ID Q502W4_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q502W4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
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DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
ON [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Glandular pool- thyroid;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC095489; AAH95489.1; -; mRNA.
DR SMR; Q502W4; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25936 MW; E2DF79AC18756AA9 CRC64;

Query Match 19.8%; Score 696; DB 2; Length 236;
Best Local Similarity 63.4%; Pred. No. 2.8e-35;
Matches 135; Conservative 28; Mismatches 48; Indels 2; Gaps 2;

QY 460 IVMTQTPTSLVAGDRVTITCKASQSVNDVAVYQKQSPKLLISYTSRRVAGVPDR 519
DB 1 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
24 IQMTQSPSSLSASVGDRTVTITCRASQGRDLGWYQKQPKAPKRLIFAASSLSQSGVPSR 83
QY 520 FSGSGYGTDFLTITSSVQAEADAAVYFCQQDYNS-PPTFGGKTKLEIKRADAAPTIVSI 578
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 FSGSGSGTEFTLTINSIQPEDFATYICLQ-YNSYPTFGGKTKVEIKRTVAAPSVFI 142
QY 579 SSEQLTSGGASVVCFLNNFYPKDINVKWDGSRQNGVNLNWTQDQSKOSTYSMTSLT 638
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
143 SDEQLKSGTASVCLNNFYPKAVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 202
QY 639 LTKDEYRHNSYTCATHTKSTSTIVKSPRNE 671
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
203 LSKADYEKKHYACEVTHQGLSSPVTKSFNRRG 235
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RESULT 72
Q6GMV9 HUMAN
ID Q6GMV9 HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6GMV9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
ON [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Spleen;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073793; AAH73793.1; -; mRNA.
DR SMR; Q6GMV9; 21-235.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

Query Match 19.7%; Score 694.5; DB 2; Length 235;
Best Local Similarity 61.6%; Pred. No. 3.4e-35;
Matches 133; Conservative 33; Mismatches 49; Indels 1; Gaps 1;

QY 457 TTSIVMTQTPTSLVAGDRVTITCKASQSV-NDVAVYQKQSPKLLISYTSRRVAG 515
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
19 TGSIVLTQSPGTLSLSPGERAAALSCRASQSVNSKYLAWYQKQPKAPRLMYAASIRATG 78
QY 516 VPRFSGSGYGTDFLTITSSVQAEADAAVYFCQQDYNSPPTFGGKTKLEIKRADAAPTIVSI 575
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
79 IPRFSGSGSGTDFLTITISPLESEDFALYFCQQYGTSPITFGGKTKVEIKRTVAAPSVFI 138
QY 576 FPPSSEQLTSGGASVVCFLNNFYPKDINVKWDGSRQNGVNLNWTQDQSKOSTYSMS 635
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Db 139 FPPSDQLSGTASVCLNNFPRKQVQKVDNALQSGNSQESVTEQDSKDSSTLSLS 198
QY 636 TLTLTKDEYERHNSYTCEATHKSTSTSPIVKSFRNE 671
Db 199 TLTLSKADYKHKVYACEVTHQGLSFPVTKSFRNGE 234

RESULT 73
Q6MZQ6 HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686G1190.
GN Names=DKFZp686G1190;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Esophagus tumor;
RG The German CDNA Consortium;
RA Bahr A., Lauber J., Newes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL EMBL; BX640947; CAE45972.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR SMR; Q6MZQ6; 20-475.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ
Query Match 19.7%; Score 694; DB 2; Length 475;
Best Local Similarity 28.6%; Pred. No. 9.7e-35;
Matches 191; Conservative 74; Mismatches 162; Indels 242; Gaps 17;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHVWQSPGKGLWIGRIINPNGVTLY 60
Db 20 EVQLLESQGLVQPGGSLRLSCLSAASGFTFRNYAMNVRQAPGKGLWVSGISSGVNTYY 79
QY 61 NQKFDDKATLTVDKSTTAYMELRLSTSDSAVYYCARSS-----TMITNYMDVWGQGT 114
Db 80 ADSVKGRFTISGISTNTLYLQHSRADDTAVYICARADYRDYQVSPAYTFDVMWGRGT 139
QY 115 SVTVSSAKTTPSPVYPLAPGSAQTNSMTVLGLVKGYFPEPVTVTWNSGSLSSGVHTFP 174
Db 140 LVSVSAASKTGPSVFLAPLAPSSKTSSTGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199
QY 175 AVLQSD-LYTLSSVTVPSSTWPESETVTCNVAHPASSTKVDDKIVPRDSGGFSEKSEELN 233
Db 200 AVLQSSGLYLSVWTVPSSSLGTQTYICNVNHPKSNITKVDKKVEPKSC----- 248
QY 234 EXDLRKKSELQGTALGNLQIYYNSKAITSSKSDAQELTNTLLPKGFFTGHPWYNDLL 293
Db 249 -----DKTHTCPPCPAPELLGGPSVFLPFPKPP--KOTL 279
QY 294 VDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPTKTCMYGGVTLHDNRLNTEEEKVPIN 353
Db 280 M-----ISRTPVET-CVVVDVS-----HEDPEVKFN 304

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QY 354 LMIWGKQITVPIDKVKTSKKEVTVQELDLQARHYLHGKGLYNSDSFGGKQVQGLIVFHS 413
Db 305 WYVDG-----VEVHNAKTKPREQ-----YNSTY-----RVSVLTVLHQ 339
QY 414 SEGSTSVSYDLFDAQGYPDTLRIYRDNTTISSTLSISLYLYTTISIVMTQTPTSLLSVA 473
Db 340 DWLNGKEY----- 347
QY 474 GDRVTITKASQSVNDVAVYQKQSPKLIISYTSRYAGVPDRFSGSGYGTDTFTLT 533
Db 348 -----KCKVS-----NKALPAP-----TEKTSKAKGP----- 371
QY 534 SSVQAEADAAYFCQQDYNSPPTFGGKLEIKRADAAPTVSIFFPSSSEOLTSGGASVWCF 593
Db 372 -----REPOVYTLPPSRDELTKNQVSLTCL 396
QY 594 LNNFPKIDINVKWKIDGSRQN-----GVLNSWTDDSDKSDSYMSSTLTTLTKDEYERHN 648
Db 397 VKGFVPSDIAVWESNGQPNKYKTPPVLDS-----DGSFFLYSKLTVDKSRWQQGN 449
QY 649 SYTCEATHK 657
Db 450 VFSCSVMHE 458

RESULT 74
Q7Z473 HUMAN PRELIMINARY; PRT; 234 AA.
ID Q7Z473;
AC Q7Z473;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Lung;
RG NIH MGC Project;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAHS6256.1; -; mRNA.
DR HSSP; P01834; 1HEZ.
DR SMR; Q7Z473; 22-234.
DR Ensembl; ENSG00000163245; Homo sapiens.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:18:35 ; Search time 51.2354 Seconds
(without alignments)
1084.369 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522

Sequence: 1 EVQLQSGDPLVKPGASVKI.....EATHKTSPIVKSFRNRES 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1108.5	31.5	489	4	PCT-US95-11405-35
2	1107	31.4	233	2	US-08-695-692B-8
3	1107	31.4	257	2	US-08-486-099-112
4	1107	31.4	257	2	US-08-360-107A-122
5	1107	31.4	257	2	US-08-484-223B-112
6	1107	31.4	257	2	US-08-919-597-112
7	1107	31.4	257	2	US-08-475-668A-112
8	1107	31.4	257	2	US-08-485-551A-112
9	1107	31.4	257	2	US-08-471-913A-112
10	1107	31.4	257	2	US-08-485-264A-112
11	1107	31.4	257	2	US-08-474-349A-112
12	1107	31.4	257	2	US-08-470-896-112
13	1107	31.4	257	2	US-08-485-546A-112
14	1107	31.4	257	2	US-08-487-266A-112
15	1107	31.4	257	2	US-08-484-741-112
16	1071	30.4	254	2	US-09-350-841A-1598
17	1059.5	30.1	445	1	US-08-353-400-33
18	1059.5	30.1	464	1	US-08-353-400-36
19	1040	29.5	226	2	US-08-896-933-24
20	1040	29.5	226	2	US-09-314-235-24
21	1040	29.5	226	2	US-09-708-008B-24
22	980.5	27.8	711	2	US-09-485-737B-90
23	980.5	27.8	711	2	US-10-071-485-90
24	966	27.4	468	1	US-08-116-247-7
25	966	27.4	468	1	US-09-348-224-7
26	960	27.3	212	1	US-08-737-129A-2
27	957	27.2	468	1	US-08-303-569B-7

28	957	27.2	468	2	US-09-795-515-7	Sequence 7, Appli
29	953.5	27.1	223	4	PCT-US94-14106-51	Sequence 51, Appl
30	948	26.9	233	2	US-08-695-692B-7	Sequence 7, Appli
31	948	26.9	257	2	US-08-486-099-113	Sequence 113, App
32	948	26.9	257	2	US-08-360-107A-123	Sequence 123, App
33	948	26.9	257	2	US-08-484-223B-113	Sequence 113, App
34	948	26.9	257	2	US-08-919-597-113	Sequence 113, App
35	948	26.9	257	2	US-08-475-668A-113	Sequence 113, App
36	948	26.9	257	2	US-08-485-551A-113	Sequence 113, App
37	948	26.9	257	2	US-08-471-913A-113	Sequence 113, App
38	948	26.9	257	2	US-08-485-264A-113	Sequence 113, App
39	948	26.9	257	2	US-08-474-349A-113	Sequence 113, App
40	948	26.9	257	2	US-08-470-896-113	Sequence 113, App
41	948	26.9	257	2	US-08-485-546A-113	Sequence 113, App
42	948	26.9	257	2	US-08-487-266A-113	Sequence 113, App
43	948	26.9	257	2	US-08-484-741-113	Sequence 113, App
44	944.5	26.8	239	1	US-08-353-400-37	Sequence 37, Appl
45	944	26.8	233	1	US-08-446-918A-4	Sequence 4, Appli
46	944	26.8	233	1	US-08-580-806-4	Sequence 4, Appli
47	941.5	26.7	219	1	US-08-353-400-34	Sequence 34, Appl
48	933	26.5	222	1	US-08-737-129A-6	Sequence 6, Appli
49	931.5	26.4	232	2	US-08-896-933-23	Sequence 23, Appl
50	931.5	26.4	232	2	US-09-314-235-23	Sequence 23, Appl
51	931.5	26.4	232	2	US-09-708-008B-23	Sequence 23, Appl
52	925	26.3	257	2	US-09-144-776B-2	Sequence 2, Appli
53	925	26.3	257	2	US-08-882-431B-2	Sequence 2, Appli
54	921	26.1	233	2	US-09-144-776B-4	Sequence 4, Appli
55	921	26.1	233	2	US-08-882-431B-4	Sequence 4, Appli
56	916	26.0	454	2	US-09-653-755A-4	Sequence 4, Appli
57	916	26.0	462	2	US-09-653-755A-6	Sequence 6, Appli
58	915.5	26.0	254	1	US-08-792-824-10	Sequence 10, Appl
59	915.5	26.0	254	1	US-08-792-824-13	Sequence 13, Appl
60	909.5	25.8	254	1	US-08-792-824-4	Sequence 4, Appli
61	909.5	25.8	254	1	US-08-792-824-7	Sequence 7, Appli
62	904.5	25.7	238	2	US-09-192-545-4	Sequence 4, Appli
63	903.5	25.7	447	6	5455030-1	Patent No. 5455030
64	901	25.6	218	4	PCT-US94-14106-57	Sequence 57, Appl
65	898	25.5	211	2	US-09-170-769A-8	Sequence 8, Appli
66	897.5	25.5	223	4	PCT-US94-14106-55	Sequence 55, Appl
67	895	25.4	215	1	US-08-737-129A-8	Sequence 8, Appli
68	893.5	25.4	219	2	US-09-254-180C-131	Sequence 131, App
69	893.5	25.4	219	2	US-09-254-180C-181	Sequence 181, App
70	892.5	25.3	599	1	US-08-442-542-18	Sequence 18, Appl
71	892.5	25.3	599	1	US-08-765-469-18	Sequence 18, Appl
72	889.5	25.3	235	2	US-09-423-439-58	Sequence 58, Appl
73	889.5	25.3	235	2	US-09-011-769A-23	Sequence 23, Appl
74	885.5	25.1	216	2	US-09-254-180C-132	Sequence 132, App
75	885.5	25.1	216	2	US-09-254-180C-183	Sequence 183, App
76	878	24.9	213	1	US-08-737-129A-4	Sequence 4, Appli
77	874.5	24.8	219	2	US-09-254-180C-180	Sequence 180, App
78	874	24.8	214	2	US-09-653-755A-5	Sequence 5, Appli
79	873	24.8	647	2	US-09-423-439-60	Sequence 60, Appl
80	872	24.8	236	1	US-08-792-824-3	Sequence 3, Appli
81	872	24.8	236	1	US-08-792-824-9	Sequence 9, Appli
82	872	24.8	236	1	US-08-792-824-12	Sequence 12, Appl
83	872	24.8	236	1	US-09-301-593-18	Sequence 18, Appl
84	870	24.7	234	2	US-09-770-916-4	Sequence 4, Appli
85	868.5	24.7	216	2	US-09-254-180C-182	Sequence 182, App
86	866.5	24.6	252	2	US-09-350-841A-1599	Sequence 1599, Ap
87	864	24.5	218	4	PCT-US94-14106-61	Sequence 61, Appl
88	863.5	24.5	472	2	US-09-301-593-30	Sequence 30, Appl
89	861	24.4	215	2	US-09-170-769A-4	Sequence 4, Appli
90	860.5	24.4	466	2	US-09-698-705-11	Sequence 11, Appl
91	858	24.4	234	4	PCT-US94-07659-4	Sequence 4, Appli
92	855.5	24.3	250	2	US-09-011-769A-21	Sequence 21, Appl
93	855.5	24.3	473	2	US-09-171-945-131	Sequence 131, App
94	855.5	24.3	473	2	US-09-910-059-131	Sequence 131, App
95	854.5	24.3	470	2	US-09-238-741-4	Sequence 4, Appli
96	852.5	24.2	235	1	US-08-303-569B-5	Sequence 5, Appli
97	852.5	24.2	235	1	US-08-116-247-5	Sequence 5, Appli
98	852.5	24.2	235	2	US-09-795-515-5	Sequence 5, Appli
99	852.5	24.2	235	2	US-09-348-224-5	Sequence 5, Appli
100	850.5	24.1	200	6	5189147-8	Patent No. 5189147

101	841	23.9	454	1	US-07-934-373C-22	Sequence 22, Appl	174	741.5	21.1	298	2	US-08-804-444A-60	Sequence 60, Appl
102	841	23.9	454	2	US-08-437-642B-22	Sequence 22, Appl	175	741.5	21.1	298	2	US-09-026-985-60	Sequence 60, Appl
103	841	23.9	454	2	US-08-146-206C-22	Sequence 22, Appl	176	741.5	21.1	298	2	US-09-121-952A-60	Sequence 60, Appl
104	841	23.9	454	2	US-09-705-686-22	Sequence 22, Appl	177	741.5	21.1	298	2	US-09-234-340A-60	Sequence 60, Appl
105	841	23.9	454	2	US-09-705-398A-22	Sequence 22, Appl	178	741.5	21.1	298	2	US-09-355-014-60	Sequence 7, Appl
106	841	23.9	454	2	US-09-705-398-22	Sequence 22, Appl	179	737	20.9	446	2	US-08-397-411-7	Sequence 7, Appl
107	841	23.9	454	4	PCR-US93-07832-22	Sequence 22, Appl	180	734.5	20.9	253	2	US-09-027-449-52	Sequence 52, Appl
108	840	23.9	206	6	5189147-9	Patent No. 5189147	181	734.5	20.9	253	2	US-09-027-449-55	Sequence 55, Appl
109	834.5	23.7	217	4	PCR-US94-14106-59	Sequence 59, Appl	182	734.5	20.9	253	2	US-08-804-444A-52	Sequence 52, Appl
110	831.5	23.6	247	4	PCR-US94-07659-2	Sequence 6, Appl	183	734.5	20.9	253	2	US-08-804-444A-55	Sequence 55, Appl
111	830	23.6	233	1	US-08-792-824-6	Sequence 6, Appl	184	734.5	20.9	253	2	US-09-026-985-52	Sequence 52, Appl
112	828.5	23.5	235	2	US-08-444-644-19	Sequence 19, Appl	185	734.5	20.9	253	2	US-09-026-985-55	Sequence 55, Appl
113	828.5	23.5	235	2	US-08-444-644-28	Sequence 28, Appl	186	734.5	20.9	253	2	US-09-121-952A-52	Sequence 52, Appl
114	827.5	23.5	215	6	5455030-3	Patent No. 5455030	187	734.5	20.9	253	2	US-09-121-952A-55	Sequence 55, Appl
115	826.5	23.5	235	2	US-08-444-644-42	Sequence 42, Appl	188	734.5	20.9	253	2	US-09-234-340A-52	Sequence 52, Appl
116	826.5	23.5	235	2	US-08-232-246A-42	Sequence 42, Appl	189	734.5	20.9	253	2	US-09-234-340A-55	Sequence 55, Appl
117	825.5	23.4	235	2	US-08-444-644-19	Sequence 19, Appl	190	734.5	20.9	253	2	US-09-355-014-52	Sequence 52, Appl
118	825.5	23.4	235	2	US-08-232-246A-19	Sequence 19, Appl	191	734.5	20.9	253	2	US-09-355-014-55	Sequence 55, Appl
119	821.5	23.3	222	2	US-09-698-705-13	Sequence 13, Appl	192	734.5	20.9	256	2	US-09-027-449-70	Sequence 70, Appl
120	819	23.3	234	1	US-07-690-192-2	Sequence 2, Appl	193	734.5	20.9	256	2	US-09-026-985-70	Sequence 70, Appl
121	818.5	23.2	472	2	US-09-301-593-43	Sequence 43, Appl	194	734.5	20.9	256	2	US-09-121-952A-70	Sequence 70, Appl
122	812	23.1	467	1	US-07-916-098A-45	Sequence 45, Appl	195	734.5	20.9	256	2	US-09-234-340A-70	Sequence 70, Appl
123	811.5	23.0	233	2	US-08-444-644-33	Sequence 33, Appl	196	734.5	20.9	256	2	US-09-355-014-70	Sequence 70, Appl
124	811.5	23.0	233	2	US-08-232-246A-33	Sequence 33, Appl	197	731	20.8	233	1	US-07-934-373C-25	Sequence 25, Appl
125	803.5	22.8	478	2	US-09-770-916-2	Sequence 2, Appl	198	731	20.8	233	2	US-08-437-642B-25	Sequence 25, Appl
126	802	22.8	255	1	US-07-690-192-4	Sequence 4, Appl	199	731	20.8	233	2	US-08-146-206C-25	Sequence 25, Appl
127	802	22.8	452	2	US-09-027-449-71	Sequence 71, Appl	200	731	20.8	233	2	US-09-705-686-25	Sequence 25, Appl
128	802	22.8	452	2	US-09-026-985-71	Sequence 71, Appl	201	731	20.8	233	2	US-09-705-398A-25	Sequence 25, Appl
129	802	22.8	452	2	US-09-121-952A-71	Sequence 71, Appl	202	731	20.8	233	2	US-09-705-398-25	Sequence 25, Appl
130	802	22.8	452	2	US-09-234-340A-71	Sequence 71, Appl	203	731	20.8	233	4	PCR-US93-07832-25	Sequence 25, Appl
131	802	22.8	452	2	US-09-355-014-71	Sequence 71, Appl	204	730.5	20.7	232	1	US-07-934-373C-34	Sequence 34, Appl
132	794.5	22.6	449	1	US-08-458-516-13	Sequence 13, Appl	205	730.5	20.7	232	2	US-08-437-642B-34	Sequence 34, Appl
133	789	22.4	473	2	US-09-828-995B-20	Sequence 20, Appl	206	730.5	20.7	232	4	PCR-US93-07832-34	Sequence 34, Appl
134	785.5	22.3	470	2	US-09-859-053-28	Sequence 28, Appl	207	729	20.7	240	2	US-09-301-593-36	Sequence 36, Appl
135	782.5	22.2	462	2	US-09-627-896B-24	Sequence 24, Appl	208	728	20.7	222	1	US-08-458-516-22	Sequence 22, Appl
136	781.5	22.2	279	2	US-08-397-411-13	Sequence 13, Appl	209	728	20.7	235	1	US-08-458-516-23	Sequence 23, Appl
137	780	22.1	230	2	US-08-952-235-2	Sequence 2, Appl	210	728	20.7	237	1	US-08-463-587A-25	Sequence 25, Appl
138	780	22.1	230	2	US-09-669-971-2	Sequence 2, Appl	211	728	20.7	237	1	US-08-463-667A-3	Sequence 3, Appl
139	778.5	22.1	253	1	US-08-398-613A-58	Sequence 58, Appl	212	728	20.7	237	2	US-08-923-854-25	Sequence 25, Appl
140	778.5	22.1	253	1	US-08-398-612A-58	Sequence 58, Appl	213	728	20.7	237	2	US-09-097-303-6	Sequence 6, Appl
141	778.5	22.1	253	1	US-08-398-611A-58	Sequence 58, Appl	214	728	20.7	237	2	US-09-097-171A-10	Sequence 10, Appl
142	778.5	22.1	253	1	US-08-491-334A-58	Sequence 58, Appl	215	728	20.7	237	2	US-09-422-712B-2	Sequence 2, Appl
143	778.5	22.1	253	2	US-09-027-449-44	Sequence 44, Appl	216	728	20.7	237	2	US-09-607-756-2	Sequence 2, Appl
144	778.5	22.1	253	2	US-08-804-444A-44	Sequence 44, Appl	217	728	20.7	237	2	US-09-460-587-6	Sequence 6, Appl
145	778.5	22.1	253	2	US-09-026-985-44	Sequence 44, Appl	218	728	20.7	237	2	US-09-940-166A-6	Sequence 6, Appl
146	778.5	22.1	253	2	US-09-121-952A-44	Sequence 44, Appl	219	728	20.7	237	4	PCR-US91-09133-26	Sequence 26, Appl
147	778.5	22.1	253	2	US-09-234-340A-44	Sequence 44, Appl	220	727.5	20.7	451	2	US-09-247-352-3	Sequence 3, Appl
148	776.5	22.1	253	1	US-08-325-014-44	Sequence 44, Appl	221	727.5	20.7	451	2	US-09-466-635-3	Sequence 3, Appl
149	776.5	22.0	232	1	US-08-425-763-2	Sequence 2, Appl	222	727.5	20.7	476	1	US-08-378-939-10	Sequence 10, Appl
150	776.5	22.0	232	2	US-08-811-757-2	Sequence 2, Appl	223	727	20.6	224	2	US-09-456-090A-46	Sequence 46, Appl
151	776.5	22.0	232	2	US-09-249-230-2	Sequence 2, Appl	224	727	20.6	224	2	US-09-453-234-46	Sequence 46, Appl
152	776.5	22.0	468	2	US-09-828-995B-5	Sequence 5, Appl	225	726	20.6	214	2	US-07-934-373C-40	Sequence 40, Appl
153	775	22.0	215	2	US-09-170-769A-6	Sequence 6, Appl	226	726	20.6	214	1	US-08-788-800-11	Sequence 11, Appl
154	774	22.0	552	4	PCR-US93-07832-23	Sequence 23, Appl	227	726	20.6	214	1	US-08-437-642B-40	Sequence 40, Appl
155	759.5	21.6	470	2	US-09-828-995B-11	Sequence 11, Appl	228	726	20.6	214	2	US-09-097-309-2	Sequence 2, Appl
156	759.5	21.6	449	2	US-09-579-397-2	Sequence 2, Appl	229	726	20.6	214	2	US-09-097-171A-2	Sequence 2, Appl
157	759	21.6	449	2	US-09-680-148-2	Sequence 2, Appl	230	726	20.6	214	2	US-09-460-587-2	Sequence 2, Appl
158	759	21.6	449	2	US-09-304-465A-2	Sequence 2, Appl	231	726	20.6	214	2	US-09-679-397-1	Sequence 1, Appl
159	759	21.6	449	2	US-10-356-974-2	Sequence 2, Appl	232	726	20.6	214	2	US-09-680-148-1	Sequence 1, Appl
160	757	21.5	468	2	US-10-104-047-3329	Sequence 3329, Ap	233	726	20.6	214	2	US-09-304-465A-1	Sequence 1, Appl
161	756.5	21.5	468	2	US-09-485-737B-67	Sequence 67, Appl	234	726	20.6	214	2	US-09-940-166A-2	Sequence 2, Appl
162	756.5	21.5	468	2	US-10-071-485-67	Sequence 67, Appl	235	726	20.6	214	4	US-10-356-974-1	Sequence 1, Appl
163	756	21.5	450	1	US-08-788-800-12	Sequence 12, Appl	236	726	20.6	214	2	PCR-US93-07832-40	Sequence 40, Appl
164	756	21.5	469	1	US-07-934-373C-23	Sequence 23, Appl	237	726	20.6	220	2	US-08-952-235-1	Sequence 1, Appl
165	756	21.5	469	2	US-08-437-642B-23	Sequence 23, Appl	238	726	20.6	220	2	US-09-669-971-1	Sequence 1, Appl
166	756	21.5	469	2	US-08-146-206C-23	Sequence 23, Appl	239	726	20.6	553	1	US-08-263-911-9	Sequence 9, Appl
167	756	21.5	469	2	US-09-705-686-23	Sequence 23, Appl	240	725.5	20.6	300	2	US-09-097-309-7	Sequence 7, Appl
168	756	21.5	469	2	US-09-705-392A-23	Sequence 23, Appl	241	725.5	20.6	300	2	US-09-097-171A-11	Sequence 11, Appl
169	756	21.5	469	2	US-09-705-398-23	Sequence 23, Appl	242	725.5	20.6	300	2	US-09-422-712B-3	Sequence 3, Appl
170	752.5	21.4	213	2	US-09-170-769A-2	Sequence 2, Appl	243	725.5	20.6	300	2	US-09-607-756-3	Sequence 3, Appl
171	748	21.2	467	2	US-09-049-672A-8	Sequence 8, Appl	244	725.5	20.6	300	2	US-09-460-587-7	Sequence 7, Appl
172	743.5	21.1	642	2	US-09-423-439-26	Sequence 26, Appl	245	725.5	20.6	300	2	US-09-940-166A-7	Sequence 7, Appl
173	741.5	21.1	298	2	US-09-027-449-60	Sequence 60, Appl	246	722	20.5	214	1	US-07-934-373C-39	Sequence 39, Appl

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257 719 20.4 220 2 US-09-301-593-17 Sequence 17, Appl
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259 719 20.4 224 2 US-09-453-234-84 Sequence 84, Appl
260 719 20.4 240 2 US-09-301-593-28 Sequence 28, Appl
261 718.5 20.4 232 1 US-07-934-373C-29 Sequence 29, Appl
262 718.5 20.4 232 2 US-08-788-800-10 Sequence 10, Appl
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272 718 20.4 467 1 US-08-704-744-81 Sequence 81, Appl
273 717.5 20.4 474 2 US-09-828-995B-17 Sequence 17, Appl
274 717 20.4 236 1 US-08-070-116A-2 Sequence 2, Appl
275 717 20.4 236 2 US-08-557-050-2 Sequence 2, Appl
276 717 20.4 473 2 US-09-049-672A-4 Sequence 4, Appl
277 716.5 20.3 232 1 US-07-934-373C-35 Sequence 35, Appl
278 716.5 20.3 232 2 US-08-437-642B-35 Sequence 35, Appl
279 716.5 20.3 232 4 PCT-US93-07832-35 Sequence 35, Appl
280 716 20.3 212 2 US-10-011-125A-5 Sequence 5, Appl
281 715.5 20.3 232 1 US-07-934-373C-32 Sequence 32, Appl
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283 715.5 20.3 232 4 PCT-US93-07832-32 Sequence 32, Appl
284 715.5 20.3 239 2 US-09-627-896B-22 Sequence 22, Appl
285 715.5 20.3 255 2 US-09-171-945-19 Sequence 19, Appl
286 715.5 20.3 255 2 US-09-910-059-19 Sequence 19, Appl
287 714 20.3 214 2 US-09-472-087-71 Sequence 71, Appl
288 714 20.3 237 1 US-08-398-612A-28 Sequence 28, Appl
289 714 20.3 237 1 US-08-398-611A-28 Sequence 28, Appl
290 714 20.3 237 1 US-08-491-334A-28 Sequence 28, Appl
291 714 20.3 237 2 US-09-027-449-25 Sequence 25, Appl
292 714 20.3 237 2 US-08-804-444A-25 Sequence 25, Appl
293 714 20.3 237 2 US-09-026-985-25 Sequence 25, Appl
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295 714 20.3 237 2 US-09-234-340A-25 Sequence 25, Appl
296 714 20.3 237 2 US-09-355-014-25 Sequence 25, Appl
297 714 20.3 238 1 US-08-398-613A-28 Sequence 28, Appl
298 713.5 20.3 443 4 PCT-US96-13152-4 Sequence 4, Appl
299 712 20.2 237 2 US-08-908-469-100 Sequence 100, Appl
300 712 20.2 491 2 US-10-011-125A-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
PCT-US95-11405-35
; Sequence 35, Application PC/TUS9511405
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PHOSPHOROUS-32 LABELING OF ANTIBODIES
; TITLE OF INVENTION: FOR CANCER THERAPY
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11405
; FILING DATE: 18-SEP-1995
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; APPLICATION NUMBER: US 08/308,103
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/599/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 35:
; LENGTH: 489 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-11405-35

Query Match 31.5%; Score 1108.5; DB 4; Length 489;
Best Local Similarity 37.1%; Pred. No. 5.1e-69;
Matches 249; Conservative 60; Mismatches 156; Indels 207; Gaps 7;

QY 1 EVOLQSGDPLVKPGASVKISKASGYSTGYVMHWKQSPGKGLGWIGRINPNNGVTLY 60
Db 23 EVOLVESGGVQPGSRSLRSCASGFDFTXXXXXWVRQAPGKGLGWIGXXXXXXX 82

QY 61 NQKFKDKATLTVDKSSTTAYMELRLTSDESAVYYCARSTMTIYVMDYMGQGTSTVSS 120
Db 83 XXXXXRFTISRDNKNTLFLQMSLRPEDTGVYFCA-SXXXXXXWQSGTPTVTVSS 141

QY 121 AKTPPSVPLAPGSAATNSMTVLCGLKGYPEPEVTWNSGLSSGVTTPAVLQSD 180
Db 142 ASKGSVPLAPSSKSTGGTAALGLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 201

QY 181 -LYTLSSSVTPSPSTWPESTVTCNVAHPASSTKDKKIVPRDGPSPSEKSEINEKDLRK 239
Db 202 GLYLSVTVTPSSSLGTQYICNVNHPKSTVKDKKVP----- 241

QY 240 KSELOGTALGNLKOIYYNSKAITSEKSAQDLTNTLLFKGFTGHPWYNDLLVDLGST 299
Db 242 -----KSCD----- 245

QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMGVGTLLHDNRLTEKKVPINLWIDGK 359
Db 246 ----- 245

QY 360 QTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKVQRLIVFHSSEGSTV 419
Db 246 -----KT-----HTCPCPM 255

QY 420 SYDLFDAQQGYPTLLRIYRDNTTISTSLISLYLTTISVMTQPTSLLSVAGDRVTI 479
Db 256 KYLL-----PTAAAGLLLAQAPAMADIQLTQSPSSLSASVGDRTVI 297

QY 480 TCASQSVNDVAVYQKQSPKLLISYTSISYAGVDPDRFSGSGVGTDTLTLSVQAE 539
Db 298 TCXXXXXXXWYQKQKPKLLIYXXXXXXGVPSPFSGSGGTDTFTTSSLOPE 357

QY 540 DAAVYECQQDYNSPPTFGGTGKLEIKRAAAPTVISIFPPSSEQLTSGASVWVFLNNFYP 599
Db 358 DIATYCYCXXXXXX-XXFGQGTKEIKRTVAAPSVFIFPPSDEQLKGTASVVCLLNNFYP 416

QY 600 KDINVKWKIDGSRQNGVLNSWTQDSKDSSTYSMSSTLTLTDKDEYERHNSYTCATHKTS 659

Db 417 REAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLTLSKADYEKHKVYACEVTHOGL 476
QY 660 TSPVKSFNRE 671
Db 477 SSPVTKSFNRGE 488

RESULT 2
US-08-695-692B-8
; Sequence 8, Application US/08695692B
; Patent No. 6514498
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; APPLICANT: Johan Hansson, Terje Kalland, Lars
; APPLICANT: Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; TITLE OF INVENTION: AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692B
; FILING DATE: August 12, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-695-692B-8

Query Match 31.4%; Score 1107; DB 2; Length 233;
Best Local Similarity 89.7%; Pred. No. 2.4e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNNSKAITSEKSAOFLTNTLLFKGFFTG 285
Db 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNNEKAITENKESDDOFLNTLLFKGFFTG 60

QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 61 HPWYNDLLVDLGSKDATNKGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120

QY 346 EEKVPINLWIDGKQTTPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 121 EEKVPINLWIDGKQTTPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180

QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNTTISSTLSISLYTT 458
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNTTINSENHLIDLTYTT 233

RESULT 3
US-08-486-099-112
; Sequence 112, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; APPLICANT: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-486-099-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNNSKAITSEKSAOFLTNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNNEKAITENKESDDOFLNTLLFKGFFTG 84

QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HPWYNDLLVDLGSKDATNKGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWIDGKQTTPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNTTISSTLSISLYTT 458
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNTTINSENHLIDLTYTT 257

RESULT 4
US-08-360-107A-122

; Sequence 122, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-360-107A-122

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

Qy 226 SEKSEINEKDLRKKSELOQTALGNLKOIYYNSKAITSEKSAQDPLTNTLLFKGFTG 285
Db 25 SEKSEINEKDLRKKSELQNALNLKQIYYNEKAITENKESDDQPLENTLLFKGFTG 84

Qy 286 HPWYNLLVDLGSSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLLHNNRLT 345
Db 85 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLLHNNRLT 144

Qy 346 EEKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGFLNSDSFGKQV 405
Db 145 EEKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGFLNSDSFGKQV 204

Qy 406 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTISSTLSISLYLYTT 458
Db 205 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTISSTLSISLYLYTT 257

RESULT 5
US-08-484-223B-112
; Sequence 112, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.

; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-484-223B-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

Qy 226 SEKSEINEKDLRKKSELOQTALGNLKOIYYNSKAITSEKSAQDPLTNTLLFKGFTG 285
Db 25 SEKSEINEKDLRKKSELQNALNLKQIYYNEKAITENKESDDQPLENTLLFKGFTG 84

Qy 286 HPWYNLLVDLGSSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLLHNNRLT 345
Db 85 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLLHNNRLT 144

Qy 346 EEKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGFLNSDSFGKQV 405
Db 145 EEKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGFLNSDSFGKQV 204

Qy 406 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTISSTLSISLYLYTT 458
Db 205 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTISSTLSISLYLYTT 257

RESULT 6
US-08-919-597-112
; Sequence 112, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/470,896
APPLICATION NUMBER: 06-JUN-1995
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-919-597-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELQGTALGNLKOIYYNSKAITSEKSDQFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDLRKSELQGNLSNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 286 HPWYNDLLVDLGSSTATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144

QY 346 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 406 RGLIVFHSSEGSTSVSYDLFDAQSQYPTDLLRIYRDNNTTSSSTLSLSLYTT 458
DB 205 RGLIVFHSSEGSTSVSYDLFDAQSQYPTDLLRIYRDNNTTSENHLDLYTT 257

RESULT 7
US-08-475-668A-112
; Sequence 112, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-475-668A-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELQGTALGNLKOIYYNSKAITSEKSDQFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDLRKSELQGNLSNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 286 HPWYNDLLVDLGSSTATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144

QY 346 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 406 RGLIVFHSSEGSTSVSYDLFDAQSQYPTDLLRIYRDNNTTSSSTLSLSLYTT 458
DB 205 RGLIVFHSSEGSTSVSYDLFDAQSQYPTDLLRIYRDNNTTSENHLDLYTT 257

RESULT 8
US-08-485-551A-112
; Sequence 112, Application US/08485551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION

```

; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,913A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-9741/8864
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-471-913A-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELGQTALGNLKOIYYNKAITSSEKSDAQFLTNTLLFKGFGFTG 285
DB 25 SEKSEINEKDLRKSELGQTALGNLKOIYYNKAITSSEKSDAQFLTNTLLFKGFGFTG 84
QY 286 HPWYNDLLVDLGSTAAATSEYSGSSVDLYGAYGYOCAGTGNKTKACMYGGVTLHNNRLT 345
DB 85 HPWYNDLLVDLGSKDATNKYKGVKVDLYGAYGYOCAGTGNKTKACMYGGVTLHNNRLT 144
QY 346 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDACQYPTDLLRIYRDNNTTISSTLSISLYTT 458
DB 205 RGLIVFHSSEGSTVSVDLFDACQYPTDLLRIYRDNNTTINSENHLIDLTYTT 257

RESULT 10
US-08-485-264A-112
; Sequence 112, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,551A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-9741/8864
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-551A-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELGQTALGNLKOIYYNKAITSSEKSDAQFLTNTLLFKGFGFTG 285
DB 25 SEKSEINEKDLRKSELGQTALGNLKOIYYNKAITSSEKSDAQFLTNTLLFKGFGFTG 84
QY 286 HPWYNDLLVDLGSTAAATSEYSGSSVDLYGAYGYOCAGTGNKTKACMYGGVTLHNNRLT 345
DB 85 HPWYNDLLVDLGSKDATNKYKGVKVDLYGAYGYOCAGTGNKTKACMYGGVTLHNNRLT 144
QY 346 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDACQYPTDLLRIYRDNNTTISSTLSISLYTT 458
DB 205 RGLIVFHSSEGSTVSVDLFDACQYPTDLLRIYRDNNTTINSENHLIDLTYTT 257

RESULT 9
US-08-471-913A-112
; Sequence 112, Application US/08471913A
; Patent No. 6093794
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP

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; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/485,264A
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-264A-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELQGTALGNLKQIYYNYSKAITSEKSADQFLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELQGNLSNLRIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 286 HPWYNLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNRLT 345
Db 85 HPWYNLLVDLGSKDANTNKGKVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 405
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 406 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNNTTSSLSISLYTT 458
Db 205 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNNTTSENHLDLYTT 257

RESULT 11
US-08-474-349A-112
; Sequence 112, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-474-349A-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELQGTALGNLKQIYYNYSKAITSEKSADQFLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELQGNLSNLRIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 286 HPWYNLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNRLT 345
Db 85 HPWYNLLVDLGSKDANTNKGKVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 405
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 406 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNNTTSSLSISLYTT 458
Db 205 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNNTTSENHLDLYTT 257

RESULT 12
US-08-470-896-112
; Sequence 112, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,896
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-470-896-112

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Query Match	31.4%;	Score 1107;	DB 2;	Length 257;
Best Local Similarity	89.7%;	Pred. No. 2.8e-69;		
Matches 209;	Conservative	9;	Mismatches 15;	Indels 0; Gaps 0;
Qy	226	SEKSEENEKDLRKKSELQGTALGNLQIYYYNKSKAITSEKSKADQFLTNTLLFKGFFTG	285	
Db	25	SEKSEENEKDLRKKSELQNALSNLRQIYYYNKSKAITENKESDDQFLNTLLFKGFFTG	84	
Qy	286	HPWYNDLLVDLGGSTAATSEYEGSSVDLYGAYYGQCAGGTENKTACMYGGVTLHDNNRLT	345	
Db	85	HPWYNDLLVDLGGSDATNKYKGGKVDLYGAYYGQCAGGTENKTACMYGGVTLHDNNRLT	144	
Qy	346	EKKVPINLMDIGKQTTVPIDKVTSKKEVTVQELDQARHYLHGKFCGLYNSDSFGGKVQ	405	
Db	145	EKKVPINLMDIGKQTTVPIDKVTSKKEVTVQELDQARHYLHGKFCGLYNSDSFGGKVQ	204	
Qy	406	RGLTVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNNTTISSTLSISLYLTT	458	
Db	205	RGLTVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENLHIDLTYLT	257	

RESULT 13
US-08-485-546A-112
; Sequence 112, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546A

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; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-546A-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0

Qy 226 SEKSEENEKDLRKSELQGTALGNLKQIYYYNSEKAITSEKSDAQFLTNTLLPKGFPTG 285
Db 25 SEKSEENEKDLRKSELQGNALSNLRQIYYNEKAITENKESDDPLENTLLFKGFPTG 84

Qy 286 HPWTNDLLVDLGSTAAITSEVGGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 345
Db 85 HPWTNDLLVDLGSKDAAITNKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 144

Qy 346 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDQARHYLHGKFGLYNSDSFGGKVQ 204

Qy 406 RGLIVFSSSEGSTVSYDLFDAQGYPPTLRLRIYRDNNTTISTSGISLIYVTT 458
Db 205 RGLIVFSSSEGSTVSYDLFDAQGYPPTLRLRIYRDNKTINSENLHDIYLYTT 257

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RESULT 14
US-08-487-266A-112
; Sequence 112, Application US/08487266A
; Patent No. 6824783
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pernie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,266A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-025
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-08-487-266A-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSSSEKSDQFLNTLLFKGFPTG 285
DB 25 SEKSEINEKDLRKSELQGNALSRLRQIYYYNKAITENKESDDQFLENTLLFKGFPTG 84
QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYYGQCAGTGNKTCACMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVDLGSKDATNKYKGKVDLYGAYYGQCAGTGNKTCACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKVPINLWIDGKQTTVPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYLYTT 458
DB 205 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTINSENHLIDLYLYTT 257

RESULT 15
US-08-484-741-112
Sequence 112, Application US/08484741
Patent No. 6951717
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT NUMBER: US/08/484,741
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-022
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-08-484-741-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSSSEKSDQFLNTLLFKGFPTG 285
DB 25 SEKSEINEKDLRKSELQGNALSRLRQIYYYNKAITENKESDDQFLENTLLFKGFPTG 84
QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYYGQCAGTGNKTCACMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVDLGSKDATNKYKGKVDLYGAYYGQCAGTGNKTCACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKVPINLWIDGKQTTVPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYLYTT 458
DB 205 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTINSENHLIDLYLYTT 257

RESULT 16
US-09-350-841A-1598
Sequence 1598, Application US/09350841A
Patent No. 6750008
GENERAL INFORMATION:
APPLICANT: Jeffs, Peter;
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
FILE REFERENCE: 7872-066-999
CURRENT APPLICATION NUMBER: US/09/350,841A
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 1946
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1598
LENGTH: 254
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1598

Query Match 30.4%; Score 1071; DB 2; Length 254;
Best Local Similarity 88.0%; Pred. No. 8.7e-67;
Matches 206; Conservative 9; Mismatches 17; Indels 2; Gaps 2;

QY 226 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSSSEKSDQFLNTLLFKGFPTG 285
DB 22 SEKSEINEKDLRKSELQGNALSRLRQIYYYNKAITENKESDDQFLENTLLFKGFPTG 81
QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYYGQCAGTGNKTCACMYGGVTLHDNNRLT 345
DB 82 HPWYNDLLVDLGSKDATNKYKGKVDLYGAYYGQCAGTGNKTCACMYGGVTLHDNNRLT 141
QY 346 EEKVPINLWIDGKQTTVPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 405
DB 142 EEKVPINLWID-KQTTVPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 200
QY 406 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYLYTT 458
DB 201 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTINSENHLIDLYLYTT 254

Qy	551	LISSVQVEDRAVIFCQDDINSEFIFGGITLRLKADAPVNSIIFPSSQLTISGGNSV	399
Db	338	-----KGRPKAPQVVTIIPPKQMAKDKVSL	363
Qy	591	VCFLNNFPKIDINVKWKIDGSEONGVLSWTDQDSKDSYTSMSSTLTLTCKDEYERHNSY	650
Db	364	TCMITDFPEDITVEWQNGQPAEN-YKNTQPMIDT-DGSFYVYVKLVKSNVQSNWEAGNTF	421
Qy	651	TCEATHK 657	
Db	422	TCSVLHE 428	
RESULT 18			
US-08-353-400-36			
: Sequence 36, Application US/08353400			
: Patent No. 5665357			
: GENERAL INFORMATION:			
: APPLICANT:			
: TITLE OF INVENTION: PROTEINS			
: NUMBER OF SEQUENCES: 37			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/353,400			
: FILING DATE:			
: CLASSIFICATION: 424			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: GB 9324819.3			
: FILING DATE: 03-DEC-1993			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: GB 9411089.7			
: FILING DATE: 03-JUN-1994			
: INFORMATION FOR SEQ ID NO: 36:			
: SEQUENCE CHARACTERISTICS:			
: LENGTH: 464 amino acids			
: TYPE: amino acid			
: STRANDEDNESS: single			
: TOPOLOGY: linear			
: MOLECULE TYPE: protein			
US-08-353-400-36			
Query Match 30.1%; Score 1059.5; DB 1; Length 464;			
Best Local Similarity 37.5%; Pred. No. 1.2e-65;			
Matches 250; Conservative 61; Mismatches 107; Indels 249; Gaps 14;			
Qy	1	EVQLQSGPDLVKPGASVKISCKASGYSTFGYYHWVKQSPGKLEWIGRIINPNNGVTLY	60
Db	20	QVQLQPGAEVLKPGASVQLSKASGYFTFGYIHWVKQRPQGQLEWIGEVNPSGTGRSDY	79
Qy	61	NRKPKDKATLVTKSSSTTAWEILRSLTSEDSAVYICARSTMI-TNYVMDYWGQGTSTVTVS	119
Db	80	NEKPKDKATLVTKSSSTTAWEILRSLTSEDSAVYICARERAYGDDMDYWGQGTSTVTVS	139
Qy	120	SAKTTTPSVYPLAPGAAQNTNSMTLGLCKLVGYFPEPVTVTWNSGSLSSGVHTFPVVLQS	179
Db	140	SAKTTTPSVYPLAPGAAQNTNSMTLGLCKLVGYFPEPVTVTWNSGSLSSGVHTFPVVLQS	199
Qy	180	DLVTLSSVTVPSSTWPSSETVTCNVAHPASTKVDKKIVPRDSGGPSEKSEEINEKDLRK	239
Db	200	DLVTLSSVTVPSSTWPSSETVTCNVAHPASTKVDKKIVPRDCG-----	243
Qy	240	KSELQGLTGNLKKQIYYVNSKAITSSSEKSDQFLNTLTLLFKGFPTGHPWYNLLVLDLGS	299
Db	244	-CPKICTVPEVSSVFIFFPK-----PKDLVLTITL-----	272
Qy	300	AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLTBEKKVPIINLWDGK	359
Db	273	-----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--	297

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QY 360 QTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQVGLIV 410
Db 298 --DVEVHTAQTPRERQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAPPIEK----- 351
QY 411 FHSSEGSTVSYDLFDAQQGVPTLLRIYRDNNTTSSLSISLYLTTTSIVMTQTPTSL 470
Db 352 -----TISKT----- 356
QY 471 VSAGDRVTTCKASQSVSNDVAWYQKPGOSPKLLISYSSRYAGVDPDRFSGSGYGTDTFT 530
Db 357 ----- 356
QY 531 LTISSVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTYSIFPPSSEQLTSGASV 590
Db 357 -----KGRPKAPQVYTTIPPKPEQNAKDKVSL 382
QY 591 VCFPLNFPKIDINVKWKIDGSRQNGVLSWTPQDSKDSYMSSTLTILTKDYEYRHNSY 650
Db 383 TCWITDFPFDITVENQWNGQPAEN-YKQTPIMDT-DGSYFYVYKLVQKSNWEAGNTF 440
QY 651 TCEATHK 657
Db 441 TCSVLHE 447
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RESULT 19
US-08-896-933-24
; Sequence 24, Application US/08096933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-24
```

```
Query Match 29.5%; Score 1040; DB 2; Length 226;
Best Local Similarity 85.2%; Pred. No. 1.1e-64;
Matches 196; Conservative 13; Mismatches 17; Indels 4; Gaps 1;

QY 229 SEINEKDLRKXSELQGTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTGHPW 288
Db 1 SEINEKDLRKXSELQARNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 60
QY 289 YNDLLVDLGSTATSEYEGSSVDLYGAYGYQCAGTGNKTAQMYGGVTLHDNNRLTEEK 348
Db 61 YNDLLVDKGSKDATNRYKKGKVDLYGAYGYQCAGTGNKTAQMYGGVTLHDNNRLTEE- 119
QY 349 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVGL 408
Db 120 ---VBKWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVGL 176
QY 409 IVFHSSEGSTVSYDLFDAQQGVPTLLRIYRDNNTTSSLSISLYLTT 458
Db 177 IVFHSSEGSTVSYDLFDAQQGVPTLLRIYRDNNTTSSLSISLYLTT 226
```

```
RESULT 20
US-09-314-235-24
; Sequence 24, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
```

```
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-24
```

```
Query Match 29.5%; Score 1040; DB 2; Length 226;
Best Local Similarity 85.2%; Pred. No. 1.1e-64;
Matches 196; Conservative 13; Mismatches 17; Indels 4; Gaps 1;

QY 229 SEINEKDLRKXSELQGTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTGHPW 288
Db 1 SEINEKDLRKXSELQARNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 60
QY 289 YNDLLVDLGSTATSEYEGSSVDLYGAYGYQCAGTGNKTAQMYGGVTLHDNNRLTEEK 348
Db 61 YNDLLVDKGSKDATNRYKKGKVDLYGAYGYQCAGTGNKTAQMYGGVTLHDNNRLTEE- 119
QY 349 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVGL 408
Db 120 ---VBKWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVGL 176
QY 409 IVFHSSEGSTVSYDLFDAQQGVPTLLRIYRDNNTTSSLSISLYLTT 458
Db 177 IVFHSSEGSTVSYDLFDAQQGVPTLLRIYRDNNTTSSLSISLYLTT 226
```

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RESULT 21
US-09-708-008B-24
; Sequence 24, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-708-008B-24
```

```
Query Match 29.5%; Score 1040; DB 2; Length 226;
Best Local Similarity 85.2%; Pred. No. 1.1e-64;
Matches 196; Conservative 13; Mismatches 17; Indels 4; Gaps 1;
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QY 229 SEBINEKDLKKSELOQTALCNLKOIYYNSKAITSEKSDAQOPLNTLLFKGFFTGHPW 288
Db 1 SEBINEKDLKKSELOQTALCNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 60
QY 289 YNDLLVDLGSSTAATSEYEGSSVDLYGAYGVCAGGTPNKTCACMGVTLHDNNRLTEEK 348
Db 61 YNDLLVDKSKDATNKFKKKVDLYGAYGTCAGGTPNKTCACMGVTLHDNNRLTEZ 119
QY 349 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVQRL 408
Db 120 ---VBRKIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVQRL 176
QY 409 IVPHSSEGSTSVSVDLFDQAQQYPTLLRIYRDNTTSSLSLSLYTT 458
Db 177 IVPHSSEGSTSVSVDLFDQAQQYPTLLRIYRDNTTSSLSLSLYTT 226
RESULT 22
US-09-485-737B-90
; Sequence 90, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90
Query Match 27.8%; Score 980.5; DB 2; Length 711;
Best Local Similarity 35.3%; Pred. No. 6.8e-60;
Matches 254; Conservative 103; Mismatches 180; Indels 183; Gaps 23;
QY 1 EVOLQSGDPLVKPGASVKISKASGYSTGYTHMHWKQSPKGLGWIGRINPNNGVTLY 60
Db 21 QVQLVQSGSELKPKGASVKISKASGYSTFDYGMNWKQAPGQGLKWMGWINTYTGESTY 80
QY 61 NQKPKDKATLVTKGSTTAYMELRSLTSDSAVYCARSTMTINYMDYKQGTSVTSS 120
Db 81 VDDFKGRFVFLSDTSVSAAYLQISSLKAEDTATYFCARRGF---YAMDYWGQGTVTSS 137
QY 121 AKTTPSPVPLAPGSAQTNSMTLGLCVKGYPEPVTVTWNSGSLSSGVHTTFAVLQSD 180
Db 138 ASTKGSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 197
QY 181 -LYTLSSSVTPSPSTWPFSTVTCNVAHPASSTKVDKIVPRDS-----GG 224
Db 198 GLYLSLSSVTPSPSSLTQITVYCNVNHKPSNTKVDKRVKPSCKDTHTCPPCAPELLGG 257
QY 225 PS-----EKSBEI-----NEKDLKKSELQGTALGNLK---QYYYN 258
Db 258 PSVFLPPPKDPTLMISRTPEVTCVVVDVSDHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 317
QY 259 S-----KAITSS-EK-----SADQ 271
Db 318 STYRVSVSLVTLHQDWLNGKEYKCKVSNKALPASIETKISKAKGQRPQVYTLPPSREE 377

QY 272 FLTN-----TLLFKGFTGHPWYNDLLVDLGSTA-ATSEYEGSS--VDLYGAYGYQCAGG 324
Db 378 MTKNQVSLTCLVKGYF-----SDIAVWESNGQPENNYKTTTPVLDSDGSGFFLYSKL-- 430
QY 325 TPNTKACMGV-----TLHD--NNRLTEEK-----KVPINLWIDGKQTTVPIDKV 368
Db 431 TVDKSRWQGNVPSVCSVMHEALHNHYTQKSLSLSPKLGSGSQVLVOSSELSKPGASV 490
QY 369 KTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVQRLIVPHSSEGSTSVSVDLFDQAQ 428
Db 491 KISK-----ASGYTFTDYGMNWKQAPGQGLKWMGWINTYTGESTYVD--DFKG 538
QY 429 QYPTDLLRIYRDNTTSSLSLS-----LYLYT----- 457
Db 539 RF-----VPSLDTVSAAYLQISSLKAEDTATYFCARRGFYAMDYWGQGTVTTVSSGGG 592
QY 458 -----TSIVMTQPTSLLSVAGDRVTITCKASQSVSNDVAVYQKPKGQSPKLLI 506
Db 593 GSGGGSGGGGSDIVLTQSPATMSAEPGERVTITCSASSISY-MFWYHQRPGQSPRLLI 651
QY 507 SYTSSRYAGVPRDFSGSGYGTDFTLTISVQAEDAAVYFCQDYNPSPTFGGQTKLEIKR 566
Db 652 YDTSNLASGVPARFSGSGGCTSYSLTISRMEPEDFATYFCHQSSSYPTFTFGQGTLEIKR 711
RESULT 23
US-10-071-485-90
; Sequence 90, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-90
Query Match 27.8%; Score 980.5; DB 2; Length 711;
Best Local Similarity 35.3%; Pred. No. 6.8e-60;
Matches 254; Conservative 103; Mismatches 180; Indels 183; Gaps 23;
QY 1 EVOLQSGDPLVKPGASVKISKASGYSTGYTHMHWKQSPKGLGWIGRINPNNGVTLY 60
Db 21 QVQLVQSGSELKPKGASVKISKASGYSTFDYGMNWKQAPGQGLKWMGWINTYTGESTY 80
QY 61 NQKPKDKATLVTKGSTTAYMELRSLTSDSAVYCARSTMTINYMDYKQGTSVTSS 120
Db 81 VDDFKGRFVFLSDTSVSAAYLQISSLKAEDTATYFCARRGF---YAMDYWGQGTVTSS 137
QY 121 AKTTPSPVPLAPGSAQTNSMTLGLCVKGYPEPVTVTWNSGSLSSGVHTTFAVLQSD 180
Db 138 ASTKGSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 197
QY 181 -LYTLSSSVTPSPSTWPFSTVTCNVAHPASSTKVDKIVPRDS-----GG 224

Db 198 GYLSLVTVVSSSLGTOTYICNVNHNKFSNTKYDKRVEPKSCDKTHTCPPCPAPPELLGG 257
QY 225 PS-----EKSEI-----NEKDLRKXSELQGTALGNLK---QIYYYN 258
Db 258 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 317
QY 259 S-----KAITSS-EK-----SADQ 271
Db 318 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIETISKAKGQPREPQVYTLPPSRRE 377
QY 272 FLTN-----TLLFKGFTTGHFWNDLLDVLGSTA-ATSEYEGSS--VDLYGAYGYQCAGG 324
Db 378 MYKNQVSLTCLVKGFY-----SDIAVEWESNGQPENNYKTPPVLDSGSPFLYSKL--- 430
QY 325 TPNKTACMYGGV-----TLHD--NNRLTEK-----KVPINLWIDGKQTTVPIDKV 368
Db 431 TVDKSRWQQGNVFCSCVMHEALHNHYTKSLSLSPGKLGGSQVQLVQSGSELKPKPGASV 490
QY 369 KTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQORGLIVPHSSEGSTVSVDLFDAG 428
Db 491 KISK-----ASGYFTFDYGMNVVKQAPGQGLKWMGINTYTGSTYVD--DFKG 538
QY 429 QYPTDLLRIYRDNNTTISSTLSIS-----LYLYT----- 457
Db 539 RP-----VPSLDTVSAAVLQISSLKAEATATYFCARRGFYAMDYWGQTTTVYSSGG 592
QY 458 -----TSIVMTQPTSLLSVAGDRVTITCKASQSVNDVAVYQKQPGQSPKLLI 506
Db 593 GSGGGSGGGSDIVLTQSPATMSAASGERVLTLCSSASSISY-MFWYHQRPGQSPRLLI 651
QY 507 SVTSSRYAGVDPDFSGSGYGTFTLTISVQAEADAAYFCQDYNSTPFGGKTKLEIKR 566
Db 652 YDTSNLASGVPAFSGSGSGTYSLTISRMEPEDFATYFCHOSSSYPTFTFGQTKLEIKR 711

RESULT 24

US-08-116-247-7
; Sequence 7, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-116-247-7

Query Match 27.4%; Score 966; DB 1; Length 468;
Best Local Similarity 34.9%; Pred. No. 3.9e-59;
Matches 241; Conservative 56; Mismatches 126; Indels 268; Gaps 14;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSPTGYMHVVKOSPGKGLRWIGRIINPNNGVTLY 60
Db 20 QVQLQSGDGLARPASVSKASGYTFRITRMHWKORPGQGLEWIGYIINPSRGYTN 79
QY 61 NQKFKDKATLTVDKSTTAYMELRLTSDSAVYYCARSTMITNYVMDYWGQTSYTVSS 120
Db 80 NQKFKDKATLTVDKSSSTAYMQLSSLTSDSAVYYCAR--YYDDHYCLDYWGQGTTLTVSS 138
QY 121 AKTTPSPVYPLAPGAAQTNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTFPVAVLQSD 180
Db 139 AKTTPSPVYPLAPVCGDITGSSVTLGCLVKGYFPEPVTITWNSGSLSSGVHTFPVAVLQSD 198
QY 181 LYTLSSTVTPSSVWPSETVTCNVAPASSTKVDKIVPRDGGPGPSEKSEINEKDLRKK 240
Db 199 LYTLSSTVTPSSVWPSETVTCNVAPASSTKVDKIVPRDGGPGPSEKSEINEKDLRKK 246
QY 241 SELQGTALGNLKOIYYYNKAITSEKSAQDQTLTNTLLFKGFTTGHFWNDLLDVLGSTA 300
Db 247 ----- 246
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKACMYGGVTLHDNNRLTEEEKVPIINLWIDGKQ 360
Db 247 -----PCKCPAPN-----LLGGPSVF----- 262
QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQORGLIVPHSSEGSTVS 420
Db 263 -----IFPPKIKDVLMI---SLSPVIT 281
QY 421 YDLFDAQQGYPTLLRIYRDNNTTISSTLSISLYLYTTSIVMTQPTSLLSVAGDRVTIT 480
Db 282 CVVDVDSDDPD-----VQISWFWNVNVEVHTAQTOT----- 312
QY 481 CKASQSVNDVAVYQKQPGQSPKLLISYTSRYAGVDPDFSGSGYGTFTLTISVQAEAD 540
Db 313 -----HREDYNSTLRVV----- 324
QY 541 AAVYFCQDYNSTPPTFGGKTKLEIKRAD-----AAPTYSIFPPSSEQLT 584
Db 325 SALPIQHQQDWMSGKEF---CKVNNKDLPAPIERTISKPGSVRAPOVYVLPPEEEMT 380
QY 585 SGGASVVCFLNNFYPKDINVKKIDGSEKQN-----GVLSNWTDDQSKDSTYSMSSTLTL 639
Db 381 KKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTPEVLDS-----DGSYFMYSKLRV 433
QY 640 TKDEYERHNSYTCETHK--TSTSPIVKSFNR 669
Db 434 EKKNWVERNSYSCSVVHGLNHNHTTKSFNR 464

RESULT 25
US-09-348-224-7
; Sequence 7, Application US/09348224
; Patent No. 6750325
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda Kay
; APPLICANT: Zivin, Robert Allan
; APPLICANT: Adair, John Robert
; APPLICANT: Achwal, Diljeet Singh
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; FILE REFERENCE: CARP0066
; CURRENT APPLICATION NUMBER: US/09/348,224

; CURRENT FILING DATE: 1999-07-06
; EARLIER APPLICATION NUMBER: 08/116,247
; EARLIER FILING DATE: 1993-09-03
; EARLIER APPLICATION NUMBER: 07/743,377
; EARLIER FILING DATE: 1991-10-04
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Mouse
US-09-348-224-7

Query Match 27.4%; Score 966; DB 2; Length 468;
Best Local Similarity 34.9%; Pred. No. 3.9e-59;
Matches 241; Conservative 56; Mismatches 126; Indels 268; Gaps 14;

QY 1 EVOLQSGPDLVPGASVKISCKASGYFTGYMHVWQSPGKLEWIGINPNNGVTLY 60
DB 20 QVQLQSGAGELARPGASVKMSCKASGYFTRYTMHWYKRPQGQLEWIGINPSRGYTN 79
QY 61 NQKPKDKATLTVKSSSTAYMELSLTSDSAVYVCARSTMTITNVMYDYGQGTSTVSS 120
DB 80 NQKPKDKATLTVKSSSTAYMELSLTSDSAVYVCARSTMTITNVMYDYGQGTSTVSS 138
QY 121 AKTTPSVYPLAPGSAQAQTNMVTGLCLVKGYPPEPVTVTNWGSLSGGVHTFPVQLQSD 180
DB 139 AKTTPSVYPLAPGSAQAQTNMVTGLCLVKGYPPEPVTVTNWGSLSGGVHTFPVQLQSD 198
QY 181 LYTLSSTVTPSPSTWPTSETVTCNVAHPASSTKVDKIKVPRDGGPSEKSEINEKDLRKK 240
DB 199 LYTLSSTVTPSPSTWPTSETVTCNVAHPASSTKVDKIKVPRDGGPSEKSEINEKDLRKK 246
QY 241 SELQGTALGNLKOIYYNNAKITSSEKSAQDLTNTLLPKGFTGHPWYNDLLVLDGSTA 300
DB 247 ----- 246
QY 301 ATSEYEGSVLDYGAAYGYQAGTGNKTAQMGVTLHDNRLTEKKVPIINLWIDGKQ 360
DB 247 -----PCKCPAPN-----LLGGPSVF----- 262
QY 361 TTVPIDKVTSKKEVTVQELDLQARHYLHGKFLGNSDSFGGKVGRLIVFHSSEGSTVS 420
DB 263 -----IFPKIKDVLMT---SLSPIT 281
QY 421 YDLFDAQGGVPTLLRIYRDNMTTISSTLSGLYLTSTVMTQTPTSLVLSAGDRVIT 480
DB 282 CVVDVSEDDPD-----VQISFVNNVEVHTAQQT----- 312
QY 481 CKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFGSGYGTDFTLTISVQAE 540
DB 313 -----HREDYNSTLRVV--- 324
QY 541 AAVYFCODVNSPPTFGGKLEIKRAD-----AAPTGISFPSSSEOLT 584
DB 325 SALPIQHDWMSGKEF---KCKVNNKDLPAPIERTISKPGSVAPQVTLVPPPEEEM 380
QY 585 SGASVVCFLNNFVKDINVKWIKDGSERON----GVLSNWTDDQDSKDYTSMSSTLT 639
DB 381 KKQVTLTCMTVDMPEDIVYEWNTNGKTELNYKNTPEVLDSE-----DGSYFMYSLRV 433
QY 640 TKDEYERHNSYTCETHK-TSTSPVKSFN 669
DB 434 EKKWVERNYSVCSVHVEGLHNHHTTKFSR 464

RESULT 26
US-08-737-129A-2
; Sequence 2, Application US/08737129A
; Patent No. 5885816
; GENERAL INFORMATION:
; APPLICANT: Ikuo FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY

; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: No. 5885816member 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-737-129A-2

Query Match 27.3%; Score 960; DB 1; Length 212;
Best Local Similarity 84.7%; Pred. No. 3.6e-59;
Matches 183; Conservative 11; Mismatches 14; Indels 8; Gaps 1;

QY 6 QSGPDLVPGASVKISCKASGYFTGYMHVWQSPGKLEWIGINPNNGVTLYNQKFK 65
DB 2 ESGTELAKPGASVKMSCKASGYFTTSYIHWVWQKRPQGQLEWIGINPSTDYTEYIOKFK 61
QY 66 DKATLTVKSSSTAYMELSLTSDSAVYVCARSTMTITNVMYDYGQGTSTVSSAKTTP 125
DB 62 DKATLTVKSSSTAYMELSLTSDSAVYVCARSTMTITNVMYDYGQGTSTVSSAKTTP 113
QY 126 PSYVPLAPGSAQAQTNMVTGLCLVKGYPPEPVTVTNWGSLSGGVHTFPVQLQSDLYLS 185
DB 114 PSYVPLAPGSAQAQTNMVTGLCLVKGYPPEPVTVTNWGSLSGGVHTFPVQLQSDLYLS 173
QY 186 SSVTPSPSTWPTSETVTCNVAHPASSTKVDKIKVPRD 221
DB 174 SSVTPSPSTWPTSETVTCNVAHPASSTKVDKIKVPRD 209

RESULT 27
US-08-303-569B-7
; Sequence 7, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia

Db 247 ----- 246
QY 301 ATSEYEGSSVDLYGAYGYQACGTPNKTACTMYGGVTLHDNNRLTEKVPINLWIDGKQ 360
Db 247 -----PCKCPAPN-----LLGGPSVF----- 262
QY 361 TTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKQVQGLIVFHSSEGSTVS 420
Db 263 -----IPFPKIKOVLMT---SLSPIVT 281
QY 421 YDLFDAQGVDPDILLRIYRDNNTTSSLSLSLYLTTSTVMQTPTPSLLVASGDRVTIT 480
Db 282 CVVDVSEDDPD-----VQISFVNVEVHTAQOT----- 312
QY 481 CKASQSVNDVAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGYGTDFTLTSSVQAE 540
Db 313 -----HREDYNSTLRVV----- 324
QY 541 AAVYFCQDYNPPTFGGKTKLEIKRAD-----AAPTVISFPPSSEQLT 584
Db 325 SALPIQHQDWMGKEF-----CKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380
QY 585 SGCASVVCFLNNFVPKDINVKWKIDGSEON-----GVLSNWDQDQSKDSTYSMSSTLT 639
Db 381 KKQVTLTCMTDWPEDILYVETWNGKTELYNKNTEPVLDS-----DGSYFMYSKLRV 433
QY 640 TKDEYERHNSYTCETHK-TSTSPIVKSFNR 669
Db 434 EKNWVERNYSYSCSVWHEGLNHHHTTKFSR 464

RESULT 29
PCT-US94-14106-51
; Sequence 51, Application PC/TUS9414106
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Process for Generating Specific Antibodies
; NUMBER OF SEQUENCES: 61
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14106
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14106-51

Query Match 27.1%; Score 953.5; DB 4; Length 223;
Best Local Similarity 83.0%; Pred. No. 1.1e-58;
Matches 185; Conservative 12; Mismatches 23; Indels 3; Gaps 2;

QY 1 EVLOQSGPLVKPGASVKISCKASGYSFTGYVHWVQSPGKGLWIGINFNNGVTLY 60
Db 1 EVLOQSGPELMMPGASVKISCKATGYTLSSYLWVQSPGKGLWIGILFGSGSAHY 60
QY 61 NQFKDKATLVTKSSSTAYMELRSLTSDSAVYCARSTMITNY--VMDYWGQGTSTV 118
Db 61 NEFKGKATFTVTSNTAYMQLSSLTSDSAVYCARGP-YGNYGDYFYWGQGTTLTV 119
QY 119 SSAKTTPPSVYPLAPGAAQTNSMTGLCIVKGVFPPEVTVTWNSGSLSSGVHTFPVLQ 178
Db 120 SSAKTTPPSVYPLAPGAAQTNSMTGLCIVKGVFPPEVTVTWNSGSLSSGVHTFPVLQ 179
QY 179 SDLYTLSSSVTVPSSTWPSSTVTCNVAHPASSTKVKDKIVPRD 221
;|||||

Db 180 SDLYTLSSSVTVPSSTWPSSTVTCNVAHPASSTKVKDKIVPRD 222

RESULT 30
US-08-695-692B-7
; Sequence 7, Application US/08695692B
; Patent No. 6514498
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlisten,
; APPLICANT: Johan Hansson, Terje Kalland, Lars
; APPLICANT: Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; TITLE OF INVENTION: AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692B
; FILING DATE: August 12, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-695-692B-7

Query Match 26.9%; Score 948; DB 2; Length 233;
Best Local Similarity 76.4%; Pred. No. 2.8e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNYSKALTSEKSDAQDLTNTLLPKGFTG 285
Db 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHDDQLQHTLLFKGFTD 60
QY 286 HPWYNLLVDLGSSTAATSEYEGSSVDLYGAYGYQACGTPNKTACMYGGVTLHDNNRLT 345
Db 61 HSWYNLLVDLGSSTADIVDKYKGGKVDLYGAYGYQACGTPNKTACMYGGVTLHDNNRLT 120
QY 346 EEKKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 405
Db 121 EEKKVPINLWIDGKQTTVPLETVTNKNQNTVQELDLQARHYLQEKYNLNSVDVFDGKVQ 180
QY 406 RGLIVFHSSEGSTVSVDLFDQAQGVDPDILLRIYRDNNTTSSLSLSLYLTT 458
Db 181 RGLIVFHTSTPEPSVNYDLFQAQGVDPDILLRIYRDNNTTSENHHDIIYLYTS 233

RESULT 31
US-08-486-099-113
; Sequence 113, Application US/08486099
; Patent No. 6013263

GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-486-099-113

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAKTENKESHDFLOHTILFKGFFTD 84

QY 286 HPWYNDLLVDLGSSTAATSEYSGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HSWYNDLLVDFDSKDIDVKYKGVLDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGCKVQ 405
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTQELDLQARRYLQEKYLYNSDSVDFGKQV 204

QY 406 RGLIVFHSSEGSTVSYDLFDAQCYQPDTLRIYRDNTTISSTLSLSLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFGAQCYQSYNTLLRIYRDNKTINSENMHIDIVLYTS 257

RESULT 32
US-08-360-107A-123
; Sequence 123, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-360-107A-123

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAKTENKESHDFLOHTILFKGFFTD 84

QY 286 HPWYNDLLVDLGSSTAATSEYSGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HSWYNDLLVDFDSKDIDVKYKGVLDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGCKVQ 405
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTQELDLQARRYLQEKYLYNSDSVDFGKQV 204

QY 406 RGLIVFHSSEGSTVSYDLFDAQCYQPDTLRIYRDNTTISSTLSLSLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFGAQCYQSYNTLLRIYRDNKTINSENMHIDIVLYTS 257

RESULT 33
US-08-484-223B-113
; Sequence 113, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.

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; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-484-223B-113

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKIYYNKAITSSEKSAQDQFLTNLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKIYYNEKAKTENKESHQDQFLQHTILFKGFFTD 84

QY 286 HPWYNLLVDLGGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HSWYNLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVKQ 405
Db 145 EEKVPINLWIDGKQNTVPLETVKTNKGNVTVOELDLQARRYLQEKYNLNSDVFQKVKQ 204

QY 406 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTISTSLISLYLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNTKNTINSENHIDIYLYTS 257

RESULT 34
US-08-919-597-113
; Sequence 113, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
```

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; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,896
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-919-597-113

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKIYYNKAITSSEKSAQDQFLTNLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKIYYNEKAKTENKESHQDQFLQHTILFKGFFTD 84

QY 286 HPWYNLLVDLGGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HSWYNLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVKQ 405
Db 145 EEKVPINLWIDGKQNTVPLETVKTNKGNVTVOELDLQARRYLQEKYNLNSDVFQKVKQ 204

QY 406 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTISTSLISLYLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNTKNTINSENHIDIYLYTS 257

RESULT 35
US-08-475-668A-113
; Sequence 113, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-475-668A-113

Query Match          26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKQIYYNYSKAITSEKSADQFLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOGTALGNLKQIYYNEKAKTENKSHDQFLQHTILFKGFFTD 84
QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 345
Db 85 HSWYNDLLVDFDSKDIDVYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVELDLQARHYLHGKFLYNSDSFGKQVQ 405
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTQVELDLQARRYLQEKYNYNSDVDFGKQVQ 204
QY 406 RGLIVPHSSEGSTVSYDLFDAQGYPDTLRLIYRDNTTISSTLSLSLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFQAQGYQNTLLRIYRDNKTINSENMHIDIYLYTS 257

RESULT 37
US-08-471-913A-113
; Sequence 113, Application US/08471913A
; Patent No. 6093794
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-475-668A-113

Query Match          26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKQIYYNYSKAITSEKSADQFLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOGTALGNLKQIYYNEKAKTENKSHDQFLQHTILFKGFFTD 84
QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 345
Db 85 HSWYNDLLVDFDSKDIDVYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVELDLQARHYLHGKFLYNSDSFGKQVQ 405
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTQVELDLQARRYLQEKYNYNSDVDFGKQVQ 204
QY 406 RGLIVPHSSEGSTVSYDLFDAQGYPDTLRLIYRDNTTISSTLSLSLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFQAQGYQNTLLRIYRDNKTINSENMHIDIYLYTS 257

RESULT 36
US-08-485-551A-113
; Sequence 113, Application US/08485551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-471-913A-113

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKKSELOQTALGNLKOIYYNSKAITSEKSAQDQFLTNLTLFKGFFTG 285
DB 25 SEKSEINEKDLRKKSELOQTALGNLKOIYYNEKAKTENKESHQDQLQHTILFKGFFTD 84
QY 286 HPWYNLLVDLGSSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 85 HSWYNLLVDFDSKIDVRYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLGNSDSFGKVKQ 405
DB 145 EEKVPINLWIDGKQNTVPLETKNKNVTQVQELDLQARRYLOEKYNLNSDVFQKVKQ 204
QY 406 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYLYTT 458
DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 38
US-08-485-264A-113
Sequence 113, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-264A-113
Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKKSELOQTALGNLKOIYYNSKAITSEKSAQDQFLTNLTLFKGFFTG 285
DB 25 SEKSEINEKDLRKKSELOQTALGNLKOIYYNEKAKTENKESHQDQLQHTILFKGFFTD 84
QY 286 HPWYNLLVDLGSSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 85 HSWYNLLVDFDSKIDVRYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLGNSDSFGKVKQ 405
DB 145 EEKVPINLWIDGKQNTVPLETKNKNVTQVQELDLQARRYLOEKYNLNSDVFQKVKQ 204
QY 406 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYLYTT 458
DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNKTINSENHIDIYLYTS 257
RESULT 39
US-08-474-349A-113
Sequence 113, Application US/08474349A
Patent No. 6333395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:


```
/ REFERENCE/DOCKET NUMBER: 7872-028
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 113:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-487-266A-113

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNKAITSSEKADQPLTNLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAKTENKESHDFLOHTILFKGFFTD 84

QY 286 HPWYNLLVDLGSTAAITSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HSWYNLLVDLDFSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 405
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARRYLOEKYNLNSDVDFGKQV 204

QY 406 RGLIVFHSSEGSTVSYDLFPAQOQYPTDLLRIYRDNTTISSTLSISLYLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFCAQOQYSNTLLRIYRDNKTINSENNHIDIYLYTS 257

RESULT 42
US-08-487-266A-113
/ Sequence 113, Application US/08487266A
/ Patent No. 6824783
/ GENERAL INFORMATION:
/ APPLICANT: Bolognesi, Dani P.
/ APPLICANT: Matthews, Thomas J.
/ APPLICANT: Wild, Carl T.
/ APPLICANT: Barney, Shawn O.
/ APPLICANT: Lambert, Dennis M.
/ APPLICANT: Petteway, Stephen R.
/ APPLICANT: Langlois, Alphonse J.
/ TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
/ OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
/ NUMBER OF SEQUENCES: 239
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/487,266A
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-025
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864

/ REFERENCE/DOCKET NUMBER: 7872-028
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 113:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-487-266A-113

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNKAITSSEKADQPLTNLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAKTENKESHDFLOHTILFKGFFTD 84

QY 286 HPWYNLLVDLGSTAAITSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HSWYNLLVDLDFSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 405
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARRYLOEKYNLNSDVDFGKQV 204

QY 406 RGLIVFHSSEGSTVSYDLFPAQOQYPTDLLRIYRDNTTISSTLSISLYLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFCAQOQYSNTLLRIYRDNKTINSENNHIDIYLYTS 257

RESULT 43
US-08-484-741-113
/ Sequence 113, Application US/08484741
/ Patent No. 6951717
/ GENERAL INFORMATION:
/ APPLICANT: Bolognesi, Dani P.
/ APPLICANT: Matthews, Thomas J.
/ APPLICANT: Wild, Carl T.
/ APPLICANT: Barney, Shawn O.
/ APPLICANT: Lambert, Dennis M.
/ APPLICANT: Petteway, Stephen R.
/ APPLICANT: Langlois, Alphonse J.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
/ OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
/ TRANSMISSION
/ NUMBER OF SEQUENCES: 273
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/484,741
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-022
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 113:
/ SEQUENCE CHARACTERISTICS:
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; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-08-484-741-113

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSAOFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDLRKXSELOGTALGNLKOIYYNEKAKTENKESHDOFLQHTILFKGFFTD 84

QY 286 HPWYNLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTKACMYGGVTLHNNRLT 345
DB 85 HSWYNLLVDLSDKVIDKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHNNRLT 144

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLGYNDSFGGKVQ 405
DB 145 EEKVPINLWLDGKQNTVPLETVTKNKNVTVQELDLQARRYLQEKYINLYNSDVFQKQV 204

QY 406 RGLIVPHSSEGSVSYDLFDAOGQYPTLLRIYRDNTTISSTLSLSLYLTT 458
DB 205 RGLIVPHSTEPSVNYDLFAGQGYNTLLRIYRDNKTINSENMHIDIYLYTS 257

RESULT 44
US-08-353-400-37
; Sequence 37, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT: PROTEINS
; TITLE OF INVENTION: 37
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-400-37

Query Match 26.8%; Score 944.5; DB 1; Length 239;
Best Local Similarity 78.1%; Pred. No. 5e-58;
Matches 185; Conservative 22; Mismatches 19; Indels 11; Gaps 3;

QY 445 SSTLSLSLYLTT-----STVMQTPTSLVSAAGDRTVITCKASQSVND-----VAVY 494
DB 3 SQAQVILLLLWVSGTGGDIVMSQSPSLAVSAGEKVTWCKSKSQSLLNSRTEKNLAWY 62

QY 495 QKPGQSPKLLISYTSRVRAGVDPDRSGSGYGTFTLTITSSVQAEAAVYFCQDYNPP 554
DB 63 QKPGQSPKLLIYWASTRTSGVDPDRFTGSGSGTFTLTITSSVQAEALAIYCKQSY-TLR 121

QY 555 TFGGKTLEIKRADAAPTVSIFPPPSSEQLTSGASVVCFLNNFYPKDINVKKIDGSEKQ 614
DB 122 TFGGKTLEIKRADAAPTVSIFPPPSSEQLTSGASVVCFLNNFYPKDINVKKIDGSEKQ 181

QY 615 NGVLNSWTDQDSKDYSTYSMSSTLTITKDEYERHNSYTCETHKTSTSPIVKGFNRNE 671
DB 182 NGVLNSWTDQDSKDYSTYSMSSTLTITKDEYERHNSYTCETHKTSTSPIVKGFNRNE 238

RESULT 45
US-08-446-918A-4
; Sequence 4, Application US/08446918A
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,918A
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 552
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-918A-4

Query Match 26.8%; Score 944; DB 1; Length 233;
Best Local Similarity 76.3%; Pred. No. 5.3e-58;
Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 227 EKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSAOFLNTLLPKGPFTH 286
DB 2 EKSEINEKDLRKXSELOGTALGNLKOIYYNEKAKTENKESHDOFLQHTILFKGFFTDH 61

QY 287 PWYNLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTKACMYGGVTLHNNRLTE 346
DB 62 SWYNLLVDLSDKVIDKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHNNRLTE 121

QY 347 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLGYNDSFGGKVQ 406
DB 122 EEKVPINLWLDGKQNTVPLETVTKNKNVTVQELDLQARRYLQEKYINLYNSDVFQKQV 181

QY 407 GLIVPHSSEGSVSYDLFDAOGQYPTLLRIYRDNTTISSTLSLSLYLTT 458
DB 182 GLIVPHSTEPSVNYDLFAGQGYNTLLRIYRDNKTINSENMHIDIYLYTS 233

RESULT 46
US-08-580-806-4
; Sequence 4, Application US/08580806

Patent No. 5935568
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
APPLICANT: Potter, Terence A.
TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-580-806-4

Query Match 26.8%; Score 944; DB 1; Length 233;
Best Local Similarity 76.3%; Pred. No. 5.3e-58;
Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 227 EKSEINEKDLRKKELOGTALGNLKOIYYNKAITSSEKSDAQFTNTLLPKGFTGH 286
Db 2 EKSEINEKDLRKKELOGTALGNLKOIYYNKAITSSEKSDAQFTNTLLPKGFTGH 61

QY 287 PWNLDLVLGSLTAATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTE 346
Db 62 SWYNDLVLDFDSDKDIDVKYKGGVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTE 121

QY 347 EKKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHVLHGKFLYNSDSFGGKVQR 406
Db 122 EKKVPINLWDGKQNTVPLETVTKNKGNVTVOELDLQARHVLHGKFLYNSDSFGGKVQR 181

QY 407 GLIVFHSSGTSYDLFDAGQGPDTLLRIYRDNMTTISSTLSLSISLYTT 458
Db 182 GLIVFHTSTPESVNYDLFGAGQVSNLLRIYRDNKNTINSENHIDIYLYTS 233

RESULT 47
US-08-353-400-34
Sequence 34, Application US/08353400
Patent No. 5665357
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BFO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/353,400
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN-1994
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-353-400-34

Query Match 26.7%; Score 941.5; DB 1; Length 219;
Best Local Similarity 83.0%; Pred. No. 7.2e-58;
Matches 181; Conservative 19; Mismatches 11; Indels 7; Gaps 2;

QY 460 IVMTOTPTSLVSGADRVTTITCKASQSVSND-----VANYQKPGQSPKLLISYTSRY 513
Db 2 IVMSQSPSSLAVSAGEKVTMCKSSQSLNLSRTRKNYLAWYQRPQSPKLLIYWASTRT 61

QY 514 AGVPDRFSGSGYGTDTLTITSSVQAEADAAVYFCQDYNSPPTFGGGTKLEIKRADAAPT 573
Db 62 SGVPDRFTGSGSGTDTLTITSSVQAEADLAIYCKQSY-TLRTFGGGTKLEIKRADAAPT 120

QY 574 SIFFPSSEQLTSGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLNSWTQDSDKSTYSM 633
Db 121 SIFFPSSEQLTSGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLNSWTQDSDKSTYSM 180

QY 634 SSTLTLTQDEYERHNSYTCEATHTSTSPIVKSFNRNE 671
Db 181 SSTLTLTQDEYERHNSYTCEATHTSTSPIVKSFNRNE 218

RESULT 48
US-08-737-129A-6
Sequence 6, Application US/08737129A
Patent No. 5885816
GENERAL INFORMATION:
APPLICANT: Ikuo FUJII et al.
TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,129A
FILING DATE: No. 5885816member 15, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850

```
;
; TELEFAX:
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-737-129A-6

Query Match 26.5%; Score 933; DB 1; Length 222;
Best Local Similarity 82.6%; Pred. No. 2.9e-57;
Matches 180; Conservative 12; Mismatches 24; Indels 2; Gaps 1;

QY 6 QSGPDLVKGASVKISCKASGVSFTGYMHVWVQSPGKGLWIGRINPNNGVTLNQKPK 65
Db 2 ESGPELVKPGSGVTISCKASGYGFTSMWNVQRPGQGLEWIGRIYPGSGDNVYNGKPK 61
QY 66 DKATLTVDKSSSTAYMELSLTSEDSAVYCAR--STMITNVMYMDYMGOGTSVTYSSAKT 123
Db 62 VRATLTAEKRSSTTVYLHLSLTSVDSAVYFCARFHYDYRRSVAMDYMGOGTSVTYSSAKT 121
QY 124 TTPSVVPLAPGSAQAQNSMVTGLCLVKGYFPPPEPTVTWNSSGSLSSGVHTFPAVLQSDLYT 183
Db 122 TTPSVVPLAPGSAQAQNSMVTGLCLVKGYFPPPEPTVTWNSSGSLSSGVHTFPAVLQSDLYT 181
QY 184 LSSSVTPSSTWPSSTVTCNVAHPASSTKVKKIVPRD 221
Db 182 LSSSVTPSSTWPSSTVTCNVAHPASSTKVKKIVPRD 219
```

```
RESULT 49
US-08-896-933-23
; Sequence 23, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
;
US-08-896-933-23
```

```
Query Match 26.4%; Score 931.5; DB 2; Length 232;
Best Local Similarity 76.0%; Pred. No. 3.9e-57;
Matches 177; Conservative 21; Mismatches 34; Indels 1; Gaps 1;

QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNYSKAITSEKSADQFLNTLLFKGFFTG 285
Db 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNYSKAITSEKSADQFLNTLLFKGFFTG 59
QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 60 HSWYNDLLVDLFDSDKDIVKYKGVKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 119
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFLYNSDSFGKVQ 405
Db 120 EEKVPINLWIDGKQNTVLETYTKNKNVTVOELDQARHYLHGKFLYNSDSVDFGKVQ 179
QY 406 RGLIVPHSSEGSTSVSYDLFDAQQYPTDLLRIYRDNNTTSSLSLSLYTT 458
Db 180 RGLIVPHTSTPEPSVNYDLFGAQQYGSNTLLRIYRDNKNTINSENMHIDIYLYTS 232
```

```
RESULT 50
US-09-314-235-23
; Sequence 23, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1994-06-02
; EARLIER FILING DATE: 1991-01-17
; EARLIER FILING DATE: 1992-06-01
; EARLIER FILING DATE: 1991-01-17
; EARLIER FILING DATE: 1990-01-17
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
;
US-09-314-235-23
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```
Query Match 26.4%; Score 931.5; DB 2; Length 232;
Best Local Similarity 76.0%; Pred. No. 3.9e-57;
Matches 177; Conservative 21; Mismatches 34; Indels 1; Gaps 1;

QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNYSKAITSEKSADQFLNTLLFKGFFTG 285
Db 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNYSKAITSEKSADQFLNTLLFKGFFTG 59
QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 60 HSWYNDLLVDLFDSDKDIVKYKGVKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 119
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFLYNSDSFGKVQ 405
Db 120 EEKVPINLWIDGKQNTVLETYTKNKNVTVOELDQARHYLHGKFLYNSDSVDFGKVQ 179
QY 406 RGLIVPHSSEGSTSVSYDLFDAQQYPTDLLRIYRDNNTTSSLSLSLYTT 458
Db 180 RGLIVPHTSTPEPSVNYDLFGAQQYGSNTLLRIYRDNKNTINSENMHIDIYLYTS 232
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RESULT 51
US-09-708-008B-23
; Sequence 23, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; EARLIER FILING DATE: 2000-11-08
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
;
US-09-708-008B-23
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ORGANISM: Staphylococcus aureus
US-09-708-008B-23

Query Match 26.4%; Score 931.5; DB 2; Length 232;
Best Local Similarity 76.0%; Pred. No. 3.9e-57;
Matches 177; Conservative 21; Mismatches 34; Indels 1; Gaps 1;
QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSDADQPLTNTLLFKGFFTG 285
Db 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHQPL-HTILFKGFFTD 59
QY 286 HPWYNLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 60 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 119
QY 346 EEKVPINLWDGKQTVPIIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 405
Db 120 EEKVPINLWDGKQTVPIETVTKNKNVTVOELDQARHYLHGKFGLYNSDSFGKQV 179
QY 406 RGLIVHSSSEGSTVSDYDLFDAQGYPTLLRIYRDNTTISSTLSISLYLYTT 458
Db 180 RGLIVHTSTEPSVNYDLFQAQGYSTLLRIYRDNTTINSENHIDILYLYTS 232

RESULT 52

US-09-144-776B-2
Sequence 2, Application US/09144776B
Patent No. 6399332

GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Acty)

CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-144-776B-2

Query Match 26.3%; Score 925; DB 2; Length 257;
Best Local Similarity 75.1%; Pred. No. 1.3e-56;
Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSDADQPLTNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHQDQFROHTILFKGFFTD 84
QY 286 HPWYNLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWDGKQTVPIIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 405
Db 145 EEKVPINLWDGKQTVPIETVTKNKNVTVOELDQARHYLHGKFGLYNSDSFGKQV 204
QY 406 RGLIVHSSSEGSTVSDYDLFDAQGYPTLLRIYRDNTTISSTLSISLYLYTT 458
Db 205 RGLIVHTSTEPSVNYDLFQAQGYSTLLRIYRDNTTINSENHIDILYLYTS 257

RESULT 53

US-08-882-431B-2
Sequence 2, Application US/08882431B
Patent No. 6713284

GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Acty)

CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431B-2

Query Match 26.3%; Score 925; DB 2; Length 257;
Best Local Similarity 75.1%; Pred. No. 1.3e-56;
Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSDADQPLTNTLLFKGFFTG 285

Db 25 SEKSEINEKDLRKSELOQTALGNLKQIYYVNEKAKTENKESHDOFRQHTILFKGFSTD 84
QY 286 HPWYNLLVDLGGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HSWYNLLVRFDSKDIDVKYKGGKVDLYGAYAGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 405
Db 145 EKKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARHYLHGKFGLYNSDSVDFGKQV 204
QY 406 RGLIVFHSSBGSTVSYDLFDAQOQYPTTLRIYRDNTTISSTLSLSLYLTT 458
Db 205 RGLIVFHTSTEPSVNDLFGAQOQYNTLLRIYRDNKTINSENMHIDIYLYTS 257

RESULT 54
US-09-144-776B-4
; Sequence 4, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Attv)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-144-776B-4

Query Match 26.1%; Score 921; DB 2; Length 233;
Best Local Similarity 75.0%; Pred. No. 2.1e-56;
Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
QY 227 EKSEINEKDLRKSELOQTALGNLKQIYYVNEKAKTENKESHDOFRQHTILFKGFSTD 286
Db 2 EKSEINEKDLRKSELOQTALGNLKQIYYVNEKAKTENKESHDOFRQHTILFKGFSTD 61
QY 287 PWNVDLLVGGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 346

Db 62 SWYNLLVRFDSKDIDVKYKGGKVDLYGAYAGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 347 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 406
Db 122 EKKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARHYLHGKFGLYNSDSVDFGKQV 181
QY 407 GLIVFHSSBGSTVSYDLFDAQOQYPTTLRIYRDNTTISSTLSLSLYLTT 458
Db 182 GLIVFHTSTEPSVNDLFGAQOQYNTLLRIYRDNKTINSENMHIDIYLYTS 233

RESULT 55
US-08-882-431B-4
; Sequence 4, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-4

Query Match 26.1%; Score 921; DB 2; Length 233;
Best Local Similarity 75.0%; Pred. No. 2.1e-56;
Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
QY 227 EKSEINEKDLRKSELOQTALGNLKQIYYVNEKAKTENKESHDOFRQHTILFKGFSTD 286
Db 2 EKSEINEKDLRKSELOQTALGNLKQIYYVNEKAKTENKESHDOFRQHTILFKGFSTD 61
QY 287 PWNVDLLVGGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 346
Db 62 SWYNLLVRFDSKDIDVKYKGGKVDLYGAYAGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 347 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 406
Db 122 EKKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARHYLHGKFGLYNSDSVDFGKQV 181


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QY 475 DRVTITKASQSVNDVAMVYQKPGQPKLLISYTSRAGVDPDRFSGSGYGTDFLTIS 534
Db 312 -----TLP IQ 316
QY 535 SVOAEDAAVYFCQDYNPSPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFL 594
Db 317 HQDMSGKEFKCKVNNKDLPSPIERTISKIGLVRAPQVYVILPPPAEQLSRKDVSLTCLV 376
QY 595 NNFPYKDIINVKIDGSEKQN-----GVLSWTDQDQSKDSTYSMSSTLTTLTKDEYERHNS 649
Db 377 VGFNPGDISVWTSNGHTTEENYKDTAPVLDS-----DGSFYISKLANMKTSKWEKTD 429
QY 650 YTCEATHK 657
Db 430 FSCNVRHE 437

RESULT 58
US-08-792-824-10
; Sequence 10, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHYEE, ELDEFRAWI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Chemical and Biological Defense
; STREET: Office of the Chief Counsel, Bldg E4435
; CITY: Aberdeen Proving Ground
; STATE: MD
; COUNTRY: U.S.
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,824
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Biffoni, U. J.
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 431-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-792-824-10

Query Match 26.0%; Score 915.5; DB 1; Length 254;
Best Local Similarity 79.2%; Pred. No. 5.7e-56;
Matches 179; Conservative 15; Mismatches 27; Indels 5; Gaps 2;

QY 1 EVOLQSQGPDLVKPGASVKISCKASGYSTGYMHVVKQSPGKLEWIGRIINPNNGVTL 60
Db 23 EVOLQSQGAEVLKPGASVKLSCTASGFNIKDTFMHVKQRPQGLEWIGRIDPANGTEY 82
QY 61 NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYYCARSTMITNYMDYWGQGTSTVTVSS 120
Db 83 DPKFGQKATITADTSSNTVNLQSLTSDTAVYYCASGGELG---FPYWGQGTTLTVSA 139
QY 121 AKTTTPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTFPAVLQSD 180
Db 140 AKTTTPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTFPAVLQSD 199
QY 181 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKKIVPRD--SGG 224
Db 200 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKKIVPRDCTSGG 245

RESULT 60
US-08-792-824-13
; Sequence 13, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHYEE, ELDEFRAWI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Chemical and Biological Defense
; STREET: Office of the Chief Counsel, Bldg E4435
; CITY: Aberdeen Proving Ground
; STATE: MD
; COUNTRY: U.S.
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,824
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Biffoni, U. J.
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 431-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-792-824-13

Query Match 26.0%; Score 915.5; DB 1; Length 254;
Best Local Similarity 79.2%; Pred. No. 5.7e-56;
Matches 179; Conservative 15; Mismatches 27; Indels 5; Gaps 2;

QY 1 EVOLQSQGPDLVKPGASVKISCKASGYSTGYMHVVKQSPGKLEWIGRIINPNNGVTL 60
Db 23 EVOLQSQGAEVLKPGASVKLSCTASGFNIKDTFMHVKQRPQGLEWIGRIDPANGTEY 82
QY 61 NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYYCARSTMITNYMDYWGQGTSTVTVSS 120
Db 83 DPKFGQKATITADTSSNTVNLQSLTSDTAVYYCASGGELG---FPYWGQGTTLTVSA 139
QY 121 AKTTTPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTFPAVLQSD 180
Db 140 AKTTTPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTFPAVLQSD 199
QY 181 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKKIVPRD--SGG 224
Db 200 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKKIVPRDCTSGG 245
```

RESULT 61
: TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
: REFERENCE: HUSOVAR, MARIE

RESULT 65
US-09-170-769A-8
; Sequence 8, Application US/09170769A
; Patent No. 644206
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: LETURCO, Didier
; APPLICANT: MORIATRY, Ann
; APPLICANT: ULEVITCH, Richard
; APPLICANT: TOBIAS, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA
; FILE REFERENCE: SCRIPI140-3
; CURRENT APPLICATION NUMBER: US/09/170,769A
; CURRENT FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/070,160
; PRIOR FILING DATE: 1993-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 8
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Murine
US-09-170-769A-8
Query Match 25.5%; Score 898; DB 2; Length 211;
Best Local Similarity 81.4%; Pred. No. 7.3e-55;
Matches 171; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
QY 462 MTQTPSLLVAGDRVTITCKASQSVNDVAVTQKPGQPKLLISYTSRYAGVDFRFS 521
DB 1 MTQTPSLLSAGDRVTITCKASQSVNDVAVTQKPGQPKLLISYTSRYAGVDFRFS 60
QY 522 GSGYGTDTLTITSSVQAEADAVFCQDYNBPTEFGGKLEIKRADAAPTISIFPPSSE 581
DB 61 GSGGTDYSLTISNLQEDPATFCQGDTPWTFGGTKLEIKRADAAPTISIFPPSSE 120
QY 582 QLTSGGASVVCFLNNFYPKDINVKKIDGSRQGVNLNWTQDQSKDSTYSMSSTLTITK 641
DB 121 QLTSGGASVVCFLNNFYPKDINVKKIDGSRQGVNLNWTQDQSKDSTYSMSSTLTITK 180
QY 642 DEVERHNSYTCETHKTSSTSPVKSFNNE 671
DB 181 DEVERHNSYTCETHKTSSTSPVKSFNNE 210
RESULT 66
PCT-US94-14106-55
; Sequence 55, Application PC/TUS9414106
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Process for Generating Specific Antibodies
; NUMBER OF SEQUENCES: 61
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14106
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14106-55
Query Match 25.5%; Score 897.5; DB 4; Length 223;
Best Local Similarity 79.4%; Pred. No. 8.5e-55;
Matches 177; Conservative 12; Mismatches 31; Indels 3; Gaps 2;

QY 1 EVLOQSGDPLVKPGASVKISKASGYSFTGYTHHWVKQSPGKGLWIGRINPNNGVTLY 60
DB 1 EVLOQSGAELMMPGASVKISKATGYTLSSSLWLVKQSPGKGLWIGRILFGSGSAHY 60
QY 61 NQFKDKATLTVDKSSSTTAYMELRSLTSEDSAVYYCARSTMTITNY--VMDYWGQGTSTTV 118
DB 61 NEXFKGKATFTVDTSSNTAYMQLSSTSEDSAVYYCARGD-YGNYGDFYWGQGTSTTV 119
QY 119 SSAKTTTPPSVYPLAPGSAQAQTSNMTLGCILVKGYFPEPTVTWNSGSLSGVHTFPAVLQ 178
DB 120 FSAKTTTPSSVYPLAAGSAQAQTSNMTLGCILVKGYLPEPTVTWNSGSLSGVHTFPAVLQ 179
QY 179 SDLYTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKIVPRD 221
DB 180 SDLYTLRSVTPSPSTWPSSETVTCNVAHPASSTKVDKIVPRD 222
RESULT 67
US-08-737-129A-8
; Sequence 8, Application US/08737129A
; Patent No. 5885816
; GENERAL INFORMATION:
; APPLICANT: Ikuo FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: No. 5885816ember 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-737-129A-8
Query Match 25.4%; Score 895; DB 1; Length 215;
Best Local Similarity 80.2%; Pred. No. 1.2e-54;
Matches 170; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 460 IVMOTPTSLVLSAGDRVTITCKASQSVNDVAVTQKPGQPKLLISYTSRYAGVDFR 519
DB 2 LVMOTPTSSMYASLGERVTITCKASQDINIYLSWFOQKPGKSPKALIYRNLGLVDGVPSR 61
QY 520 FSGSGYGTDTLTITSSVQAEADAVFCQDYNBPTEFGGKLEIKRADAAPTISIFPPS 579

TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 599 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-442-542-18

Query Match 25.3%; Score 892.5; DB 1; Length 599;
Best Local Similarity 32.4%; Pred. No. 7.1e-54;
Matches 219; Conservative 73; Mismatches 118; Indels 265; Gaps 16;
QY 1 EVLOQSGDPLVPGASVKISCKASGYSFTGYVMHWKQSPGKLEWIGRI--NPNGVT 58
DB 155 QVKLQSGGGGLVQPKGSLKLSKAASGFTFNFMNVRQAPGKLEWVARIRKSNYAT 214
QY 59 LYNQKFKDKATLVDSKSTTAYMELRSLTSEDSAVYYCARSTMTITNYVMDYWGQGSVTV 118
DB 215 SYGDSVKDRFTVSRDSDSQSMFYLMNNLKTEDTAMYYCYR---VVYGMNDYWGQGSVTV 271
QY 119 SSAKTTTPPSVYPLAPG--SAAQTNSMVTGLCKLVKGYFPEPTVTWNSGSLSSGVHTFPVAV 176
DB 272 SSAKTTTPPSVYPLAPGSRSAQTNSMVTGLCKLVKGYFPEPTVTWNSGSLSSGVHTFPVAV 331
QY 177 LQSDLYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDDKIVPRDGGPSEKSEINEKD 236
DB 332 LQSDLYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDDKIVPRDCG----- 378
QY 237 LRKKSLEQGTALGNLQIYYNSKAITSEKSAQDLTNTLFPKFTGHPWYNDLLVDL 296
DB 379 -----CKPCTVPEVSSVFIFPPK-----PKDVLITL----- 407
QY 297 GSTAATSEYEGSSVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLTEKKVPINLWI 356
DB 408 -----TP-KVTCVVVDIS-----KDDPEVQFSWFV 431

QY 357 DGKQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVORG 407
DB 432 D-----DVEVHTAQTPREEQFNSTFRVSELPIHQDWLNGKEFKCRVNSAAFPAPIEK- 486
QY 408 LIVFHSSEGSTVSYDLFDAQGYQPDTLRLIYRDNTTISSTLSISLYLYTTSIVMTQTP 467
DB 487 -----TISKI----- 491
QY 468 SLLVSAGDRVTITCKASQSVSNVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGGYGT 527
DB 492 ----- 491
QY 528 DFTLTSSVQAEAAVYFCQDYNSPPTFGGTTKLEIKRADAAPTVSIIRPPSSEQLTSGG 587
DB 492 -----KGRPKAPQVVTIIPPKQWAKDK 514
QY 588 ASVVCFLNFPYKPDINVKWIDGSEKQ-----GVLSNWTDOBSKDSYMSSTLTITKD 642
DB 515 VSLTCMTIDTFEPEDITVEMQNGQPAENYKNTQPINMT-----NGSYFVYKLVNQKS 567
QY 643 EYERHNSYTCEATHK 657
DB 568 NWEAGNTFTCSVLHE 582

RESULT 71
US-08-765-469-18
Sequence 18, Application US/08765469
Patent No. 6069301
GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine B.
APPLICANT: Kozziel, Michael G.
TITLE OF INVENTION: Antibodies which Bind to Insect Gut
TITLE OF INVENTION: Proteins and their Use

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,469
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/267,641
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC 1750
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 599 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-765-469-18

Query Match 25.3%; Score 892.5; DB 2; Length 599;
Best Local Similarity 32.4%; Pred. No. 7.1e-54;
Matches 219; Conservative 73; Mismatches 118; Indels 265; Gaps 16;
QY 1 EVLOQSGDPLVPGASVKISCKASGYSFTGYVMHWKQSPGKLEWIGRI--NPNGVT 58
DB 155 QVKLQSGGGGLVQPKGSLKLSKAASGFTFNFMNVRQAPGKLEWVARIRKSNYAT 214
QY 59 LYNQKFKDKATLVDSKSTTAYMELRSLTSEDSAVYYCARSTMTITNYVMDYWGQGSVTV 118
DB 215 SYGDSVKDRFTVSRDSDSQSMFYLMNNLKTEDTAMYYCYR---VVYGMNDYWGQGSVTV 271
QY 119 SSAKTTTPPSVYPLAPG--SAAQTNSMVTGLCKLVKGYFPEPTVTWNSGSLSSGVHTFPVAV 176
DB 272 SSAKTTTPPSVYPLAPGSRSAQTNSMVTGLCKLVKGYFPEPTVTWNSGSLSSGVHTFPVAV 331
QY 177 LQSDLYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDDKIVPRDGGPSEKSEINEKD 236
DB 332 LQSDLYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDDKIVPRDCG----- 378
QY 237 LRKKSLEQGTALGNLQIYYNSKAITSEKSAQDLTNTLFPKFTGHPWYNDLLVDL 296
DB 379 -----CKPCTVPEVSSVFIFPPK-----PKDVLITL----- 407
QY 297 GSTAATSEYEGSSVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLTEKKVPINLWI 356
DB 408 -----TP-KVTCVVVDIS-----KDDPEVQFSWFV 431
QY 357 DGKQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVORG 407
DB 432 D-----DVEVHTAQTPREEQFNSTFRVSELPIHQDWLNGKEFKCRVNSAAFPAPIEK- 486
QY 408 LIVFHSSEGSTVSYDLFDAQGYQPDTLRLIYRDNTTISSTLSISLYLYTTSIVMTQTP 467
DB 487 -----TISKI----- 491
QY 468 SLLVSAGDRVTITCKASQSVSNVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGGYGT 527

Db 492 ----- 491
QY 528 DFTLTSSVOAEDAAYFCQDYNSSPTFGGGTKLEIKRADAPTIVSIIPPSPSEQLTSGG 587
Db 492 -----KGRPKAPQVYTTIPPKQEQMAKDK 514
QY 588 ASVVCFNNFYPKDINVKMKIDGSRQN-----GVLSNWTQDQSKDSTYSMSSTLTLT KD 642
Db 515 VSLTCMITDFPEDITVEQWNGQPAENYKNTOPIMNT-----NGSYFVYSKLVNQKS 567
QY 643 EVERHNSYTCETHK 657
Db 568 NWEAGNTFTCSVLHE 582

RESULT 72
US-09-423-439-58
; Sequence 58, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-NO. 6339070-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-423-439-58

Query Match 25.3%; Score 889.5; DB 2; Length 235;
Best Local Similarity 77.1%; Pred. No. 3.3e-54;
Matches 172; Conservative 19; Mismatches 31; Indels 1; Gaps 1;
QY 449 LGSILYLYTTSIVMTQTPTSLLSVAGDRVITTCASQSVSNVDVAMVYQKPGQSPKLLISY 508
Db 13 ISASVIMSGQTVLSQSPAILSSAPGKVTMTCRASSVTY-IHWYQKPGSSPKSWIYA 71
QY 509 TSSRYAGVDPFRSGSGYGTDFTLTSSVQAEADAAYFCQDYNSSPTFGGGTKLEIKRAD 568
Db 72 TSNLASGVPARFSGSGSGTSYSLTISRVEADAATYICQHWSSKPTFGGGTKLEIKRAD 131
QY 569 AAPTVSIFPPSSQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLSNWTDDQSKD 628
Db 132 AAPTVSIFPPSSQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLSNWTDDQSKD 191
QY 629 STYSMSSTLTLTKDEYERHNSYTCETHKSTSTSPIVKSFNRNE 671
Db 192 STYSMSSTLTLTKDEYERHNSYTCETHKSTSTSPIVKSFNRNE 234

RESULT 73
US-09-011-769A-23
; Sequence 23, Application US/09011769A
; Patent No. 6436691
; GENERAL INFORMATION:
; APPLICANT: SLATER, Anthony M.
; BLAKEY, David C.
; DAVIES, David H.
; HENNAM, John F.
; HENNEQUIN, Laurent F.A.
; MARSHAM, Peter R.
; DOWELL, Robert I.
; TITLE OF INVENTION: Chemical Compounds
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, LLP
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,769A
; FILING DATE: 13-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9612295.7
; FILING DATE: 12-JUN-1996
; APPLICATION NUMBER: GB 9611019.2
; FILING DATE: 25-MAY-1996
; APPLICATION NUMBER: GB 9516810.0
; FILING DATE: 16-AUG-1995
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-011-769A-23
Query Match 25.3%; Score 889.5; DB 2; Length 235;
Best Local Similarity 77.1%; Pred. No. 3.3e-54;
Matches 172; Conservative 19; Mismatches 31; Indels 1; Gaps 1;
QY 449 LGSILYLYTTSIVMTQTPTSLLSVAGDRVITTCASQSVSNVDVAMVYQKPGQSPKLLISY 508
Db 13 ISASVIMSGQTVLSQSPAILSSAPGKVTMTCRASSVTY-IHWYQKPGSSPKSWIYA 71
QY 509 TSSRYAGVDPFRSGSGYGTDFTLTSSVQAEADAAYFCQDYNSSPTFGGGTKLEIKRAD 568
Db 72 TSNLASGVPARFSGSGSGTSYSLTISRVEADAATYICQHWSSKPTFGGGTKLEIKRAD 131
QY 569 AAPTVSIFPPSSQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLSNWTDDQSKD 628
Db 132 AAPTVSIFPPSSQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLSNWTDDQSKD 191
QY 629 STYSMSSTLTLTKDEYERHNSYTCETHKSTSTSPIVKSFNRNE 671
Db 192 STYSMSSTLTLTKDEYERHNSYTCETHKSTSTSPIVKSFNRNE 234
RESULT 74
US-09-254-180C-132

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; Sequence 132, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; FILE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Mouse
US-09-254-180C-132

Query Match 25.1%; Score 885.5; DB 2; Length 216;
Best Local Similarity 80.0%; Pred. No. 5.6e-54;
Matches 172; Conservative 14; Mismatches 24; Indels 5; Gaps 1;

QY 460 IVMTQTPTSLVLSAGDRVTITCKASQSVSND-----VAVYQKPGQSPKLLISYTSRYA 514
Db 2 VLMTQTPLSLPVSLGDAQSISCKSSQSIHSSGNTYFEWYLPKQPGSPKLLIYKVSNRFS 61
QY 515 GVPDRFSGSGYGTDFLTITSSVQAEADAAVYFCQDYNNSPPTFGGGTKLEIKRADAAPTVS 574
Db 62 GVPDRFSGSGGTDFLTIKISRVEAEDLGYYVYCFQGSHPPTFGSGTKLEIKRADAAPTVS 121
QY 575 IPPPSSEQLTSGGASVVCFLNNFPKDIINVKWIDGSRQNGVLNSWTDQDSKDYTSMS 634
Db 122 IPPPSSEQLTSGGASVVCFLNNFPKDIINVKWIDGSRQNGVLNSWTDQDSKDYTSMS 181
QY 635 STLTLTKDEYERHNSYTCEATHKTSPIVKSFNR 669
Db 182 STLTLTKDEYEWHSNTYCEATHKTSPIVKSFNR 216

RESULT 75
US-09-254-180C-183
; Sequence 183, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; FILE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 183
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-180C-183

Query Match 25.1%; Score 885.5; DB 2; Length 216;
Best Local Similarity 80.0%; Pred. No. 5.6e-54;
Matches 172; Conservative 14; Mismatches 24; Indels 5; Gaps 1;

QY 460 IVMTQTPTSLVLSAGDRVTITCKASQSVSND-----VAVYQKPGQSPKLLISYTSRYA 514
Db 2 VLMTQTPLSLPVSLGDAQSISCKSSQSIHSSGNTYFEWYLPKQPGSPKLLIYKVSNRFS 61
QY 515 GVPDRFSGSGYGTDFLTITSSVQAEADAAVYFCQDYNNSPPTFGGGTKLEIKRADAAPTVS 574
Db 62 GVPDRFSGSGGTDFLTIKISRVEAEDLGYYVYCFQGSHPPTFGSGTKLEIKRADAAPTVS 121
QY 575 IPPPSSEQLTSGGASVVCFLNNFPKDIINVKWIDGSRQNGVLNSWTDQDSKDYTSMS 634
Db 122 IPPPSSEQLTSGGASVVCFLNNFPKDIINVKWIDGSRQNGVLNSWTDQDSKDYTSMS 181
QY 635 STLTLTKDEYERHNSYTCEATHKTSPIVKSFNR 669
Db 182 STLTLTKDEYEWHSNTYCEATHKTSPIVKSFNR 216

Search completed: February 15, 2006, 20:20:13
Job time : 60.2354 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 15, 2006, 20:34:11 ; Search time 170.042 Seconds
(without alignments)
1651.247 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522

Sequence: 1 EVLOQSGPLVKPGASVKI.....EATHKTSPIVKSPFRNES 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- Published Applications AA_Main:*
- 1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*
 - 2: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep:*
 - 3: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
 - 4: /cgn2_6/ptodata/1/pubppa/US10A_PUBCOMB.pep:*
 - 5: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep:*
 - 6: /cgn2_6/ptodata/1/pubppa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3522	100.0	672	3	US-09-900-766-1
2	1832.5	52.0	478	4	US-10-679-620-72
3	1832.5	52.0	478	6	US-11-132-143-72
4	1832.5	52.0	509	4	US-10-679-620-90
5	1832.5	52.0	509	6	US-11-132-143-90
6	1653	46.9	552	4	US-10-679-620-86
7	1653	46.9	552	6	US-11-132-143-86
8	1350	38.3	750	6	US-11-084-080-16
9	1339	38.0	750	6	US-11-084-080-24
10	1321.5	37.5	669	5	US-10-900-328-3
11	1317.5	37.4	751	6	US-11-084-080-26
12	1308.5	37.2	759	6	US-11-084-080-28
13	1260	35.8	488	6	US-11-084-080-18
14	1260	35.8	488	6	US-11-084-080-22
15	1257	35.7	669	3	US-09-807-721-2
16	1257	35.7	750	6	US-11-084-080-20
17	1218	34.6	233	3	US-09-900-766-2
18	1130	32.1	233	3	US-09-900-766-3
19	1107	31.4	233	3	US-09-900-766-7
20	1107	31.4	233	4	US-10-283-838-8
21	1107	31.4	257	4	US-10-267-682-112
22	1107	31.4	257	4	US-10-267-748-112
23	1107	31.4	257	4	US-10-428-817A-188
24	1072	30.4	248	3	US-09-870-759-16
25	1072	30.4	248	3	US-09-751-708A-16
26	1072	30.4	248	4	US-10-428-817A-12
27	1072	30.4	248	5	US-10-937-758A-16

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Sequence 12, Appl
Sequence 11, Appl
Sequence 9, Appl
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Sequence 14, Appl
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Sequence 13, Appl
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Sequence 6, Appl
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Sequence 67, Appl
Sequence 84, Appl
Sequence 9, Appl
Sequence 10, Appl
Sequence 2, Appl
Sequence 71, Appl

101	903	25.6	233	2	US-08-882-431-4	Sequence 4, Appl1	174	832.5	23.6	468	6	US-11-004-639-12	Sequence 12, Appl1
102	901.5	25.6	219	4	US-10-683-815-10	Sequence 10, Appl1	175	832.5	23.6	624	5	US-10-723-003-30	Sequence 30, Appl1
103	900.5	25.6	462	4	US-10-281-479A-23	Sequence 23, Appl1	176	832.5	23.6	624	6	US-11-004-639-30	Sequence 30, Appl1
104	900.5	25.6	462	4	US-10-286-132A-23	Sequence 23, Appl1	177	832.5	23.6	639	5	US-10-723-003-32	Sequence 32, Appl1
105	900.5	25.6	464	4	US-10-375-180A-23	Sequence 23, Appl1	178	832.5	23.6	639	6	US-11-004-639-32	Sequence 32, Appl1
106	895	25.4	214	5	US-10-488-074-69	Sequence 69, Appl1	179	830	23.6	235	5	US-10-516-429-11	Sequence 11, Appl1
107	895	25.4	216	5	US-10-488-074-85	Sequence 85, Appl1	180	827.5	23.5	470	4	US-10-216-484-143	Sequence 143, Appl1
108	894	25.4	218	4	US-10-679-620-80	Sequence 80, Appl1	181	827.5	23.5	470	4	US-10-384-933-143	Sequence 143, Appl1
109	894	25.4	218	6	US-11-132-143-80	Sequence 80, Appl1	182	825.5	23.4	470	4	US-10-216-484-145	Sequence 145, Appl1
110	894	25.4	712	4	US-10-679-620-116	Sequence 116, Appl1	183	825.5	23.4	470	4	US-10-384-933-145	Sequence 145, Appl1
111	894	25.4	712	6	US-11-132-143-116	Sequence 116, Appl1	184	825	23.4	442	5	US-10-822-300-124	Sequence 124, Appl1
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114	890.5	25.3	215	4	US-10-679-620-120	Sequence 120, Appl1	187	824.5	23.4	470	4	US-10-216-484-117	Sequence 117, Appl1
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124	883	25.1	218	5	US-10-488-074-66	Sequence 66, Appl1	197	818.5	23.2	472	4	US-10-159-006-43	Sequence 43, Appl1
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128	872	24.8	236	5	US-10-877-467A-8	Sequence 8, Appl1	201	816	23.2	446	5	US-10-822-300-136	Sequence 136, Appl1
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134	870	24.7	234	5	US-10-496-059-4	Sequence 5, Appl1	207	813.5	23.1	447	5	US-10-822-300-134	Sequence 134, Appl1
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160	845.5	24.0	626	6	US-11-004-639-44	Sequence 44, Appl1	233	800	22.7	471	6	US-11-021-874-4	Sequence 4, Appl1
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164	844	24.0	237	5	US-10-997-690-11	Sequence 11, Appl1	237	798	22.7	452	5	US-10-861-049-17	Sequence 17, Appl1
165	844	24.0	446	5	US-10-822-300-121	Sequence 121, Appl1	238	798	22.7	452	5	US-10-861-049-20	Sequence 20, Appl1
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167	843.5	23.9	384	4	US-10-822-231-5	Sequence 5, Appl1	240	798	22.7	452	6	US-11-021-874-20	Sequence 20, Appl1
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249	795.5	22.6	368	5	US-10-880-320-47	Sequence 47, Appl
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268	793	22.5	467	4	US-10-699-874-30	Sequence 30, Appl
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272	792	22.5	448	4	US-10-353-708-60	Sequence 60, Appl
273	792	22.5	448	4	US-10-731-984-16	Sequence 16, Appl
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276	792	22.5	467	4	US-10-171-452A-41	Sequence 41, Appl
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278	792	22.5	467	4	US-10-171-452A-59	Sequence 59, Appl
279	792	22.5	467	4	US-10-353-708-41	Sequence 41, Appl
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ALIGNMENTS

RESULT 1
US-09-900-766-1
; Sequence 1, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0/10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PSPTIDE
; LOCATION: (1)..(672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1

Query Match 100.0%; Score 3522; DB 3; Length 672;
Best Local Similarity 100.0%; Pred. No. 4.6e-152;
Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-679-620-72
; Sequence 72, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING


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RESULT 6
US-10-679-620-86
; Sequence 86, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinel, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 86
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plSBCL736, see Example 15
US-10-679-620-86

Query Match 46.9%; Score 1653; DB 4; Length 552;
Best Local Similarity 51.5%; Pred. No. 2.1e-67;
Matches 351; Conservative 40; Mismatches 85; Indels 206; Gaps 7;

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QY 174 PAVLQSDLYTLSSSVTVPSSTWPSSTVTCNVAHPASSTKVDKKIIVPRDGGPSEKSEIN 233
Db 245 PAVLQSDLYTLSSSVTVPSSTWPSSTVTCNVAHPASSTKVDKKIIVPRDCGG----- 295
QY 234 EKDLRKSELOQTALGNLKQIYYNSKAITSEKSDAQFLTNTLLPKGFTGHPWYNDLL 293
Db 296 -----GKRTIQDSA-----TDT----- 307
QY 294 VDLGSAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGVTLHDNNRLTEKKVPIIN 353
Db 308 VDLGAELHRDDPPPTASDI----- 326
QY 354 LMIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVQGLIVFHS 413
Db 327 -----GKRGKRGD----- 335
QY 414 SEGSTVSVDLFDAGQGYPTLLRIIRDNTTISSTLSLSLYLTYSIVMTQPTSLLYSA 473
Db 336 -----IVLTQSPASLAVSL 349
QY 474 GDRVTITCKASQSVN-----DVAWYQKPGQPKLLISYTSRYAGVPRFSGSGYGTDF 529
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
```

```
Db 350 GQRATISCRASESDVNYGFSFMNWFQKPGQPPKLLIYAI SNRGSGVPARFSGSGSGTDF 409
QY 530 TLTISVQAEDAAVYFCQDYNSTPFTGGTCKLEIKRADAAPTIVSIFPPSSQOLTSGGAS 589
Db 410 SLNIHVEEDDPAMVFCQQTKEVPWTFGGTCKLEIKRADAAPTIVSIFPPSSQOLTSGGAS 469
QY 590 VVCFLNFPYKDIINVKWIDGSRQNGVLNSWTDQDSDSTYSMSSTLTLTUTKDEYERHNS 649
Db 470 VVCFLNFPYKDIINVKWIDGSRQNGVLNSWTDQDSDSTYSMSSTLTLTUTKDEYERHNS 529
QY 650 YTCEATHKTSTSPIVKSFNENE 671
Db 530 YTCEATHKTSTSPIVKSFNENE 551

RESULT 7
US-11-132-143-86
; Sequence 86, Application US/11132143
; Publication No. US20050207977A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinel, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/11/132,143
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 86
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plSBCL736, see Example 15
US-11-132-143-86

Query Match 46.9%; Score 1653; DB 6; Length 552;
Best Local Similarity 51.5%; Pred. No. 2.1e-67;
Matches 351; Conservative 40; Mismatches 85; Indels 206; Gaps 7;

QY 1 EVLOQSGDPLVKPGASVKISKASGYSTGYMHWVKSPQKGLWIGRINPNNGVTLY 60
Db 65 EVDLVESGDLVKPGGSLKLSCAASGFTFSHYGMSWVRQTPDKRLEWVATIGSRGTTHY 124
QY 61 NQKFKDKATLTVDKSTTAYMELRSITSDSAVYYCARSTMITNY-----VMDYWGOG 113
Db 125 PDSVGRFTISRDNKALYLQMSLKSEDTAMYCYARRSEFYFGNTYYGAMDYWGOG 184
QY 114 TSVTVSSAKTTTPSVYPLAPGSAQAQNSMVTLCGLVKGYFPBPVTVTNWNSGLSSGVHTF 173
Db 185 ASVTSSAKTTTPSVYPLAPGSAQAQNSMVTLCGLVKGYFPBPVTVTNWNSGLSSGVHTF 244
QY 174 PAVLQSDLYTLSSSVTVPSSTWPSSTVTCNVAHPASSTKVDKKIIVPRDGGPSEKSEIN 233
Db 245 PAVLQSDLYTLSSSVTVPSSTWPSSTVTCNVAHPASSTKVDKKIIVPRDCGG----- 295
QY 234 EKDLRKSELOQTALGNLKQIYYNSKAITSEKSDAQFLTNTLLPKGFTGHPWYNDLL 293
Db 296 -----GKRTIQDSA-----TDT----- 307
QY 294 VDLGSAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGVTLHDNNRLTEKKVPIIN 353
Db 308 VDLGAELHRDDPPPTASDI----- 326
QY 354 LMIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVQGLIVFHS 413
Db 327 -----GKRGKRGD----- 335
```

QY 414 SEGSTVSYDLFDAQGOYPTLLRIYRDNTTISSTLSISLYLVTGIVMTQPTTSLVSA 473
Db 336 -----IVLTQSPASLAVSL 349
QY 474 GORVTTICKASQSVN----DVAWYQOKGCPKLIISYTSSRYAGVPDRFSGSGYGTDF 529
Db 350 GQATITSCRASESVDNYGFSFMWFQOKPGQPKLLIYALISNRGSGVPAKFSGSGGTDF 409
QY 530 TTITSSVOAEDAAYVFCQDQYNSPPTFGGCTKLEIKRADAAPTVSIFPPSSSEQLTSGGAS 589
Db 410 SLNIHVEEDDPAMYFCQTKVEPWFPGGCTKLEIKRADAAPTVSIFPPSSSEQLTSGGAS 469
QY 590 VVCFLLNFPKIDINVKKIDGSRQNGVLSWTDQDSKSTYSMSSTLTITKDEYERHNS 649
Db 470 VVCFLLNFPKIDINVKKIDGSRQNGVLSWTDQDSKSTYSMSSTLTITKDEYERHNS 529
QY 650 YTCEATHKTSTSPIVKSFENE 671
Db 530 YTCEATHKTSTSPIVKSFENRNE 551
RESULT 8
US-11-084-080-16
; Sequence 16, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDORRN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSCH, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084, 080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845
US-11-084-080-16
Query Match 38.3%; Score 1350; DB 6; Length 750;
Best Local Similarity 41.8%; Pred. No. 1.5e-53;
Matches 321; Conservative 101; Mismatches 208; Indels 138; Gaps 19;
QY 1 EVOLQSGDPLVKPGASVKISCKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
Db 23 EVOLVSGDGLVPGGSGVRISCAASGYFTFYGNVWVKQPGKLEWIGRINPNNGVTLY 82
QY 61 NQKPKDKATLVDSSTTAYMELRSLTSEDSAVYVCARSTMITNYVMDYWGQGTSTVTS 120
Db 83 ADSFKGRFTSLQTSASAAYLQINSLRAEDTAVYCARPAI-----KGDYWGQGTSTVTS 138
QY 121 AKTTPPSVPLAPGSAAGTNSMTLGLVKYGPPEPVTWNSGSLSSGVHTTFAVLQSD 180
Db 139 ASTKGFSEVPLAPGSSKSTSGGTAALGLVKVDYFPPEPVTWNSGSLTSGVHTTFAVLQSS 198
QY 181 -LYTLSSSVTPSPSTWPFSEVTCNVAPASSTKVDKKIIVPRDGGGPFSEKSEINEKDLRK 239
Db 199 GLYSLSVSVTPSPSSLTGTQYICNVNHPKSNKTVDKKVEPKSC-----TRHQPRG 249

QY 240 KSELQGTALGNLKQIYYNYSKAITSEKSAQDQFLNTLLPKFGFTGHPWVND---LLVDL 296
Db 250 WEQLNVTYFNFLGEAYEP---TFTQDLRLNLAGKTPVCQLPVTLTQTTIADKRFLVDI 305
QY 297 GSTAATSEVEGSSVDLYGAY-YGYQCAGCTPNK-----TACMYGGVTLHDNRL 344
Db 306 --TTTSKTKVKVAIDVTVVVGVDKWDGKORAVFLDKVPTVATSKLPGV7-----NRV 359
QY 345 TBEKKVPINLWIDGK-QTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGK 403
Db 360 T-----LTFDGSYQKLVAAKADRKALEGLVKNLEFSI-EAIGHK-----TINGQ 403
QY 404 -----VQRGLIVFHSSEGSTVSYDLFDAQGOYPTLLRI 437
Db 404 EAAKFLFIQIOMVSEAAEFKYTEVVDRLG--YGSFKPNFKVLNLENMNGDISDAIHKS 461
QY 438 YRDNTTISSTLSIS-----LYLYTTS----- 459
Db 462 SPOCTTINPALQILISPSNDPWWNVKVSQISPDGMILKFKSSKMKYLLPTAAAGLLLLAAQ 521
QY 460 -----IVMTQTPTSLIVSAGDRVITITCKASQSV--SNDVA---WYQKPGQSPK 503
Db 522 PAMAHHHHHHDITQMTQSPSSLSASVGDRTIICRSTKSLHNSNGITYLYWYQKPGKAPK 581
QY 504 LLISYTSRYAGVDPDRFSGSGYGTDTFTLTISSSVQAEADAAYVFCQDQYNSPPTFGGKTLE 563
Db 582 LLTYQMSNLASGVPSRFSFGSGGTDTFTLTISSLQPEDFATYCAQNLEIPRTFGQGTKE 641
QY 564 IKRADAAPTVSIFPPSSSEQLTSGASVWCFLLNFPKIDINVKKIDGSRQNGVLSWTD 623
Db 642 LKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAVQWKVQNALQSGNSQESVTE 701
QY 624 QDSKSTYSMSSTLTITKDEYERHNSYTCEATHKTSTSPIVKSFENRNE 671
Db 702 QDSKSTYSLSSTLTITLTKADYKHKYVACEVTHQGLSSPVTKSFNRGE 749
RESULT 9
US-11-084-080-24
; Sequence 24, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDORRN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSCH, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084, 080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-24
Query Match 38.0%; Score 1339; DB 6; Length 750;
Best Local Similarity 41.6%; Pred. No. 4.9e-53;
Matches 320; Conservative 101; Mismatches 202; Indels 146; Gaps 20;

```
QY 1 EVOLQSGDPLVKPGASVKISKASGYSFTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVOLVSGDGLVPGGSGVRISCAASGYTFNYGMNWKQAPGKLEWGMWINTYTGESTY 88
QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSEDSAVYYCARSTMTITNYVMDYWGQGTSTVTS 120
Db 89 ADSFKGRFTFSLDTSASAYLQINSLRAEDTAVYYCARFAI-----KGDIWGQGTLLTVSS 144
QY 121 AKTTPSVVPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
Db 145 ASTKGSVPFLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 204
QY 181 -LYTLSSSVTPSSSTWPESTVTCNVAHPASSTKVDKKIIPRDSGGSEKSEINEKDLRK 239
Db 205 GLYSLSVVTPSSSLGTQYICNVNHPKSNKTKVDKKEPKSC-----M 248
QY 240 KSLQGTALG-----NLKQIYYNSKAITSEKSAQDQFLTNLLFKGF 282
Db 249 KYLLPTAAAGLLLAQAQAMAYNTVSFNLGEAYEP-----TFQLDLNELAKGTPVCQLP 304
QY 283 FTGHPWYND---LLVDLGSTAAATSEYEGSSVDLYGAY-YGYCAGAGTPNK-----328
Db 305 VTLQTTIADDKRFVLVDI--TTTSKTKVKAIDVDVYVVGQYQDKWDGKRAVFLDKVPTV 362
QY 329 -TACMYGGVTLHDNNRLTEKKVPINLWIDGK-QTTVPIDKVKTSKKEVTVOELDLQARH 386
Db 363 ATSKLFPGVV-----NRVT-----LTFDGSYQKLVNAKADRKALEGVNKLFSI-E 409
QY 387 YLHGKFGLYNSDGGK-----VORGLIVFHSSEGSTVS 420
Db 410 AIHGK-----TINGQEAARKFLLIVQMVEAARFKYIETEVVDRLG--YGSFKENFKV 460
QY 421 YDLFDAGQVPTDLLRIYRDNNTI-----SSTLSLSLYLYTTS--459
Db 461 LNLNNWGDIDSAIHKSPPQCTTINPALQLISPDNPWVNVKVSQISPDGMILKFKSKT 520
QY 460 -----LVMTQTPTSLVASGDRVTITCKASQSV--SNDVA---WYQCKPQOSP 502
Db 521 RHQPRGWQLDIQMTQSPSSLSASVGDRTVTICRSTKSLHSHNGITYLYWYQCKPGKAP 580
QY 503 KLLIYSYTSRYAGVPRDFSGSGYGTDFTLTITSSVQAEADAAYFCOODYNSPPTFGGQTKL 562
Db 581 KLLIYQMSNLASGVPRFSFGSSGSGTDFTLTITSSLPQEDPATYICACQNLEIPRTFGQTKV 640
QY 563 EIKRAADAAPTYSIFPPSSSEQLTSGGASVVCFLNFPKQINVKWKIDGSRQNGVNSWT 622
Db 641 ELKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQMWKDVALQSGNSQESVT 700
QY 623 DQSKDSTYSMSSTLTLTDEYERHNSYTCEATHKSTSTSPVKSFNRNE 671
Db 701 EQSKDSTYSLSSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGE 749
```

RESULT 10

```
US-10-900-928-3
; Sequence 3, Application US/10900928
; Publication No. US2005006952A1
; GENERAL INFORMATION:
; APPLICANT: Bleck, Gregory T.
; APPLICANT: Collins, Ian
; TITLE OF INVENTION: Fusion Antibodies
; FILE REFERENCE: GALA-09135
; CURRENT APPLICATION NUMBER: US/10/900, 928
; CURRENT FILING DATE: 2004-07-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
```

US-10-900-928-3

```
Query Match 37.5%; Score 1321.5; DB 5; Length 669;
Best Local Similarity 40.8%; Pred. No. 2,7e-52;
Matches 303; Conservative 94; Mismatches 199; Indels 147; Gaps 17;
```

```
QY 1 EVOLQSGDPLVKPGASVKISKASGYSFTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVOLVSGGCVQPGRLSLRSLSCASGDFTTTVMWSWRQAPGKLEWIGEIHEDSDSTINY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSEDSAVYYCARSTMTITNYVMDYWGQGTSTVTS 120
Db 61 AFSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCA-SLYFGFPPFAFWGQGTPTVTS 119
QY 121 AKTTPSVVPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
Db 120 ASTKGSVPFLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 179
QY 181 -LYTLSSSVTPSSSTWPESTVTCNVAHPASSTKVDKKIIPRDS-----GG 224
Db 180 GLYSLSVVTPSSSLGTQYICNVNHPKSNKTKVDKKEPKSCDKTHTTCCPPAPPELLGG 239
QY 225 PSEKSEINEKD---LRKSELGQTALGNLKOIYYNSKAITSEKSAQDQFLTNLLFKG 281
Db 240 PSVFLFPPPKDQTLMSRTPETVCVVVD-----VSHEDPEVKF-----277
QY 282 FTGHPWYND-LLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPTNKACMYGGVTLHD 340
Db 278 -----NWYVDGVEVHNKTKPREEQNRYRVVSVL-----TVLHQ 313
QY 341 NNRLTEKKVPINLWIDGKQ-----TTVPIDK-----VKTSKKEV 375
Db 314 D-----WLNKGEYKCKVSNKALPAPIEKTISKAKQPREPQVYVTLPPSREEM 360
QY 376 TVOELDQARHYLHGKFGLYNSDPSGCKGVORGLIVFHSSEGS-----TVSYDLDFAQGY 430
Db 361 TKQVSLTCL-----VKGFPYSD-----IAVEWESNGQPENNYKTPPVLDSDGSF 406
QY 431 -----PDTLLRIYRDNNTITSTLSLSLYLYTT--SIWMTQTPTS 468
Db 407 FLYSKLTVDKSRWQQGNVFCVSMHEALNNHYTKLSLSPGLFHATQADIQLTQSPSS 466
QY 469 LLVASGDRVTITCKASQSVNDVAVYQCKPQSPGKLLIYSYTSRYAGVPRDFSGSGYGT 528
Db 467 LNASGDRVTITCKASQSDYGTSVAVYQCKPGKAPKLLIYWTSTRTHTGVSPRFSGSGGTD 526
QY 529 FTLTISVQAEADAAYFCOODYNSPPTFGGQTKLEIKRAADAAPTYSIFPPSSQLTSGGA 588
Db 527 FTFITSSLPQEDIATYTCQ--YSLYRSFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTA 585
QY 589 SVVCFLNFPKQDINVKWKIDGSRQNGVNSWTQDSDKSDTYSMSSTLTLTDEYERHN 648
Db 586 SVVCLLNNFYPREAKVQMWKDVALQSGNSQESVTEQDSKSDTYSLSSTLTLSKADYEKKH 645
QY 649 SYTCEATHKSTSTSPVKSFNRNE 671
Db 646 VIACEVTHQGLSPVTKSFNRGE 668
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RESULT 11

```
US-11-084-080-26
; Sequence 26, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDORF, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTHWISTLE, Joycelyn
; APPLICANT: BOSCH, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
```

```

; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 751
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-gelonin
US-11-084-080-26

Query Match      37.4%; Score 1317.5; DB 6; Length 751;
Best Local Similarity 41.6%; Pred. No. 4.6e-52;
Matches 320; Conservative 101; Mismatches 208; Indels 141; Gaps 26;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYVMHWKSPGKGLWIGINPNNGVTLY 60
DB 23 EVQLVSGDPLVPGGSRVIRISCAASGYTFNYGMWVKQAPGKGLWMMGWINTYTGESTY 82
QY 61 NQKFKDKATLVDSKSTTAYMELRSLTSDSAVYCARSTMITNYVMYDYGQGTSTVTS 120
DB 83 ADSFKGRFTFSLDTSASAAVLQINSRAEDTAVYCARFAI-----KGDYWGQGTSLTVSS 138
QY 121 AKTTPSVVPLAPGSAQAQNSMTYTLGCLVKGYPEPVTYVWNSGSLSSGVHTFPVQLQSD 180
DB 139 ASTKGPVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVTYVWNSGALTSVHTFPVQLQSS 198
QY 181 -LYTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKKIIVP-----DSG 223
DB 199 GLYSLSVVTPSSSLGTQYICNVNHPKNTKVDKKVPEKSTRHRQPRGWELGLDVT 258
QY 224 GPSEKSE-----INEKLRKSKELQGTALGNLQIYYNSKAITSSSEKSDAQFLTNT 276
DB 259 SFSTKATITYYVFNLE--LRVKLKPEG-----NSHGIPLLRKKCD----- 299
QY 277 LIFKGPFTGHPWYNDLLDGLGTAATSEYEGSSVDLYGAY-YGYQCAG-----GTPN-- 327
DB 300 -----PGKCFVLVALSND--NGQLAEIAIDVTSVVVGYYQVNRYSYFPKADPAA 347
QY 328 -----KTACMYGG--VTLHDNNRLTEKKV--PINLWDGKQTTVPIDKVK----- 369
DB 348 YEGLFKNTIKTRLHFSGSYPSLEGEKAYRETTDLGIEPRLIGIK-KLDENAIIDNYKPT 406
QY 370 TSKKEVTVOELDIQARH-YLHGKFGLYNSDSFGKQV--RGLIVFHSSEGSTVSYDL--F 424
DB 407 ASLLVVIQWSEAAFTFENQI-----RNNFOORIRPTNNTISLENKWK-LSFQIRTS 461
QY 425 DAQGVPTDLRLIYRDN-----TTSSTSLSTL-----LYLYTS----- 459
DB 462 GANGMFSEA-VELERANGKYYVYTAVDQVKPKIALLKFDVKDKPKMYLLPTAAAGLLLA 520
QY 460 -----IVMTQPTSLVAGDRVTTICKASQSV--SNDVA---WYQKPGQS 501
DB 521 AQPAMAHHHHHDIQMTQSPSSLSASVGGDRVTTICRSTKSLHSNGITYLYWYQKPGKA 580
QY 502 PKLLISYTSRYAGVDRPSGSGYDFTLTISVQAEADAAYFCQODYNSPPTFGGGTK 561
DB 581 PKLLIQMNLASGVPSRFSSSGSGDFTLTISLQPEDFATYCAQNLEIPRTFQGT 640
QY 562 LETKRAADAAPTWSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLSW 621
DB 641 VELKRTVAAPSVIFPPSDQLKSGTASVVCLLNNFYPEAKYQWKVDNALQSGNSQESV 700
QY 622 TDQDSKDSYMSSTLTILKDEYERHNSYTCETHTKTSTSPIVKSFRNE 671
DB 701 TEQDSKDSYLSSTLTILSKADYEKKHVACEVTHQGLSPVTKSFRNGE 750
```

RESULT 12

```

US-11-084-080-28
; Sequence 28, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDORF, Koehn
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSCH, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-011
US-11-084-080-28
```

Query Match 37.2%; Score 1308.5; DB 6; Length 759;

Best Local Similarity 40.3%; Pred. No. 1.2e-51;

Matches 312; Conservative 109; Mismatches 212; Indels 141; Gaps 20;

```

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYVMHWKSPGKGLWIGINPNNGVTLY 60
DB 23 QVQLVESGGGVQPGKSLRLSCAASGFFPRSPAMHWVRQALGKLEWVAIVISDGSTKY 82
QY 61 NQKFKDKATLVDSKSTTAYMELRSLTSDSAVYCARSTMITN-----YVMYWGQGT 115
DB 83 ADSVKGRFTISRTSKNTVYKMSLRTEDTAVYVCARDQSLGDYDHYGLDVMWKGTT 142
QY 116 VYSSAKTTPPSVYPLAPGSAQAQNSMTYTLGCLVKGYFPEPVTYVWNSGSLSSGVHTFPA 175
DB 143 VTSSASTKGPSPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTYVWNSGALTSVHTFPA 202
QY 176 VLQSD-LYTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKKIIVPRDSGGPSEKSEBINE 234
DB 203 VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKKVPEKSC-----TRH 253
QY 235 KDLRKSKELQGTALGNLQIYYNSKAITSSSEKSDAQFLTNTLLFKGFTFGHPWYND--- 291
DB 254 RQPRGWEQLYNTVSNFLGEAYEP---TFIQDLRNLAKGTVCQQLPVTIQTADDKRF 309
QY 292 LLVDLGSTTAATSEYEGSSVDLYGAY-YGYQCAGGTPNK-----TACMYGGVTLH 339
DB 310 VLVDI--TTTSKTKTVKVAIDVTDVYVVGQDKWDGKDAVFLDKVPTVATVSKLPPGVT-- 365
QY 340 DNNRLTEKKVPINLWDGK-QTTVPIDKVKTSKKEVTVOELDIQARHYLHGKFGLYNSD 398
DB 366 --NRVT-----LTFDGSYQKLNVAAKADRAKALELVNKLFEFSI-EAHGK----- 407
QY 399 SFEGK-----VORGLIVFHSSEGSTVSYDLFDAQGYPD 432
DB 408 TINGQEAQKFFLIVIQWSEAAAFKVIETEVVDRL--YGSFKPNFKVLNLENNWGDID 465
QY 433 TLLRIYRDNVTTISSTSLSTIS-----VORGLIVFHSSEGSTVSYDLFDAQGYPD 459
DB 466 AIHKSPQCTTINPALQLISPSNDPWVNVKVSQISPDMLGILKPKSKMKYLLPTAAAGLL 525
```


QY 460 -----IVMTQPTSLVSAGDRVTITCKASQSVND-VAVYQOKPGQSP 502
Db 526 LLAAQAPAMAHHHHDIVLTQSPGTLTSLSPGERATLSCRASQSVSSSYLAWYQOKPGQAP 585
QY 503 KLLISYTSRYAGVPRFSGSGVGTDTLTITISSVQAEADAAYPCQQDYNSSP-----TFG 557
Db 586 RLLIYGASTRATGMPRFGSGSGTDTLTITISLREPEDFAVYVCOQ-YGSSQTPOITFG 644
QY 558 GGTGLRIKRAADAPTYISFPPSSEQLTSGASVCFVCLNNFYPKDINVWKIDGSRQNGV 617
Db 645 GGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNS 704
QY 618 LNSWTDQSDKSTYSMSSLTTLTKDYERHNSVTCETHSTSPVKSFNRE 671
Db 705 QESVTEQDSKSTYSLSLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGE 758

RESULT 13
US-11-084-080-18
; Sequence 18, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: HELLENDORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB5-845
US-11-084-080-18

Query Match 35.8%; Score 1260; DB 6; Length 488;
Best Local Similarity 40.6%; Pred. No. 1.2e-49;
Matches 275; Conservative 66; Mismatches 118; Indels 218; Gaps 8;

QY 1 EVOLQSGDPLVKPGASVKISCKASGYFTGYMHVVKQSPGKLEWIGRINPNNGVTLY 60
Db 23 EVOLVSGGELVQPGGSRVISAASGYFTFYGMNVVKQAPGKLEWGMWINTYTGESTY 82
QY 61 NOKFKDKATLVDPKSTTAYMELRSLTSDSAVYYCARSTMITNYMDYWGQSTVTVSS 120
Db 83 ADSFKGRFTFSLDTSASAAYLQINSLRAEDTAVYYCARFAI-----KGDYWGQGTLLTVSS 138
QY 121 AKTPPSVYPLAPGSAQNTNSMWTLCGLVKGYPEPVTVTWNSGSLSSGVHPTPAVLQSD 180
Db 139 ASTKGSVYPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 198
QY 181 -LYTLSSVTVPSSTWPESTVTCNVAHPASSTVDKKIIVPRDGGSGPSEKSEINEKDLRK 239
Db 199 GLYSLSVTVPSSSLGTYICNVNPKSNTKVDKKVEP----- 238
QY 240 KSELOGTALGNLKIYYNYSKAITSSSEKSAQFLTNLTLLFKGFTTGHPPWYNDLLVLDLST 299
Db 239 -----KSCMKYLLPT----- 248

QY 300 AATSEVEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLLHNNRLTEKKVPINLWIDGK 359
Db 249 -----AAAGLLLLAAQP----- 260
QY 360 QTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQKGLIVFHSSEGSTV 419
Db 261 -----AMAHHHH----- 268
QY 420 SYDLFDAQOQYPTDLLRIYRDNTTISSTLSLSLYLYTTSIVMTQPTSLLSVAGDRVTI 479
Db 269 -----HDIQMTQSPSSLSASVGRVTI 290
QY 480 TCKASQSV--SNDVA---WYQKPGQSPKLLISYTSRVRGVPDRFSGSGYGTDFLTITIS 534
Db 291 TCRSTKSLHNSGITYLYWYQKPGKAPKLLIYQMSNLASGVPSRFSSGSGGTDFLTITIS 350
QY 535 SVQAEDAAYVFCQQDYNSSPPTFGGQTKLEIKRAADAPTYISFPPSSEQLTSGGASVCFV 594
Db 351 SLQPEDFATYCAQNLEIPRTFGQTKVELKRTVAAPSVFIFPPSDEQLKSGTASVVCLL 410
QY 595 NNFYPKIDINVWKIDGSRQNGVLNSWTDQSDKSTYSMSSLTTLTKDYERHNSVTCFA 654
Db 411 NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSLTLSKADYERKHVYACEV 470
QY 655 THKTSSTSPVKSFNRE 671
Db 471 THQGLSSPVTKSFNRGE 487

RESULT 14
US-11-084-080-22
; Sequence 22, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: HELLENDORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-NVH-de-bouganin
US-11-084-080-22

Query Match 35.8%; Score 1260; DB 6; Length 750;
Best Local Similarity 40.6%; Pred. No. 1.9e-49;
Matches 275; Conservative 66; Mismatches 118; Indels 218; Gaps 8;

QY 1 EVOLQSGDPLVKPGASVKISCKASGYFTGYMHVVKQSPGKLEWIGRINPNNGVTLY 60
Db 285 EVOLVSGGELVQPGGSRVISAASGYFTFYGMNVVKQAPGKLEWGMWINTYTGESTY 344
QY 61 NOKFKDKATLVDPKSTTAYMELRSLTSDSAVYYCARSTMITNYMDYWGQSTVTVSS 120
Db 345 ADSFKGRFTFSLDTSASAAYLQINSLRAEDTAVYYCARFAI-----KGDYWGQGTLLTVSS 400


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121 AKTTPSVYPLAPGSAQTNSMWTGCLVKGYPPEPVTVTWNSGSLSSSGVHTTFAVLQSD 180
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 401 ASTKGPSVPLAPSSKSTSGTAALGCLVKGYPPEPVTVSMNSGALTSVHTTFAVLQSS 460
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 181 -LYTLSSVTVPSSTWPESTVTCNVNAPASSTKVDKIIIVPRDGGGSEKSEINEKDLRK 239
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 461 GLYSLSSVTVPSSTLGTQYICNVNHPKNTKVDKKEVP- 500
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 240 KSELQGTALGNLQIYYYNKSAITSSSEKSAOFLTNTLLFKGFFTGHPWYNLLVDLGS 299
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 501 - 510
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 300 AATSEYEGSSVDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLTEKKVPINLMIDGK 359
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 511 - 522
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 360 OTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVORGLIVFHSSEGSTV 419
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 523 - 530
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 420 SYDLFDAQGYPTDLLRIYRDNTTISSTLSLSLYLVTTSIVMTQPTPTSLVSAGDRVTI 479
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 531 - 552
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 480 TKASQSV--SNDVA--WYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFLTIS 534
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 553 TCRSTKSLHNSGITYLYWYQKPGKAPKLLIYQMSNLASGVPSRFSSSSGGTDFLTIS 612
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 535 SVQAEADAUVFCODVNSPPTFGGKLEIKRADAAPTIVIPPPSEQLTSGGASVVCFL 594
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 613 SLOPEDFATYCAQNLBIPRTFGGKVELKRTVAAPSVFIPPPSEQLSGTASVVCLL 672
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 595 NNFPYKIDINVKWIDGSRQGVNSMTDODSKDSTYSMSSTLTLTDEYERHNSYTCEA 654
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 673 NNFPYKQVQWVDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEV 732
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 655 THKTSTSPIVKSFNRE 671
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 733 THQGLSSPVTKSFNRGE 749
| | | | | : : : | | | | | : | | | | | : | | | | |

RESULT 15
US-09-807-721-2
; Sequence 2, Application US/09807721
; Patent No. US20020174453A1
; GENERAL INFORMATION:
; APPLICANT: AUBURN UNIVERSITY
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS
; FILE REFERENCE: 1463-PCT-US-00
; CURRENT APPLICATION NUMBER: US/09/807,721
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: PCT/US01/06274
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-721-2
Query Match 35.7%; Score 1257; DB 3; Length 669;
Best Local Similarity 41.6%; Pred. No. 2.3e-49;
Matches 308; Conservative 87; Mismatches 201; Indels 144; Gaps 23;

Qy 2 VQLQQSGPDLVKFGASVKISCKASGYSTGYTHWVKQSPKGLWIGRINPNNGVTLYN 61
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 3 VQLQQSGPDLVKFGASVKISCKASGYSTGYTHWVKQSPKGLWIGRINPNNGVTLYN 62
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 62 QKFKDKATLTVDKSSITAYMELSLTSEDASVYCAT- 121
| | | | | : : : | | | | | : | | | | | : | | | | |
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```
Db 63 QKFKDKATLTVDKSSITAYMELSLTSEDASVYCAT- 115
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 122 KTTPPSVYPLAPGSAQTNSMWTGCLVKGYPPEPVTVTWNSGSLSSSGVHTTFAV--LQ 178
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 116 SPTSFKVFLSLDSTPDQGNV--VACLVOGFFQEPPLSVTWSESGQNVARTARNPPSODAS 174
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 179 SDLYTLSSSVTVPSSTWTP--SETVTCNVNAPASSTKVDKIIIVPRDGGGSEKSEINEKDL 237
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 175 GDLYTTSSQLTLPATCPDGKSVTCHVKHTNSQ--DVTVPCRVPPPP- 224
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 238 RKSELOGTALGNLQIYYYNKSAITSSSEKSAOFLTNTLLFKGFFTGHPWYNLLVDLGS 297
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 225 HPLSLHRLPALEDL- 258
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 298 STAATSEYEGSSV-- 334
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 259 AATTWTPSSGKSAVOGPPERDLGCYSVSSVLPCCAQPNHGETFTCTAAHPELKTPLTA 318
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 335 GVTLHDNNRLTEKKVP- 368
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 319 NITKSGNTFRPEVHLLPPPESEELANLNLVTLTCLARGFSKDVLRVWLOGSQ--ELPREKY 377
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 369 KT--SKKE- 418
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 378 LTWASROEPSGQTTTAVTSILRVAEDMKKG- 424
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 419 VSYDLFDAQGYPTDLLRIYRDNTTISSTLSLSLYL- 471
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 425 FTQKTTIDRLAGKP- 469
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 472 SAGDRVITTCASQSVNSDVANVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 470 SPGEKVTITCSASSMSVY--MHWFOQKPGTSPKMLYSTNSLNSGVPARFSGSGSGTSYSL 528
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 532 TISSVQAEADAUVFCODVNSPPTFGGKLEIKRADAAPTIVIPPPSEQLTSGGASVV 591
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 529 TISMAEADAATYCHQRTSYPTFGGKLEIKRTVAAPSVFIPPPSEQLSGGTASVV 589
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 592 CFLNFPYKIDINVKWIDGSRQGVNSMTDODSKDSTYSMSSTLTLTDEYERHNSYT 651
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 589 CLLNFPYKQVQWVDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYA 648
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 652 CEATHKTSTSPIVKSFNRE 671
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 649 CEVTHQGLSSPVTKSFNRGE 668
| | | | | : : : | | | | | : | | | | | : | | | | |

RESULT 16
US-11-084-080-20
; Sequence 20, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDORF, Koehn
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSCH, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGAINVILLEA PROTEINS, CYTOTOXINS AND METHODS AND USES
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 750
```



```
QY 406 RGLIVFHSSEGSTSVSYDLFDAQOQYPTDLLRIYRDNTTSSLSLSLYTT 458
|||||
Db 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTDLLRIYRDNTTSENHIALYLYTT 233

RESULT 19
US-09-900-766-7
; Sequence 7, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, PER
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0:10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-7

Query Match 31.4%; Score 1107; DB 3; Length 233;
Best Local Similarity 89.7%; Pred. No. 5.3e-43;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLQIYYNYSKAITSEKSDAQFLNTLLFKGFFTG 285
|||||
Db 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
|||||

QY 286 HPWYNLLVDLGSTATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
|||||
Db 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
|||||

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 405
|||||
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 180
|||||

QY 406 RGLIVFHSSEGSTSVSYDLFDAQOQYPTDLLRIYRDNTTSSLSLSLYTT 458
|||||
Db 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTDLLRIYRDNTTSENHIALYLYTT 233

RESULT 20
US-10-283-838-8
; Sequence 8, Application US/10283838
; Publication No. US20030092894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; Johan Hansson, Terje Kalland, Lars
; Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,838
; FILING DATE: 30-Oct-2002
```

```
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692
; FILING DATE: August 12, 1996
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-283-838-8

Query Match 31.4%; Score 1107; DB 4; Length 233;
Best Local Similarity 89.7%; Pred. No. 5.3e-43;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLQIYYNYSKAITSEKSDAQFLNTLLFKGFFTG 285
|||||
Db 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
|||||

QY 286 HPWYNLLVDLGSTATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
|||||
Db 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
|||||

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 405
|||||
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 180
|||||

QY 406 RGLIVFHSSEGSTSVSYDLFDAQOQYPTDLLRIYRDNTTSSLSLSLYTT 458
|||||
Db 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTDLLRIYRDNTTSENHIALYLYTT 233

RESULT 21
US-10-267-682-112
; Sequence 112, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Peteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
```

; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484, 223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
; US-10-267-682-112

Query Match 31.4%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 5.8e-43;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SKSEINEKDKRKSELQGTALGNLKQIYYNYSKAITSEKSDAQFLNTLLFKGFFTG 285
Db 25 SKSEINEKDKRKSELQGNLSNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 406 RGLIVPHSSEGSTSVSYDLFDAQGYPDPTLLRIYRDNNTTSSLSLSLYTT 458
Db 205 RGLIVPHSSEGSTSVSYDLFDAQGYPDPTLLRIYRDNNTTSSLSLSLYTT 257

RESULT 22
US-10-267-748-112
; Sequence 112, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484, 223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
; US-10-267-748-112

Query Match 31.4%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 5.8e-43;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SKSEINEKDKRKSELQGTALGNLKQIYYNYSKAITSEKSDAQFLNTLLFKGFFTG 285
Db 25 SKSEINEKDKRKSELQGNLSNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 406 RGLIVPHSSEGSTSVSYDLFDAQGYPDPTLLRIYRDNNTTSSLSLSLYTT 458
Db 205 RGLIVPHSSEGSTSVSYDLFDAQGYPDPTLLRIYRDNNTTSSLSLSLYTT 257

RESULT 23
US-10-428-817A-188
; Sequence 188, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 188
; LENGTH: 257

```
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-188

Query Match      31.4%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 5.8e-43;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

Qy 226 SEKSEINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLTNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLTNTLLFKGFFTG 84

Qy -286 HPWYNLLVLDLSTAASTSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HPWYNLLVLDLSTAASTSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

Qy 346 EEKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 405
Db 145 EEKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204

Qy 406 RGLIVHSSSGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTT 458
Db 205 RGLIVHSSSGSTVSVDLFDAGQGYPTLLRIYRDNTTINSENHLHIDLYLYTT 257

RESULT 24
US-09-751-708A-16
; Sequence 16, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-16

Query Match      30.4%; Score 1072; DB 3; Length 248;
Best Local Similarity 90.2%; Pred. No. 2.2e-41;
Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

Qy 226 SEKSEINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLTNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLTNTLLFKGFFTG 84

Qy 286 HPWYNLLVLDLSTAASTSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HPWYNLLVLDLSTAASTSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

Qy 346 EEKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 405
Db 145 EEKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204

Qy 406 RGLIVHSSSGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTT 449
Db 205 RGLIVHSSSGSTVSVDLFDAGQGYPTLLRIYRDNTTINSEN 248

RESULT 25
US-09-751-708A-16
; Sequence 16, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
```

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; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-16

Query Match      30.4%; Score 1072; DB 3; Length 248;
Best Local Similarity 90.2%; Pred. No. 2.2e-41;
Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

Qy 226 SEKSEINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLTNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLTNTLLFKGFFTG 84

Qy 286 HPWYNLLVLDLSTAASTSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HPWYNLLVLDLSTAASTSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

Qy 346 EEKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 405
Db 145 EEKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204

Qy 406 RGLIVHSSSGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTT 449
Db 205 RGLIVHSSSGSTVSVDLFDAGQGYPTLLRIYRDNTTINSEN 248

RESULT 26
US-10-428-817A-12
; Sequence 12, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-12

Query Match      30.4%; Score 1072; DB 4; Length 248;
Best Local Similarity 90.2%; Pred. No. 2.2e-41;
Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

Qy 226 SEKSEINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLTNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLTNTLLFKGFFTG 84
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QY 286 HPWYNLLVLDLGGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HPWYNLLVLDLGGKDATNKYKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVPHSSEGSTSVYDLFDAQQGYPTDLLRIYRDNTTISSTSL 449
Db 205 RGLIVPHSSEGSTSVYDLFDAQQGYPTDLLRIYRDNTTINSENL 248

RESULT 27
US-10-937-758A-16
; Sequence 16, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; PRIOR FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-937-758A-16

Query Match 30.4%; Score 1072; DB 5; Length 248;
Best Local Similarity 90.2%; Pred. No. 2.2e-41;
Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELQALGNLKOIYYNSKAITSEKSADQFLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELQALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 286 HPWYNLLVLDLGGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HPWYNLLVLDLGGKDATNKYKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVPHSSEGSTSVYDLFDAQQGYPTDLLRIYRDNTTISSTSL 449
Db 205 RGLIVPHSSEGSTSVYDLFDAQQGYPTDLLRIYRDNTTINSENL 248

RESULT 28
US-10-334-235-38
; Sequence 38, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 532682000920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585

; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of 574Sabl
US-10-334-235-38

Query Match 30.4%; Score 1069; DB 4; Length 600;
Best Local Similarity 37.9%; Pred. No. 6.9e-41;
Matches 254; Conservative 20; Mismatches 60; Indels 336; Gaps 9;
QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60
Db 23 EVLOQSGPDLVKPGASVKISCKASGYSTGYVMHWKQSHGKSLWIGRINPNNGVTLY 82
QY 61 NQKFKDKATLTVDKSSTTAYMELSLTSDSAVYICARSTMITNYVMDYMGQTSVTSS 120
Db 83 NQKFKDKATLTVDKSSTTAYMELSLTSDSAVYICARSTMITNYVMDYMGQTSVTSS 141
QY 121 AKTTPSPVPLAPGAAQNTNSMVTGLCLVKGYFPEPVTVWNSGSLSSGVHTFPAVLQSD 180
Db 142 ----- 141
QY 181 LYTLSSVTVPSSTWPSSEITVCNVAHPASSTKVDKIVIPRDGSGPSEKSEINEKDLRKK 240
Db 142 -----SGG----- 144
QY 241 SELQGTALGNLKOIYYNSKAITSEKSADQFLNTLLFKGFFTGHPWYNLDDLGLSTA 300
Db 145 ----- 144
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db 145 -----GGSGGGT----- 154
QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRLIVPHSSEGSTVS 420
Db 155 -----GG----- 156
QY 421 YDLFDAQQGYPTDLLRIYRDNTTISSTSLISLYLTTISVMTQTPTSLLSAGDRVTIT 480
Db 157 -----SSIVMTQTPTFLLSAGDRVTIT 179
QY 481 CKASQSVSNDAVWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGCYGTDFTLTLSVQAED 540
Db 180 CKASQSVSNDAVWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGCYGTDFTLTLSVQAED 239
QY 541 AAVYFCQDDYNSPPTFGGKTLEIKRADA-APTVSIFPPPSSEQLTSGGASVVCFLANFYP 599
Db 240 LAVYFCQDDYNSPPTFGGKTLEIKRATGKGSVFPPLAPSSKTSKGTGAALGCLVKDYFP 299
QY 600 KDINVKWK-----IDGSEKQGVLSNWTQDQSKDSTYSMSSTLTLTLDKDEYERHNSYTCBAT 655
Db 300 EPTVTSWNSGALTSGVHTFPAVLQSD-----SGLYSLSSVTVTPSSSLGT-QTYICNVN 351
QY 656 HKTSTSPIVK 665
Db 352 HKPSNTKVDK 361

RESULT 29
US-10-742-405-12
; Sequence 12, Application US/10742405
; Publication No. US20040213761A1
; GENERAL INFORMATION:

; APPLICANT: Bowman, Edward P.
; APPLICANT: Chan, Jason R.
; APPLICANT: Moore, Kevin
; APPLICANT: Nguyen, Nhung
; APPLICANT: Churakova, Tatyana
; APPLICANT: Chen, Shi-Juan
; APPLICANT: Cua, Daniel J.
; TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
; FILE REFERENCE: DX01578K
; CURRENT APPLICATION NUMBER: US/10/742,405
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-742-405-12

Query Match 29.6%; Score 1042; DB 4; Length 467;
Best Local Similarity 37.4%; Pred. No. 9.1e-40;
Matches 249; Conservative 57; Mismatches 110; Indels 250; Gaps 14;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYVMHWKQSPGKLEWIGRINPNNGVTL 60
DB 20 QVLOQPGAEVLVPGASGKLSCKASGYSTSYWMNVKQRPQGQLEWIGMIDPLDSETH 79
QY 61 NQFKDKATLTVDKSTTAYMELRSLTSEDYAVYCARSTMTITNYVMDYMGQGSTVTVSS 120
DB 80 NQMFKDKATLTVDKSSSTAYMQLSSLTSEDYAVYCARGD--NYAYMDYMGQGSTVTVSS 137
QY 121 AKTTPSVYPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTFAVLQSD 180
DB 138 AKTTPSVYPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTFAVLQSD 197
QY 181 LYTLSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIVPRDSCGPESEINEKDLRKK 240
DB 198 LYTLSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIVPRDSCG-----240
QY 241 SELQGTALGNLKOIYYNYSKAITSEKSAQDQFLNTLLPKGFTTGHWPYNDLLVDLGSTA 300
DB 241 CKPCICTVPEVSVFIPPK-----PKDVLITIL-----269
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTAQMYGGVTLHDNNRLTBKVKPINLWIDGKQ 360
DB 270 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD---294
QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSPGKVGQRLIVF 411
DB 295 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEK-----348
QY 412 HSSEGSTSVSYDLFDAQCYQPDTLRLIYRDNTTISSTLSISLYLYTTSIVMTQPTSLV 471
DB 349 -----TISK-----353
QY 472 SAGDRVITTCASQSVSNDAVYQKPGOSPKLLISYTSRYAGVDPFRFSGSGYGTDFTL 531
DB 354 -----353
QY 532 TISSVQAEADAAYFCQDYNSTPFGGTGKLEIKRADAAPTIVSIFPPSSQOLTSGGASVV 591
DB 354 -----KGRPKAPQVYTIPTPKKEQMAKDKVSLT 380
QY 592 CFLNPFYKIDNGSERONGVNSWTDODSKDSTYSMSSTLTLTDEYERHNSYT 651
DB 381 CMITDFPEDITVEWMQNGQPAEN--YKNTQPIKDS--DGSYFYVSKLVNQQSNWEAGNTFT 438
QY 652 CEATHK 657
DB 439 CSVLHE 444

RESULT 30

US-09-903-327A-11
; Sequence 11, Application US/09903327A
; Patent No. US2002016433A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Erqiang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
; OTHER INFORMATION: and TNF alpha mature peptide
US-09-903-327A-11

Query Match 29.2%; Score 1028; DB 3; Length 597;
Best Local Similarity 37.2%; Pred. No. 4.9e-39;
Matches 253; Conservative 53; Mismatches 115; Indels 260; Gaps 15;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYVMHWKQSPGKLEWIGRINPNNGVTL 60
DB 20 EVLOQSGPELVKPGASVKISCKASGYTFTDYNMHWKQSHGKSLSEWIGVIYIPKGGTGY 79
QY 61 NQFKDKATLTVDKSTTAYMELRSLTSEDYAVYCARSTMTITNYVMDYMGQGSTVTVSS 120
DB 80 NQFKDKATLTVDSSNTAYMELRSLTSDASAVYCARG-----IAYMGQGLTVTVA 132
QY 121 AKTTPSVYPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTFAVLQSD 180
DB 133 AKTTPSVYPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTFAVLQSD 192
QY 181 LYTLSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIVPRDSCGPESEINEKDLRKK 240
DB 193 LYTLSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIVPRDSCG-----235
QY 241 SELQGTALGNLKOIYYNYSKAITSEKSAQDQFLNTLLPKGFTTGHWPYNDLLVDLGSTA 300
DB 236 CKPCICTVPEVSVFIPPK-----PKDVLITIL-----264
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTAQMYGGVTLHDNNRLTBKVKPINLWIDGKQ 360
DB 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD---289
QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSPGKVGQRLIVF 411
DB 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEK-----343
QY 412 HSSEGSTSVSYDLFDAQCYQPDTLRLIYRDNTTISSTLSISLYLYTTSIVMTQPTSLV 471
DB 344 -----TISK-----348
QY 472 SAGDRVITTCASQSVSNDAVYQKPGOSPKLLISYTSRYAGVDPFRFSGSGYGTDFTL 531
DB 349 -----348
QY 532 TISSVQAEADAAYFCQDYNSTPFGGTGKLEIKRADAAPTIVSIFPPSSQOLTSGGASVV 591
DB 349 -----KGRPKAPQVYTIPTPKKEQMAKDKVSLT 375
QY 592 CFLNPFYKIDNGSERONGVNSWTDODSKDSTYSMSSTLTLTDEYERHNSYT 651
DB 376 CMITDFPEDITVEWMQNGQPAEN--YKNTQPIKDS--DGSYFYVSKLVNQQSNWEAGNTFI 433

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QY 652 CEATHKTSPIVKSFNRNES 672
Db 434 CSVLHE-----FVRSSTRPS 449

RESULT 31
US-10-216-484-9
; Sequence 9, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 9
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-216-484-9

Query Match 29.1%; Score 1025.5; DB 4; Length 464;
Best Local Similarity 36.2%; Pred. No. 5e-39;
Matches 243; Conservative 64; Mismatches 106; Indels 259; Gaps 14;

QY 1 EVLOQSGDPLVKPGASVKISCKASYSTGYMHVVKQSPKGLIEWIGRINPNNGVTLY 60
Db 20 QVLOQPGAEVLKPGASVKLSCKASYTFTSYMQVWKQRPQGLEWIGRIDPSDSYTN 79

QY 61 NQKFKDKATLVDKSSTAYMELRSITSEDSAVYYCARS-TWITNYVMYWGQTSVTVS 119
Db 80 NQKFKGKATLVDTSSSTAYMQLSSLTSEDSAVYYCARNRDYSNNWYFDVWGTTTVTS 139

QY 120 SAKTTPPSVYPLAPGSAQTNSMVTLGCLVKGYFPEPPTVTWNSGLSSGVHTFPVAVLS 179
Db 140 SAKTTPPSVYPLAPGSAQTNSMVTLGCLVKGYFPEPPTVTWNSGLSSGVHTFPVAVLS 199

QY 180 DLYTLSSSVTVPSSTWPSQVTCNVAHPASSTKVDKKIIVPRDSGGPSEKSEINEKDLRK 239
Db 200 DLYTLSSSVTVPSSTWPSQVTCNVAHPASSTKVDKKIIVPRDCG----- 243

QY 240 KSELOQTALGNLKQIYYYNKSKAITSEKSAQDLFTNLLFKGFTGHPWYNLDDLGLST 299
Db 244 -CKPCICTVPESSVVFPPK-----PKDVLTTTL----- 272

QY 300 AATSEVEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGK 359
Db 273 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD-- 297

QY 360 QTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVGQRLIV 410
Db 298 --DVEVHTAQTPREEQFNSTFRSVSELPIMHQNLNGKEFKCRVNSAAPPAPIEK---- 351

QY 411 FHSSEGSVSYDLFDAQGOVPTDLLRIYRDNTTISSTLSISLYLTYTTSIVMTQTPTSL 470
Db 352 -----TISKT----- 356

QY 471 VSAGDRVTITCKASQSVSNDVAMVYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDTFT 530
Db 357 ----- 356

QY 531 LTISSVQABDAAYFCQDYNPPTFGGKTKLBKIRADAAPTIVSIFPPSSEQITSGGASV 590
Db 357 -----KGRPKAPQVYTIPTPPKEQMAKDKVSL 382
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QY 591 VCFLANFYPKDINVKWKIDGSRQN-----GVLNSWTDQSDKDYTSMSSTLTLTKEYE 645
Db 383 TCMTIDTFPDEDITVEWMQNGQPAENYKNTQPIMNT-----NGSYFVYSKLVNQSKEW 435

QY 646 RHNSYTCEATHK 657
Db 436 AGNTFTCSVLHE 447

RESULT 32
US-10-384-933-9
; Sequence 9, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 9
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-384-933-9

Query Match 29.1%; Score 1025.5; DB 4; Length 464;
Best Local Similarity 36.2%; Pred. No. 5e-39;
Matches 243; Conservative 64; Mismatches 106; Indels 259; Gaps 14;

QY 1 EVLOQSGDPLVKPGASVKISCKASYSTGYMHVVKQSPKGLIEWIGRINPNNGVTLY 60
Db 20 QVLOQPGAEVLKPGASVKLSCKASYTFTSYMQVWKQRPQGLEWIGRIDPSDSYTN 79

QY 61 NQKFKDKATLVDKSSTAYMELRSITSEDSAVYYCARS-TWITNYVMYWGQTSVTVS 119
Db 80 NQKFKGKATLVDTSSSTAYMQLSSLTSEDSAVYYCARNRDYSNNWYFDVWGTTTVTS 139

QY 120 SAKTTPPSVYPLAPGSAQTNSMVTLGCLVKGYFPEPPTVTWNSGLSSGVHTFPVAVLS 179
Db 140 SAKTTPPSVYPLAPGSAQTNSMVTLGCLVKGYFPEPPTVTWNSGLSSGVHTFPVAVLS 199

QY 180 DLYTLSSSVTVPSSTWPSQVTCNVAHPASSTKVDKKIIVPRDSGGPSEKSEINEKDLRK 239
Db 200 DLYTLSSSVTVPSSTWPSQVTCNVAHPASSTKVDKKIIVPRDCG----- 243

QY 240 KSELOQTALGNLKQIYYYNKSKAITSEKSAQDLFTNLLFKGFTGHPWYNLDDLGLST 299
Db 244 -CKPCICTVPESSVVFPPK-----PKDVLTTTL----- 272

QY 300 AATSEVEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGK 359
Db 273 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD-- 297

QY 360 QTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVGQRLIV 410
Db 298 --DVEVHTAQTPREEQFNSTFRSVSELPIMHQNLNGKEFKCRVNSAAPPAPIEK---- 351

QY 411 FHSSEGSVSYDLFDAQGOVPTDLLRIYRDNTTISSTLSISLYLTYTTSIVMTQTPTSL 470
Db 352 -----TISKT----- 356

QY 471 VSAGDRVTITCKASQSVSNDVAMVYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDTFT 530
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Db 357 ----- 356
QY 531 LTISSVQAEAAVYFCQDYNSTPFTGGGKLEIKRADAAPTYSIFPPSSQELTSGASV 590
Db 357 -----KGRPKAPQVYTIIPPKQAKDKVSL 382
QY 591 VCLNNFPKIDINVKKIDGSRQN-----GVLSNWTQDSKDSYMSSTLTLTDEYE 645
Db 383 TCMTIDFPEDITVEMQWQPAENYKNTQPIWNT-----NGSYFVYSKLVNQSWE 435
QY 646 RHNSYTCETHK 657
Db 436 AGNTFTCSVLHE 447
RESULT 33
US-09-903-327A-14
; Sequence 14, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Erguang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
; OTHER INFORMATION: and SCF mature peptide
US-09-903-327A-14
Query Match 29.1%; Score 1024.5; DB 3; Length 613;
Best Local Similarity 37.3%; Pred. No. 7.3e-39;
Matches 250; Conservative 51; Mismatches 115; Indels 255; Gaps 14;
QY 1 EVLOQSGDPLVKPGASVKISCKASGYFTGYMHVWKQSPGKGLWIGRINPNNGVTLY 60
Db 20 EVLOQSGDPLVKPGASVKISCKASGYFTGYMHVWKQSPGKGLWIGRINPNNGVTLY 60
61 NQKFKDKATLTVDKSSSTAYMELSLTSDSAVYYCARSTMITYVMDYWGQTSVTSS 120
Db 80 NQKFKSKATLTVDSSNTAYMELSLTSDSAVYYCARG-----IAYWQGGTLVTVA 132
QY 121 AKTTPPSVYPLAPGSAQAQNSMTVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
Db 133 AKTTPPSVYPLAPGSAQAQNSMTVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTTTPAVLQSD 192
QY 181 LYTLSSTVTPSSVTPSWSETVTCNVAHPASSTKVDKIKVPRDSGSPSEKSEINEKDLRKK 240
Db 193 LYTLSSTVTPSSVTPSWSETVTCNVAHPASSTKVDKIKVPRDCG----- 235
QY 241 SELQGTALGNLKOIYYNSKAITSEKSDAQFLTNTLLFKGFTGHPWYNLLVDLGSTA 300
Db 236 CKFCICTVPEVSSVFIPPK-----PKDVLITL----- 264
QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHVLHGK-FGL-YNSDSGFGKVQRGILVF 411
Db 290 -DVEVHTAQTPREEQNFSTRSVELPIMHQDWLNGKEFKCRVNSAAPPAPIEK----- 343

QY 412 HSESGTYSYDLFDAQGGYPTDLLRIYRDNNTTISSTLSLSLYLYTTSIVMTQPTSLLV 471
Db 344 -----TISK----- 348
QY 472 SAGDRVITITKASQSVSNDAVYQQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
Db 349 ----- 348
QY 532 TISSVQAEAAVYFCQDYNSTPFTGGGKLEIKRADAAPTYSIFPPSSQELTSGASV 591
Db 349 -----KGRPKAPQVYTIIPPKQAKDKVSLT 375
QY 592 CFLNNFPKIDINVKKIDGSRONGVLSNWTQDSKDSYMSSTLTLTDEYERHNSYT 651
Db 376 CMITDFFPEDITVEMQWQPAEN-YKNTQPIWNT-DGSYFVYSKLVNQSWEAGNTFI 433
QY 652 CEATHKSTSP 662
Db 434 CSVLHEFCRYP 444
RESULT 34
US-09-903-327A-2
; Sequence 2, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Erguang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: DAV-1 heavy chain, penton base monoclonal antibody
US-09-903-327A-2
Query Match 29.1%; Score 1023.5; DB 3; Length 456;
Best Local Similarity 37.4%; Pred. No. 6.1e-39;
Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;
QY 1 EVLOQSGDPLVKPGASVKISCKASGYFTGYMHVWKQSPGKGLWIGRINPNNGVTLY 60
Db 20 EVLOQSGDPLVKPGASVKISCKASGYFTGYMHVWKQSPGKGLWIGRINPNNGVTLY 60
61 NQKFKDKATLTVDKSSSTAYMELSLTSDSAVYYCARSTMITYVMDYWGQTSVTSS 120
Db 80 NQKFKSKATLTVDSSNTAYMELSLTSDSAVYYCARG-----IAYWQGGTLVTVA 132
QY 121 AKTTPPSVYPLAPGSAQAQNSMTVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
Db 133 AKTTPPSVYPLAPGSAQAQNSMTVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTTTPAVLQSD 192
QY 181 LYTLSSTVTPSSVTPSWSETVTCNVAHPASSTKVDKIKVPRDSGSPSEKSEINEKDLRKK 240
Db 193 LYTLSSTVTPSSVTPSWSETVTCNVAHPASSTKVDKIKVPRDCG----- 235
QY 241 SELQGTALGNLKOIYYNSKAITSEKSDAQFLTNTLLFKGFTGHPWYNLLVDLGSTA 300
Db 236 CKFCICTVPEVSSVFIPPK-----PKDVLITL----- 264
QY 301 ATSEYEGSSVDLYGAYYQACAGTGNKTAACMGVGTGTLHNNRLTEKKVPINLWDGKQ 360

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Db 265 -----TP-KVTCVVVDIS-----KDDPEVQSFWD--- 289
Qy 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQORGLIYF 411
Db 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAPIEK----- 343
Qy 412 HSEGSTVSVDLFDAGQGYPDTLRLIYRDNTHISSTLSLSISLYLYTTSIWMQTPTSLLV 471
Db 344 -----TISK----- 348
Qy 472 SAGDRVITICKASQSVNDVAVYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
Db 349 ----- 348
Qy 532 TISSVQAEDAAYVFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVV 591
Db 349 -----KGRPKAPQVYTIPTPPKEQMAKDKVSLT 375
Qy 592 CFLNFPYPKDINVKKIDGSRQNGVLNSWTDDSDKSTYSMSSTLTLTKDEYERHNSYT 651
Db 434 CSVLHE 439
Qy 376 CMITDFPEDITVEWQNGQPAEN-YKNTQPIMDT-DGSYFYVYSKLVNOKSNWEAGNTFI 433
Qy 652 CEATHK 657
Db 434 CSVLHE 439

RESULT 35
US-09-903-327A-13
; Sequence 13, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
; OTHER INFORMATION: and EGF mature peptide
US-09-903-327A-13

Query Match 29.1%; Score 1023.5; DB 3; Length 493;
Best Local Similarity 37.4%; Pred. No. 6.6e-39;
Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;

Qy 1 EVLOQSGDPLVKPGASVKISKASGYFTGYIMHWVKQSPGKLEWIGRIINPNNGVTLY 60
Db 20 EVLOQSGPELVKPGASVKISKASGYFTDYNMHWVKQSHGKSLWIGYIYPKGGTGY 79
Qy 61 NQKFKDKATLVTDKSTTAYMELRSLTSDSAVYICARSTMTITNYMDYWGQGTSTVTVSS 120
Db 80 NQKFKSKATLTTDSSNTAYMELRSLTSDSAVYICARG-----IAYWQQTLLTVSA 132
Qy 121 AKTTPPSVPLAPGSAQTNSMTVLGCLVKGYPEPEPTVTWNVSGSLSSGGVHTFPVQLQSD 180
Db 133 AKTTPSVPLAPGSAQTNSMTVLGCLVKGYPEPEPTVTWNVSGSLSSGGVHTFPVQLQSD 192
Qy 181 LYTSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKIVPRDSDGGPSEKSEETNEKDLRKK 240
Db 193 LYTSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKIVPRDCG----- 235
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Qy 241 SELOQTALGNLKOIYYNNSKAITSSSEKSADQLTTLTKGFFTGHPWYNLLVDLGSTA 300
Db 236 CRPKCTVPESSSVFIFFPK-----PKVLTITL----- 264
Qy 301 ATSEYEGSSVDLYGAYYGYQCAGGTPTNKTACMYGGVTLHDNNRLTBEKKVPINLWIDGKQ 360
Db 265 -----TP-KVTCVVVDIS-----KDDPEVQSFWD--- 289
Qy 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQORGLIYF 411
Db 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAPIEK----- 343
Qy 412 HSEGSTVSVDLFDAGQGYPDTLRLIYRDNTHISSTLSLSISLYLYTTSIWMQTPTSLLV 471
Db 344 -----TISK----- 348
Qy 472 SAGDRVITICKASQSVNDVAVYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
Db 349 ----- 348
Qy 532 TISSVQAEDAAYVFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVV 591
Db 349 -----KGRPKAPQVYTIPTPPKEQMAKDKVSLT 375
Qy 592 CFLNFPYPKDINVKKIDGSRQNGVLNSWTDDSDKSTYSMSSTLTLTKDEYERHNSYT 651
Db 376 CMITDFPEDITVEWQNGQPAEN-YKNTQPIMDT-DGSYFYVYSKLVNOKSNWEAGNTFI 433
Qy 652 CEATHK 657
Db 434 CSVLHE 439

RESULT 36
US-09-903-327A-12
; Sequence 12, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
; OTHER INFORMATION: and IGF-1 mature peptide
US-09-903-327A-12

Query Match 29.1%; Score 1023.5; DB 3; Length 510;
Best Local Similarity 37.4%; Pred. No. 6.8e-39;
Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;

Qy 1 EVLOQSGDPLVKPGASVKISKASGYFTGYIMHWVKQSPGKLEWIGRIINPNNGVTLY 60
Db 20 EVLOQSGPELVKPGASVKISKASGYFTDYNMHWVKQSHGKSLWIGYIYPKGGTGY 79
Qy 61 NQKFKDKATLVTDKSTTAYMELRSLTSDSAVYICARSTMTITNYMDYWGQGTSTVTVSS 120
Db 80 NQKFKSKATLTTDSSNTAYMELRSLTSDSAVYICARG-----IAYWQQTLLTVSA 132
Qy 121 AKTTPPSVPLAPGSAQTNSMTVLGCLVKGYPEPEPTVTWNVSGSLSSGGVHTFPVQLQSD 180
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Db 133 AKTTPSVPLAPGSAQTNSMTLGLVKGYFPFVTVWNSGSLSSGVHTFPAVLQSD 192
Qy 181 LYTLSSTVTPSSTWSEVTCNVHPASSTKVDKIVPRDSDGPGSEKSEINEKDLRKK 240
Db 193 LYTLSSTVTPSSTWSEVTCNVHPASSTKVDKIVPRDSDGPGSEKSEINEKDLRKK 235
Qy 241 SELQGTALGNLKOIYYNSKAITSSSEKADQFTLTLFKGFTGHPWYNLDLVLGSTA 300
Db 236 CKPCICTVPEVSSVFIFPPK-----PKDVLITL----- 264
Qy 301 ATSEYEGSSVDLYGAYGYOCAGGTNKTACMYGGVTLHNNRLTBKPKVPINLWDGKQ 360
Db 265 -----TP-KVTCVVVDIS-----KODPEVQFSWFVD--- 289
Qy 361 TTVPIDKVTSKKEV-----TVQELDLQARHLYHGK-FGL-YNDSDFGKVGQGLIVF 411
Db 290 -DVEHTAQTPREQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPAPIEK----- 343
Qy 412 HSSEGSTVSYDLFDAQGYPTLLRIYRDNTTSSLSISLYLYTTSIVMTQPTSLLV 471
Db 344 -----TISK----- 348
Qy 472 SAGDRVTITCKASQSVNSDVAMVYQKPGQPKLLISYTSRYAGVDPFRSGSGYGTDFTL 531
Db 349 ----- 348
Qy 532 TISSVQAEADAAYFCQDYNPSPTFGGTYKLEIKRADAAPTIVSIFPPSSBOLTSGGASVV 591
Db 349 -----KGRPKAPQVYTIPPPKEQMAKDKVSLT 375
Qy 592 CFLNFPYPKDINVKKIDSERQNGVLSNWTODSDKSTYSMSLTTLTKDEYERHNSYT 651
Db 376 CMITDFPEPDIIVEMQWNGQPAEN-YKNTQPIMDT-DGSYFVYKLVNOKSNWEAGNTFI 433
Qy 652 CEATHK 657
Db 434 CSVLHE 439
RESULT 37
US-09-903-327A-6
; Sequence 6, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Erluang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: Portion of DAV-1 heavy chain used for fusion protein
; OTHER INFORMATION: bifunctional antibody
US-09-903-327A-6
Query Match 29.0%; Score 1022.5; DB 3; Length 438;
Best Local Similarity 37.4%; Pred. No. 6.5e-39;
Matches 249; Conservative 111; Mismatches 111; Indels 255; Gaps 14;
Qy 1 EVQLQSGDPLVPGASVKISKASGYFTGYIMHWYKQSPGKLEWIGRINPNNGVTLY 60
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Db 20 EVQLQSGDPLVPGASVKISKASGYFTGYIMHWYKQSHGKSLSEWIGYIYPKGTGY 79
Qy 61 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYCARSTMTIYNYVDYMGQGTSTVTSS 120
Db 80 NQKFKSKATLTVDKSTTAYMELRSLTSDSAVYCARSTMTIYNYVDYMGQGTSTVTSS 132
Qy 121 AKTTPSVPLAPGSAQTNSMTLGLVKGYFPFVTVWNSGSLSSGVHTFPAVLQSD 180
Db 133 AKTTPSVPLAPGSAQTNSMTLGLVKGYFPFVTVWNSGSLSSGVHTFPAVLQSD 192
Qy 181 LYTLSSTVTPSSTWSEVTCNVHPASSTKVDKIVPRDSDGPGSEKSEINEKDLRKK 240
Db 193 LYTLSSTVTPSSTWSEVTCNVHPASSTKVDKIVPRDSDGPGSEKSEINEKDLRKK 235
Qy 241 SELQGTALGNLKOIYYNSKAITSSSEKADQFTLTLFKGFTGHPWYNLDLVLGSTA 300
Db 236 CKPCICTVPEVSSVFIFPPK-----PKDVLITL----- 264
Qy 301 ATSEYEGSSVDLYGAYGYOCAGGTNKTACMYGGVTLHNNRLTBKPKVPINLWDGKQ 360
Db 265 -----TP-KVTCVVVDIS-----KODPEVQFSWFVD--- 289
Qy 361 TTVPIDKVTSKKEV-----TVQELDLQARHLYHGK-FGL-YNDSDFGKVGQGLIVF 411
Db 290 -DVEHTAQTPREQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPAPIEK----- 343
Qy 412 HSSEGSTVSYDLFDAQGYPTLLRIYRDNTTSSLSISLYLYTTSIVMTQPTSLLV 471
Db 344 -----TISK----- 348
Qy 472 SAGDRVTITCKASQSVNSDVAMVYQKPGQPKLLISYTSRYAGVDPFRSGSGYGTDFTL 531
Db 349 ----- 348
Qy 532 TISSVQAEADAAYFCQDYNPSPTFGGTYKLEIKRADAAPTIVSIFPPSSBOLTSGGASVV 591
Db 349 -----KGRPKAPQVYTIPPPKEQMAKDKVSLT 375
Qy 592 CFLNFPYPKDINVKKIDSERQNGVLSNWTODSDKSTYSMSLTTLTKDEYERHNSYT 651
Db 376 CMITDFPEPDIIVEMQWNGQPAEN-YKNTQPIMDT-DGSYFVYKLVNOKSNWEAGNTFI 433
Qy 652 CEATHK 656
Db 434 CSVLH 438
RESULT 38
US-10-679-620-94
; Sequence 94, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reini, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94
; LENGTH: 700
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBC1773, see Example 14
US-10-679-620-94
Query Match 28.4%; Score 1000; DB 4; Length 700;
```



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; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
; US-10-071-485-90

Query Match      27.8%; Score 980.5; DB 4; Length 711;
Best Local Similarity 35.3%; Pred. No. 8.3e-37;
Matches 254; Conservative 103; Mismatches 180; Indels 183; Gaps 23;

QY 1 EVLOQSGDPLVKPGASVKISKASGYSTGYIMHWKQSPGKGLGWIGRINPNNGVTLY 60
Db 21 QVQLVQSGSELKPGASVKISKASGYTFTDYGMNVKQAPOGQGLKMMGWINTYTGESTY 80
QY 61 NQPKDKATLTVDKSSITTAAMELSLTSDSAVYICARSTMTITNYVDYWGQGTSTVTS 120
Db 81 VDDFKGRFVFLSDTSVAAYLQISSLKAEADTATYFCARRGF---YANDYWGQGTSTVTS 137
QY 121 AKTTPSVPLAPGSAQTNSMTVLGCLVKGYPEPTVTWNSGSLSSGVHTTTPAVLQSD 180
Db 138 ASTKGSVPLAPSSKSTSGTAAALGCLVKDYPEPTVTWNSGALTSGVHTTTPAVLQSS 197
QY 181 -LYTSSSVTPSSTWSPSETVTCNVAHPASTKVDKKIIPRDS-----GG 224
Db 198 GLYSLSVTPSSSLGTQTYICNVNHPKSNTKVDKRVPEKSCDKTHCTPCPAPELLGG 257
QY 225 PS-----EKSEI-----NEKDLRKKSELOGTALGNLK---QIYYN 258
Db 258 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPRBEQYN 317
QY 259 S-----KAITSS-EK-----SADQ 271
Db 318 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPASIETISKAKGQPREPOVYTLPPSREE 377
QY 272 FLTN-----TLLPKGFTGHPWYNDLLVDLGSTA-ATSEYEGSS--VDLYGAYGYQCAGG 324
Db 378 MTKNQVSLTCLVKGFYP-----SDIAVEWESNGOPENNYKTTTPVLDSDGSGFLYSKL-- 430
QY 325 TPNTKATCMYGGV-----TLHD--NNRLTEEK-----KVPINLWIDCKQTTPIDKY 368
Db 431 TVDKSRWQQGNVPSFCVSMHEALHNYTKQSLSLSPGKLGSGSQVLVQSGSELKPGASV 490
QY 369 KTSKKEVTVQELDLQARHYLHGKFGLYNSDFGKVGQRLIVFHSSEGSVSYDLPDAQ 428
Db 491 KISCK-----ASGYTFTDYGMNVKQAPOGQGLKMMGWINTYTGESTYVD--DFKG 538
QY 429 QYPTDLLRIYRDNTTISSTSLIS-----LYLYT----- 457
Db 539 RF-----VPSLDTSVSAAYLQISSLKAEADTATYFCARRGFYANDYWGQGTSTVTS 592
QY 458 -----TSIVMTQPTSLLSAGDRVTTICKASQSVNDVAHYQKPGQSPKLLI 506
Db 593 GSGGGSGGGGSDIVLTQSPATMSAEPGERVLTCTCSASSISY-MFWYHQPQSGSPRLI 651
QY 507 SYTSSRYAGVDPDRFSGSGYGTDFLTATISSVQAEDAAVYFCQQDYNSPPTFGGQTKLEIKR 566
Db 652 YDTSNLSAGVPAFPFGSGSGTSLTISRMEPEDFATYFCHQSSSYPTFGQGTKEIKR 711

RESULT 41
US-10-985-581-90
; Sequence 90, Application US/10985581
; Publication No. US20050129693A1
; GENERAL INFORMATION:
; APPLICANT: Buysee, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: 11362.0015.DVUS02
; CURRENT APPLICATION NUMBER: US/10/985,581
; CURRENT FILING DATE: 2004-11-10
```

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RESULT 42
US-10-410-907A-36
; Sequence 36, Application US/10410907A
; Publication No. US20030215880A1
; GENERAL INFORMATION:
; APPLICANT: Dennis R. Burton
; APPLICANT: R. Anthony Williamson
; APPLICANT: Gianluca Moroncini
; TITLE OF INVENTION: MOTIF-GRAFTED HYBRID POLYPEPTIDES AND
; TITLE OF INVENTION: US$ THEREOF
; FILE REFERENCE: 22908-1229
; CURRENT APPLICATION NUMBER: US/10/410,907A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/371,610
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D18 Heavy Chain
US-10-410-907A-36

Query Match      27.8%; Score 979.5; DB 4; Length 223;
Best Local Similarity 87.4%; Pred. No. 3.1e-37;
Matches 194; Conservative 7; Mismatches 16; Indels 5; Gaps 2;

QY 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHVWVKQSPGKGLIEWIGRINPNNGVTL 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 EVQLLEQSGPELVKPGSSVKISKASRYFTDNDMDVVKQSHKRLIEWIGYIPNTGV 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 YNQKFKDKATLTVDKSGSTTAYMELRLTSDSDSAVYYCARSTMITNYMDYWGQTSVT 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 YNQRFKGKATLTVDKSSSTAYMELRLTSDSDSAVYYCAG----FYGYMDYWGQTSVT 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 SAKTTPPSVYVPLAPGSAQTNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQS 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 SAKTTPPSVYVPLAPGSAQTNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQY 178
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 DLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKKIIVPRD 221
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 179 DLYTMSSTVTVPSSTWPSSETVTCNVAHPASSTKVDKKIIVPRD 220
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 43
US-10-334-235-37
; Sequence 37, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingsman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingsman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 532682000920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 243

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mature secreted protein of 574 scFv, designated
; OTHER INFORMATION: 5T4scFv.1
US-10-334-235-37

Query Match      27.6%; Score 972.5; DB 4; Length 243;
Best Local Similarity 40.1%; Pred. No. 6.9e-37;
Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHVWVKQSPGKGLIEWIGRINPNNGV 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHVWVKQSHGSKLEWIGRINPNNGV 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NQKPKDKATLTVDKSGSTTAYMELRLTSDSDSAVYYCARSTMITNYMDYWGQTSVT 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFKDKATLTVDKSGSTTAYMELRLTSDSDSAVYYCARSTMITNYMDYWGQTSVT 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 AKTTPPSVYVPLAPGSAQTNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 -----
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 LYTLSSTVTVPSSTWPSSETVTCNVAHPASSTKVDKKIIVPRDGGPSEKSEINEKOLRK 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 -----SGG-----
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 SELQGTALGNLKQIYYNSKAITSEKSDAQFLTNLLFKGFTGHPWYNDLLVDLGSTA 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 -----
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 ATSEYEGSSVDLYGAYGYQCAGTGNKTACVMYGGVTLHDNNRLTBEKKVPINLWIDGK 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 -----GGGGGGT-----
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVKORGLIVFHSSEGSTVS 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 133 -----GG-----
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 YDLFDAQQGYPTLLRIYRDNTTISTSLISLYLTTSIVMTQTPTSLVSGADRVTTIT 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 135 -----SSIVMTQTPTSLVSGADRVTTIT 157
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 CKASQSVNDVAWYQKPGQSPKLLISYTSRSYAGVDPDRFSGSGYGTDTFTLTISVQAE 540
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 158 CKASQSVNDVAWYQKPGQSPKLLISYTSRSYAGVDPDRFSGSGYGTDTFTLTISLQAE 217
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 541 AAVYFCQQDYNSPPTFGGQTKLEIKR 566
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 218 LAVYFCQQDYNSPPTFGGQTKLEIKR 243
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 44
US-10-334-235-39
; Sequence 39, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingsman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingsman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 532682000920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
```

; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of B7-1.5T4.1
US-10-334-235-39

Query Match 27.5%; Score 967.5; DB 4; Length 488;
Best Local Similarity 40.0%; Pred. No. 2.3e-36;
Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;
QY 1 EVOLQSGPDLVPGASVKISCKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
Db |||||
QY 247 EVOLQSGPDLVPGASVKISCKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 306
Db |||||
QY 61 NQKFKDKATLTVDKSSTTAYMELRSLTSDSAVYICARSTMTITNYVMDYWGQTSVTSS 120
Db |||||
QY 307 NQKFKDKATLTVDKSSTTAYMELRSLTSDSAVYICARSTMTITNYVMDYWGQTSVTSS 365
Db |||||
QY 121 AKTTPPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTTTPAVLQSD 180
Db -----
QY 366 ----- 365
QY 181 LYTLSSSVTPSPSTWSEPTVCNVAHPASSTKVDKVIIPRDSGGPSEKSEINEKDLRKK 240
Db |||||
QY 366 -----SGG----- 368
QY 241 SELQGTALGNLKOIYYNSKAITSEKSDAQFLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db -----
QY 369 ----- 368
QY 301 ATSEYEGSSVDLYGAYGYQCAGTGNKTAQMWGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db |||||
QY 369 -----GGSGGGT----- 378
QY 361 TTVPIDKVTSSKEVTVQELDLQARHVLHGKFLGYNLSDSFGKVGQRLIVFHSSEGSTVS 420
Db |||||
QY 379 -----GG----- 380
QY 421 YDLFDAQGVPTDLLRIYRDNTTISSTLSLSLYLTTSIVMTQTPTSLVLSAGDRVTIT 480
Db :|||||
QY 381 -----SSIVMTQTPTFLVLSAGDRVTIT 403
QY 481 CKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGGYGTDFTLTITSSVOAED 540
Db |||||
QY 404 CKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGGYGTDFTLTITSSVOAED 463
Db |||||
QY 541 AAVYFCQDYNPSPTFGGKLEIK 565
Db |||||
QY 464 LAVYFCQDYNPSPTFGGKLEIK 488
Db |||||

RESULT 45

US-10-473-127-1954
; Sequence 1954, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 1954
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1954

Query Match 27.5%; Score 967.5; DB 5; Length 488;
Best Local Similarity 40.0%; Pred. No. 2.3e-36;
Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;
QY 1 EVOLQSGPDLVPGASVKISCKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
Db |||||
QY 247 EVOLQSGPDLVPGASVKISCKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 306
Db |||||
QY 61 NQKFKDKATLTVDKSSTTAYMELRSLTSDSAVYICARSTMTITNYVMDYWGQTSVTSS 120
Db |||||
QY 307 NQKFKDKATLTVDKSSTTAYMELRSLTSDSAVYICARSTMTITNYVMDYWGQTSVTSS 365
Db |||||
QY 121 AKTTPPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTTTPAVLQSD 180
Db -----
QY 366 ----- 365
QY 181 LYTLSSSVTPSPSTWSEPTVCNVAHPASSTKVDKVIIPRDSGGPSEKSEINEKDLRKK 240
Db |||||
QY 366 -----SGG----- 368
QY 241 SELQGTALGNLKOIYYNSKAITSEKSDAQFLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db -----
QY 369 ----- 368
QY 301 ATSEYEGSSVDLYGAYGYQCAGTGNKTAQMWGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db |||||
QY 369 -----GGSGGGT----- 378
QY 361 TTVPIDKVTSSKEVTVQELDLQARHVLHGKFLGYNLSDSFGKVGQRLIVFHSSEGSTVS 420
Db |||||
QY 379 -----GG----- 380
QY 421 YDLFDAQGVPTDLLRIYRDNTTISSTLSLSLYLTTSIVMTQTPTSLVLSAGDRVTIT 480
Db :|||||
QY 381 -----SSIVMTQTPTFLVLSAGDRVTIT 403
QY 481 CKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGGYGTDFTLTITSSVOAED 540
Db |||||
QY 404 CKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGGYGTDFTLTITSSVOAED 463
Db |||||
QY 541 AAVYFCQDYNPSPTFGGKLEIK 565
Db |||||
QY 464 LAVYFCQDYNPSPTFGGKLEIK 488
Db |||||

RESULT 46

US-10-473-127-1963
; Sequence 1963, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21

```
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1963
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1963

Query Match      27.5%; Score 967.5; DB 5; Length 488;
Best Local Similarity 40.0%; Pred. No. 2.3e-36;
Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRINPNNGVTLY 60
DB EVLOQSGDPLVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRINPNNGVTLY 306
QY 61 NQKFKDKATLTVDKSTTAYMELRLSLTSDSAVYYCARSTMTITNYMDYWGQTSVTSS 120
DB 307 NQKFKDKATLTVDKSTTAYMELRLSLTSDSAVYYCARSTMTITNYMDYWGQTSVTSS- 365
QY 121 AKTTTPSVVPLAPGSAQAQNSMVTGLCLVKGYFPEPVTTVWNSGSLSSGVHTFPAVLQSD 180
DB 366 -----
QY 181 LYTSSSVTPSPSTWPESETVTCNVAHPASSTKVDKIIIPRDGGPSEKSEINEKDLRKK 240
DB 366 -----
QY 241 SELQGTALGNLKIYYNYSKAITSEKSAQDLTNTLLFKGPTGHPWYNLLVDLGSTA 300
DB 369 -----
QY 301 ATSEYEGSDVLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTBEKKVPINLMIDGKQ 360
DB 369 -----
QY 361 TTVPIDKVTSKKEVTVQELDLQARHYLHGKPGCLYNSDFSGKVGKQLIVFHSSEGSTVS 420
DB 379 -----
QY 421 YDLFDAQGGYPTDLLRIYRDNNTTISSTLSLSLYLTTISVMTQTPTSLLSAGDRVTIT 480
DB 381 -----
QY 481 CKASQSVNDVAMVYQKPGQSKLLISYTSRYAGVDRFSGSGYGTDTFTLTSSVQABD 540
DB 404 CKASQSVNDVAMVYQKPGQSKLLISYTSRYAGVDRFSGSGYGTDTFTLTSSVQABD 463
QY 541 AAVYFCQDYNSPPTFGGKTLEIK 565
DB 464 LAVYFCQDYNSPPTFGGKTLEIK 488

RESULT 47
US-10-488-074-83
; Sequence 83, Application US/10488074
; Publication No. US20050118638A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Bernard Rees
; APPLICANT: Furmaniak, Jadwiga
; APPLICANT: Sanders, Jane Pina
; TITLE OF INVENTION: Epitope Regions of a Thyrotrophin (TSH) Receptor, Uses Thereof and
; FILE REFERENCE: 7500.412USMO
; CURRENT APPLICATION NUMBER: US/10/488,074
```

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; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: PCT/GB02/03831
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: GB 0120649.9
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: GB 0215212.2
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 209
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Figures 45 & 46
US-10-488-074-83

Query Match      27.4%; Score 966.5; DB 5; Length 209;
Best Local Similarity 87.4%; Pred. No. 1.1e-36;
Matches 187; Conservative 9; Mismatches 13; Indels 5; Gaps 1;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRINPNNGVTLY 60
DB 1 DVQLXHSGLPELVKPGASMKISCKASGYSTGYTMNVWKSHGKNLDWIGLINPYNGGTSY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRLSLTSDSAVYYCARSTMTITNYMDYWGQTSVTSS 120
DB 61 DQKFKGKATLTVDKSSSTAYMELLSLTSDSAVYYCARDGL-----MDYWGQTSVTSS 115
QY 121 AKTTTPSVVPLAPGSAQAQNSMVTGLCLVKGYFPEPVTTVWNSGSLSSGVHTFPAVLQSD 180
DB 116 AKTTTPSVVPLAPGSAQAQNSMVTGLCLVKGYFPEPVTTVWNSGSLSSGVHTFPAVLQSD 175
QY 181 LYTSSSVTPSPSTWPESETVTCNVAHPASSTKVD 214
DB 176 LYTSSSVTPSPSTWPESETVTCNVAHPASSTKVD 209

RESULT 48
US-10-682-845-38
; Sequence 38, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: LanzaVecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 468
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: OKT3 heavy chain with signal peptide
US-10-682-845-38

Query Match      27.4%; Score 966; DB 4; Length 468;
Best Local Similarity 34.9%; Pred. No. 2.5e-36;
Matches 241; Conservative 56; Mismatches 126; Indels 268; Gaps 14;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRINPNNGVTLY 60
DB 20 QVLOQSGDELARPGASVKMSCKASGYFTRTYTMHWKQRPQGGLEWIGYINPSRYTNY 79
QY 61 NQKFKDKATLTVDKSTTAYMELRLSLTSDSAVYYCARSTMTITNYMDYWGQTSVTSS 120
```



```

; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/11/132,143
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 74
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBC1741 , see Example 13
US-11-132-143-74

Query Match      27.4%; Score 965.5; DB 6; Length 510;
Best Local Similarity 77.7%; Pred. No. 2.9e-36;
Matches 188; Conservative 13; Mismatches 30; Indels 11; Gaps 1;

QY 441 NNTTISTSLISLYL-----TTSIVMTQPTPTSLLSAGDRVTITCKASQSVSN 489
DB 5 NTMVNKHFLSLVLLGLSSNLTAGMLDIVMTQSHKFMSTSVGDRVSIITCKASQDVNT 64
QY 490 DVANVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGVGTDTFTLTISVQAEADAIVFCQD 549
DB 65 AVANVYQKPGHSPKLLIYASFRYTGVPDRFTGNRSGTDTFTTISVQAEADLAIVYCCQH 124
QY 550 YNSPPTFGGTTKLEIKRADAAPTIVSIFPPSSQLTSGGASVVCFLNNFYPKDINVWKID 609
DB 125 YTPPTFGGTTKLEIKRADAAPTIVSIFPPSSQLTSGGASVVCFLNNFYPKDINVWKID 184
QY 610 GSERQNGVLNSWTDQDQSDSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNR 669
DB 185 GSERQNGVLNSWTDQDQSDSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNR 244
QY 670 NE 671
DB 245 NE 246

RESULT 52
US-11-132-143-92
; Sequence 92, Application US/11132143
; Publication No. US2005020797A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/11/132,143
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBC1767, see Example 13
US-11-132-143-92

Query Match      27.4%; Score 965.5; DB 6; Length 510;
Best Local Similarity 77.7%; Pred. No. 2.9e-36;
Matches 188; Conservative 13; Mismatches 30; Indels 11; Gaps 1;

QY 441 NNTTISTSLISLYL-----TTSIVMTQPTPTSLLSAGDRVTITCKASQSVSN 489
DB 5 NTMVNKHFLSLVLLGLSSNLTAGMLDIVMTQSHKFMSTSVGDRVSIITCKASQDVNT 64
QY 490 DVANVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGVGTDTFTLTISVQAEADAIVFCQD 549
DB 65 AVANVYQKPGHSPKLLIYASFRYTGVPDRFTGNRSGTDTFTTISVQAEADLAIVYCCQH 124
QY 550 YNSPPTFGGTTKLEIKRADAAPTIVSIFPPSSQLTSGGASVVCFLNNFYPKDINVWKID 609
DB 125 YTPPTFGGTTKLEIKRADAAPTIVSIFPPSSQLTSGGASVVCFLNNFYPKDINVWKID 184
QY 610 GSERQNGVLNSWTDQDQSDSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNR 669
DB 185 GSERQNGVLNSWTDQDQSDSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNR 244
QY 670 NE 671
DB 245 NE 246

RESULT 53
US-10-679-620-84
; Sequence 84, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 84
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p4D5Lt-TOPO, see Example 11
US-10-679-620-84

Query Match      27.2%; Score 958; DB 4; Length 214;
Best Local Similarity 86.3%; Pred. No. 2.8e-36;
Matches 183; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 460 IVMTQTPTSLLSAGDRVTITCKASQSVSNDAVYQKPGQSPKLLIYSTSRVAGVDPDR 519
DB 2 IVMTQSHKFMSTSVGDRVSIITCKASQDVNTAVAWYQKPGHSPKLLIYASFRYTGVPDR 61
QY 520 FSGSGVGTDTFTLTISVQAEADAIVFCQDQDYNPPTFGGTTKLEIKRADAAPTIVSIFPPS 579
DB 62 FTGNRSGTDTFTTISVQAEADLAIVYCCQHYTTPPTFGGTTKLEIKRADAAPTIVSIFPPS 121
QY 580 SEQLTSGGASVVCFLNNFYPKDINVWKIDGSRQNGVLNSWTDQDQSDSTYSMSSTLT 639
DB 122 SEQLTSGGASVVCFLNNFYPKDINVWKIDGSRQNGVLNSWTDQDQSDSTYSMSSTLT 181
QY 640 TKDEYERHNSYTCETHKTSPIVKSFNRNE 671
DB 182 TKDEYERHNSYTCETHKTSPIVKSFNRNE 213

RESULT 54
US-11-132-143-84
; Sequence 84, Application US/11132143
; Publication No. US2005020797A1
```

```

Best Local Similarity 77.7%; Pred. No. 2.9e-36;
Matches 188; Conservative 13; Mismatches 30; Indels 11; Gaps 1;

QY 441 NNTTISTSLISLYL-----TTSIVMTQPTPTSLLSAGDRVTITCKASQSVSN 489
DB 5 NTMVNKHFLSLVLLGLSSNLTAGMLDIVMTQSHKFMSTSVGDRVSIITCKASQDVNT 64
QY 490 DVANVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGVGTDTFTLTISVQAEADAIVFCQD 549
DB 65 AVANVYQKPGHSPKLLIYASFRYTGVPDRFTGNRSGTDTFTTISVQAEADLAIVYCCQH 124
QY 550 YNSPPTFGGTTKLEIKRADAAPTIVSIFPPSSQLTSGGASVVCFLNNFYPKDINVWKID 609
DB 125 YTPPTFGGTTKLEIKRADAAPTIVSIFPPSSQLTSGGASVVCFLNNFYPKDINVWKID 184
QY 610 GSERQNGVLNSWTDQDQSDSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNR 669
DB 185 GSERQNGVLNSWTDQDQSDSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNR 244
QY 670 NE 671
DB 245 NE 246

RESULT 53
US-10-679-620-84
; Sequence 84, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 84
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p4D5Lt-TOPO, see Example 11
US-10-679-620-84

Query Match      27.2%; Score 958; DB 4; Length 214;
Best Local Similarity 86.3%; Pred. No. 2.8e-36;
Matches 183; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 460 IVMTQTPTSLLSAGDRVTITCKASQSVSNDAVYQKPGQSPKLLIYSTSRVAGVDPDR 519
DB 2 IVMTQSHKFMSTSVGDRVSIITCKASQDVNTAVAWYQKPGHSPKLLIYASFRYTGVPDR 61
QY 520 FSGSGVGTDTFTLTISVQAEADAIVFCQDQDYNPPTFGGTTKLEIKRADAAPTIVSIFPPS 579
DB 62 FTGNRSGTDTFTTISVQAEADLAIVYCCQHYTTPPTFGGTTKLEIKRADAAPTIVSIFPPS 121
QY 580 SEQLTSGGASVVCFLNNFYPKDINVWKIDGSRQNGVLNSWTDQDQSDSTYSMSSTLT 639
DB 122 SEQLTSGGASVVCFLNNFYPKDINVWKIDGSRQNGVLNSWTDQDQSDSTYSMSSTLT 181
QY 640 TKDEYERHNSYTCETHKTSPIVKSFNRNE 671
DB 182 TKDEYERHNSYTCETHKTSPIVKSFNRNE 213

RESULT 54
US-11-132-143-84
; Sequence 84, Application US/11132143
; Publication No. US2005020797A1
```

GENERAL INFORMATION:
APPLICANT: Large Scale Biology
APPLICANT: Reini, Stephen J.
APPLICANT: Edwards, Patricia C.
TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
FILE REFERENCE: 34150-004A
CURRENT APPLICATION NUMBER: US/11/132,143
CURRENT FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: US/10/679,620
PRIOR FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: 60/415,940
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.2
SEQ ID NO 84
LENGTH: 214
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: p4D5Lt-TOPO, see Example 11
US-11-132-143-84

Query Match 27.2%; Score 958; DB 6; Length 214;
Best Local Similarity 86.3%; Pred. No. 2.8e-36;
Matches 183; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVVSAGDRVTITCKASQSVNDVAVYQKQSPKLLISYTSRYAGVDR 519
DB 2 IVMTQSHKPMSTSGDRVSTCKASQDVNTAVAYQKQSPKLLISYTSRYAGVDR 61

QY 520 FSGSGVGTDTLTISVQAEADAVYFCQDYNPPTFGGTTKLEIKRAADAPTVPSPPS 579
DB 62 FTGNRSGDTFTTISVQAEADAVYFCQDYNPPTFGGTTKLEIKRAADAPTVPSPPS 121

QY 580 SEQLTSGGASVVCFLNFPKDNVWKIDGSRQNGVLSWTDQSKDSTYSMSSTLTLL 639
DB 122 SEQLTSGGASVVCFLNFPKDNVWKIDGSRQNGVLSWTDQSKDSTYSMSSTLTLL 181

QY 640 TKDEYERHNSYTCETHAKTSTSPVKSFNRE 671
DB 182 TKDEYERHNSYTCETHAKTSTSPVKSFNRE 213

RESULT 55
US-09-795-515-7
Sequence 7, Application US/09795515
Publication No. US20030039645A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:

NAME: Trujillo, Doreen Yanko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-795-515-7

Query Match 27.2%; Score 957; DB 3; Length 468;
Best Local Similarity 34.7%; Pred. No. 6.5e-36;
Matches 240; Conservative 56; Mismatches 127; Indels 268; Gaps 14;

QY 1 EVQLQSGDPLVKGASVKISKASGYSTGYMHVWQSPKGLGWIGRINPNNGVTLY 60
DB 20 QVQLQSGAELARPGASVQMSCKASGYTFTYTHVWVKORPGQGLEWIGYINPSRGYTN 79

QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYYCARSTMTITNYVMDYMGQGTSTVSS 120
DB 80 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYYCARSTMTITNYVMDYMGQGTSTVSS 138

QY 121 AKTTPSVYPLAPGSAQAQNSVMVTLGCLVKGFPPEPTVTWNSGSLSSGVHTTFAVLQSD 180
DB 139 AKTTPSVYPLAPGSAQAQNSVMVTLGCLVKGFPPEPTVTWNSGSLSSGVHTTFAVLQSD 198

QY 181 LYTSSSVTPSPSTWPESETVTCNVVAPASSTKVDDKIIVPRDGGPSEKEEINEKDLRKK 240
DB 199 LYTSSSVTPSTWPESETVTCNVVAPASSTKVDDKIIVPRDGGPSEKEEINEKDLRKK 246

QY 241 SELQGTALNLAQIYYVNSKAITSEKSDAQFLTNLLFKGPTFGHPWYNLLVDLGSTA 300
DB 247 -----

QY 301 ATSEYEGSSVDLYGAYYQYQAGGTPNKTAKMYGGVTLHDNNRLTEBEKVPINLWIDGKQ 360
DB 247 -----

QY 361 TTVPIDKVTSKKEVTVQELDLQARHYLHGKGLYNSDSFGGKVGKGLIVFHSSEGSTVS 420
DB 263 -----

QY 421 YDLFDAQGOVPTLLRIYRDNTTISSTLSISLYLTTSIVMTQTPTSLVSVAGDRVTIT 480
DB 282 CVVVDVSEDDPD-----VQISFVNNVEVHTAQOT----- 312

QY 481 CKASQSVSNDVAVYQKQSPKLLISYTSRYAGVDRFSGSGYGTDTLTITSSVQAE 540
DB 313 -----HREDYNSTLRVV----- 324

QY 541 AAVYFCQDYNPPTFGGTTKLEIKRAADAPTVPSPPS 584
DB 325 SALPIOHQDMSGKEF-----KCKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380

QY 585 SGGASVVCFLNFPKDNVWKIDGSRQNGVLSWTDQSKDSTYSMSSTLTLL 639
DB 381 KQVTLTCTWTFMPEDIIVETWNNKTELYNKNTEPVLDS-----DGSYFWSYKLRV 433

QY 640 TKDEYERHNSYTCETHAKTSTSPVKSFNRE 669
DB 434 EKQNVWERNYSYCSVVVHGLHNHHTTKSF 464

RESULT 56
US-10-704-352-7
Sequence 7, Application US/10704352
Publication No. US20040071693A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.


```
Db 20 QVLOQSGAELARPGASVKMSCKASGYTFTRYTHHWKQRPQGLEWIGVINPSRGYTNV 79
Qy 61 NQFKDKATLTVDKSSTAYMELRSLTSEDSAVYYCARSTMTITNYMDYWGQGTSTVTS 120
Db 80 NQFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCAR-YDDHCLDYWGQGTTLTVSS 138
Qy 121 AKTTPSVYPLAPGSAQAQNSMTLGLVKGYPEPVPVTVWNSGSLSSGVHTTFAVLQSD 180
Db 139 AKTTAPSVYPLAPVCGDGTGSSVTLGLVKGTPEPVPVTLTWNSGSLSSGVHTTFAVLQSD 198
Qy 181 LYTLSSTVPSVTSWPSSETVTCNVAPASSTKVDKIVPRDSGPGSEKSEINEKDLRKK 240
Db 199 LYTLSSTVTSWPSQSITCNVAHPASSTKVDKIEPR---GPTIKPCP----- 246
Qy 241 SELQGTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db 247 ----- 246
Qy 301 ATSEYEGSSVDLYGAYGYQACGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db 247 -----PCKCPAPN-----LLGGPSVF----- 262
Qy 361 TTVPIDKVKTSKEVTVQELDLQARHVLHGKFGLYNSDSFGGKVQGRGLIVFHSSEGSTVS 420
Db 263 -----IPPKIKOVLMI---SLSPIVT 281
Qy 421 YDLFDAQGVDPDTLRLRIYRDNMTTISSTLSISLYLTTSIVMTQTPTSLLSVAGDRVIT 480
Db 282 CVVDVSEDDPD-----VQISFVNVEVHTAQQT----- 312
Qy 481 CKASQSVSNDAVYQKPGQSKLLISYTSRYAGVDPDRFSGSGYGTDFTLTSSVQAE 540
Db 313 -----HREDYNSTLRV----- 324
Qy 541 AAVYFCQDYNPSPTFGGTKLEIKRAD-----AAPTVISIPSSSEQLT 584
Db 325 SALPIQHDMWSGKEF-----KCKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380
Qy 585 SGASVVCFLNFPYKDIQVWKIDGSEKQ-----GVLSWTDQDSKDSYMSSTLTL 639
Db 381 KKQVTLTCMTDMPEDIYVEWTNNGKTELNYKNTPEVLDS-----DGSYFMYSKLRV 433
Qy 640 TKDEYERHNSYTCETHK-TSTSPIVKSFN 669
Db 434 EKKNWVERNSYSCSVVHGLNHHHTTKFSR 464

RESULT 58
US-10-703-963-7
; Sequence 7, Application US/10703963
; Publication No. US20040202662A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; Athwal, Diljeet S.
; Entage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10703,963
; FILING DATE: 07-Jan-2003
; CLASSIFICATION: 424
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-703-963-7

Query Match 27.2%; Score 957; DB 4; Length 468;
Best Local Similarity 34.7%; Pred. No. 6.5e-36;
Matches 240; Conservative 56; Mismatches 127; Indels 268; Gaps 14;

Qy 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYTHHWKQSPGKLEWIGRINPNNGVTLY 60
Db 20 QVLOQSGAELARPGASVKMSCKASGYTFTRYTHHWKQRPQGLEWIGVINPSRGYTNV 79
Qy 61 NQFKDKATLTVDKSSTAYMELRSLTSEDSAVYYCARSTMTITNYMDYWGQGTSTVTS 120
Db 80 NQFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCAR-YDDHCLDYWGQGTTLTVSS 138
Qy 121 AKTTPSVYPLAPGSAQAQNSMTLGLVKGYPEPVPVTVWNSGSLSSGVHTTFAVLQSD 180
Db 139 AKTTAPSVYPLAPVCGDGTGSSVTLGLVKGTPEPVPVTLTWNSGSLSSGVHTTFAVLQSD 198
Qy 181 LYTLSSTVPSVTSWPSSETVTCNVAPASSTKVDKIVPRDSGPGSEKSEINEKDLRKK 240
Db 199 LYTLSSTVTSWPSQSITCNVAHPASSTKVDKIEPR---GPTIKPCP----- 246
Qy 241 SELQGTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db 247 ----- 246
Qy 301 ATSEYEGSSVDLYGAYGYQACGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db 247 -----PCKCPAPN-----LLGGPSVF----- 262
Qy 361 TTVPIDKVKTSKEVTVQELDLQARHVLHGKFGLYNSDSFGGKVQGRGLIVFHSSEGSTVS 420
Db 263 -----IPPKIKOVLMI---SLSPIVT 281
Qy 421 YDLFDAQGVDPDTLRLRIYRDNMTTISSTLSISLYLTTSIVMTQTPTSLLSVAGDRVIT 480
Db 282 CVVDVSEDDPD-----VQISFVNVEVHTAQQT----- 312
Qy 481 CKASQSVSNDAVYQKPGQSKLLISYTSRYAGVDPDRFSGSGYGTDFTLTSSVQAE 540
Db 313 -----HREDYNSTLRV----- 324
Qy 541 AAVYFCQDYNPSPTFGGTKLEIKRAD-----AAPTVISIPSSSEQLT 584
Db 325 SALPIQHDMWSGKEF-----KCKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380
Qy 585 SGASVVCFLNFPYKDIQVWKIDGSEKQ-----GVLSWTDQDSKDSYMSSTLTL 639
Db 381 KKQVTLTCMTDMPEDIYVEWTNNGKTELNYKNTPEVLDS-----DGSYFMYSKLRV 433
Qy 640 TKDEYERHNSYTCETHK-TSTSPIVKSFN 669
Db 434 EKKNWVERNSYSCSVVHGLNHHHTTKFSR 464

RESULT 59
```



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Db 20 QVLOQSGAELARPGASVRMSCKASGYTFTRYTMHWKORPGGLEWIGYINPSRGYTN 79
Qy 61 NOKFKDKATLTVDKSSSTTAYMELSLTSDSAVYCYCARSTMTITNYMDYWGQSTVTVSS 120
Db 80 NOKFKDKATLTDDKSSSTAYMQLSLTSDSAVYCYCAR-YDDHYCLDYWGQSTVTVSS 138
Qy 121 AKTTTPSVPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
Db 139 AKTTASVPLAPVCGDITGSSVTLGCLVKGTPEPVTLTWNSGSLSSGVHTTTPAVLQSD 198
Qy 181 LYTSSSVTVPSSTWSPSETVTCNVNHPASSTKVKKIIVPRDSCGPGSEKSEINEKDLRKK 240
Db 199 LYTSSSVTVPSSTWSPSQSITCNVHPASSTKVKKIEPR---GPTIKPCP----- 246
Qy 241 SELQGTALGNLKOIYYNKAITSSEKSAQDQFLTNLLFKGFTGHPWYNLDDLVLGSTA 300
Db 247 ----- 246
Qy 301 ATSEYEGSSVDLYGAYYGYQCAGGTGPNKTACMYGGVTLHDNNRLTBEKKVPINLWIDGKQ 360
Db 247 -----PCKCPAPN-----LLGSPSVF----- 262
Qy 361 TTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGRLIVFHSSEGSTVS 420
Db 263 ----- 281
Qy 421 YDLFDAQGGYQPDTLRIYRDNTTISSTLSISLYLTTSIVMTQTPTSLLSVAGDRVIT 480
Db 282 CVVDVSEDDPD-----VOISFVNNVEVHTAQQT----- 312
Qy 481 CRASQSVNDVAWYQKPGSQPKLLISYTSRYAGVPDRFSGSGYGTDFTLTISVQAE 540
Db 313 -----HREDYNSTLRV----- 324
Qy 541 AAVYFCQDYNPSPTFGGKTKLEIKRAD-----AAPTVISIFFPSSSEQLT 584
Db 325 SALPIQHQDWMGSKF-----KCKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380
Qy 585 SGGASVVCFLNFPKDIWKKIDGSERON-----GVLSWTDQDSKOSTYSMSSTLT 639
Db 381 KKQVTLTCMVTDMPEDIVYEWNTNGKTELNYKNTPEVLDS-----DGSYFMYSKLRV 433
Qy 640 TKDEYERHNSYTCETHK-TSTSPIVKSFR 669
Db 434 EKQWVERNSYSCSVVHEGLNHHHTTKSFR 464
```

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RESULT 61
US-10-703-344-7
; Sequence 7, Application US/10703344
; Publication No. US20050202529A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
;            Athwal, Diljeet S.
;            Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10703,344
; FILING DATE: 07-Nov-2003
```

```
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/846, 658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yacko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-703-344-7
```

Query Match 27.2%; Score 957; DB 5; Length 468;
Best Local Similarity 34.7%; Pred. No. 6.5e-36;
Matches 240; Conservative 56; Mismatches 127; Indels 268; Gaps 14;

```
Qy 1 EVLOQSGDPLVKPGASVKISKASGYSTGYIMHWKQSPKGLWIGRINPNNGVTV 60
Db 20 QVLOQSGAELARPGASVRMSCKASGYTFTRYTMHWKORPGGLEWIGYINPSRGYTN 79
Qy 61 NOKFKDKATLTVDKSSSTTAYMELSLTSDSAVYCYCARSTMTITNYMDYWGQSTVTVSS 120
Db 80 NOKFKDKATLTDDKSSSTAYMQLSLTSDSAVYCYCAR-YDDHYCLDYWGQSTVTVSS 138
Qy 121 AKTTTPSVPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
Db 139 AKTTASVPLAPVCGDITGSSVTLGCLVKGTPEPVTLTWNSGSLSSGVHTTTPAVLQSD 198
Qy 181 LYTSSSVTVPSSTWSPSETVTCNVNHPASSTKVKKIIVPRDSCGPGSEKSEINEKDLRKK 240
Db 199 LYTSSSVTVPSSTWSPSQSITCNVHPASSTKVKKIEPR---GPTIKPCP----- 246
Qy 241 SELQGTALGNLKOIYYNKAITSSEKSAQDQFLTNLLFKGFTGHPWYNLDDLVLGSTA 300
Db 247 ----- 246
Qy 301 ATSEYEGSSVDLYGAYYGYQCAGGTGPNKTACMYGGVTLHDNNRLTBEKKVPINLWIDGKQ 360
Db 247 -----PCKCPAPN-----LLGSPSVF----- 262
Qy 361 TTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGRLIVFHSSEGSTVS 420
Db 263 -----IPPKIKQVLM-----SLSPIVT 281
Qy 421 YDLFDAQGGYQPDTLRIYRDNTTISSTLSISLYLTTSIVMTQTPTSLLSVAGDRVIT 480
Db 282 CVVDVSEDDPD-----VOISFVNNVEVHTAQQT----- 312
Qy 481 CRASQSVNDVAWYQKPGSQPKLLISYTSRYAGVPDRFSGSGYGTDFTLTISVQAE 540
Db 313 -----HREDYNSTLRV----- 324
Qy 541 AAVYFCQDYNPSPTFGGKTKLEIKRAD-----AAPTVISIFFPSSSEQLT 584
Db 325 SALPIQHQDWMGSKF-----KCKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380
Qy 585 SGGASVVCFLNFPKDIWKKIDGSERON-----GVLSWTDQDSKOSTYSMSSTLT 639
Db 381 KKQVTLTCMVTDMPEDIVYEWNTNGKTELNYKNTPEVLDS-----DGSYFMYSKLRV 433
Qy 640 TKDEYERHNSYTCETHK-TSTSPIVKSFR 669
Db 434 EKQWVERNSYSCSVVHEGLNHHHTTKSFR 464
```

```

RESULT 62
US-10-516-429-10
; Sequence 10, Application US/10516429
; Publication No. US20050191617A1
; GENERAL INFORMATION:
; APPLICANT: INOUE, Makoto
; APPLICANT: HASEGAWA, Mamoru
; APPLICANT: HIRONAKA, Takashi
; TITLE OF INVENTION: Paramyxoviral Vectors Encoding
; FILE REFERENCE: Antibodies and Uses Thereof
; CURRENT APPLICATION NUMBER: 50026/049001
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: PCT/JP03/07005
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 2002-161964
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: an immunoglobulin IN-1 heavy chain
US-10-516-429-10

Query Match 27.1%; Score 955.5; DB 5; Length 244;
Best Local Similarity 82.9%; Pred. No. 4.1e-36;
Matches 184; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYSFTGYMHVWVKSPGKLEWIGRIINPNNGVTL 60
DB 22 EVKLHSGPLVRPGSVKISCKASGYFTNYWLGVWVKRPGHLEWIGDIYPGGGYTRY 81
QY 61 NOKFKDKATLTVDKSTTAYMELRLSTSDSAVYICARSTMTINY-VMDYWGQGTSTVTS 119
DB 82 NEKFKGKATLTADTSSTAYMQLSLTSDSAVYFCARFYGSSYWFYFDVWGQGTITVTS 141
QY 120 SAKTTPPSVYPLAPGSAQTNSMVTGLCLVKGFPEPPTVTVNWSGLSGVHTFPVAVLOS 179
DB 142 SAKTTPPSVYPLAPGSAQTNSMVTGLCLVKGFPEPPTVTVNWSGLSGVHTFPVAVLOS 201
QY 180 DLYTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKKIVPRD 221
DB 202 DLYTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKKIVPRD 243

RESULT 63
US-10-860-322-4
; Sequence 4, Application US/10860322
; Publication No. US20050138692A1
; GENERAL INFORMATION:
; APPLICANT: Hilary Koprowski
; APPLICANT: Kieung Ko
; APPLICANT: Pauline Rudd
; TITLE OF INVENTION: Production of Cancer Specific
; FILE REFERENCE: Antibodies in Plants
; CURRENT APPLICATION NUMBER: 08321-0146 US1
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US/10/860,322
; PRIOR FILING DATE: 2003-06-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-860-322-4

Query Match 27.1%; Score 954; DB 5; Length 239;
Best Local Similarity 82.7%; Pred. No. 4.7e-36;

Matches 186; Conservative 14; Mismatches 23; Indels 2; Gaps 1;

QY 449 LSIISLYLYTT--SIWMTQPTPTSLLYSAGDRVTITCKASQSVNDVAVYQOKPGQSPKLLI 506
DB 13 ISILLWLYGADGNIVNTQSPKSMSSVGBRVTLTCKASENVVTYVSWYQOKPGQSPKLLI 72
QY 507 SYTSRYAGVPDRFSGSGYGTDTLTITSSVQAEADAAYVFCQDDYNSPPTFGGQTKLEIKR 566
DB 73 YGASNRYTGVPDRFTGSGSATDTLTITSSVQAEADLADYHCGQGYSPYTFGGQTKLEIKR 132
QY 567 ADAAPTVISIFPPSSSQLTSGASVVCFLNNFYPKQINVKWKIDGSRQNGVLNSWTDQDS 626
DB 133 ADAAPTVISIFPPSSSQLTSGASVVCFLNNFYPKQINVKWKIDGSRQNGVLNSWTDQDS 192
QY 627 KDSYMSSTLTLTLDKDEYERHNSYTCETHKSTSTSPIVKSPNRNE 671
DB 193 KDSYMSSTLTLTLDKDEYERHNSYTCETHKSTSTSPIVKSPNRNE 237

RESULT 64
US-10-679-620-82
; Sequence 82, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinkl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p4D5Hy-TOPO, see Examl 11
US-10-679-620-82

Query Match 27.0%; Score 952; DB 4; Length 222;
Best Local Similarity 81.4%; Pred. No. 5.4e-36;
Matches 180; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYSFTGYMHVWVKSPGKLEWIGRIINPNNGVTL 60
DB 1 QVQLQSGPELVKPGASLKSCTASGFNIKDTYIHWVKQRPEQGLEWIGRIYPTNGVTRY 60
QY 61 NOKFKDKATLTVDKSTTAYMELRLSTSDSAVYICARSTMTINYVMDYWGQGTSTVTS 120
DB 61 DPKFQDKATITADTSNTAYLQVSRLTSEDYAVYCSRWGGDGFYAMDYWGQASVTSS 120
QY 121 AKTTPPSVYPLAPGSAQTNSMVTGLCLVKGFPEPPTVTVNWSGLSSGVHTFPVAVLOS 180
DB 121 AKTTPPSVYPLAPGSAQTNSMVTGLCLVKGFPEPPTVTVNWSGLSSGVHTFPVAVLOS 180
QY 181 LYTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKKIVPRD 221
DB 181 LYTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKKIVPRD 221

RESULT 65
US-11-132-143-82
; Sequence 82, Application US/11132143
; Publication No. US20050207977A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinkl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
```



```
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/11/132,143
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p4DSHy-TOPO, see Examl 11
US-11-132-143-82

Query Match      27.0%; Score 952; DB 6; Length 222;
Best Local Similarity 81.4%; Pred. No. 5.4e-36;
Matches 180; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY      1  EVLOQSGDPLVKPGASVKISCKASGYSTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1  QVLOQSGDELVKPGASLKLSCCTASGFNKTDTIHHVWKQPEQGLEWIGRIYPTNGYTRY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      61  NQKFKDKATLTVDKSSSTTAYMELRSLTSEDSAVYYCARSTMTITNYVMDYWGQGTSTVTVSS 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  DPRFQDKATITADTSSNTAYLQVSRLTSEDTAVYYCSRWGGDGFYAMDYWGQASVTVSS 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      121  AKTTPSVVPLAPGSAQAQNSMTGLCLVKGYFPEPVPTVNSGSLSSGVHPTPAVLQSD 180
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121  AKTTPSVVPLAPGSAQAQNSMTGLCLVKGYFPEPVPTVNSGSLSSGVHPTPAVLQSD 180
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      181  LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKVIKIPRD 221
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181  LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKVIKIPRD 221
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 66
US-09-900-766-4
; Sequence 4, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-4

Query Match      26.9%; Score 948; DB 3; Length 233;
Best Local Similarity 76.4%; Pred. No. 8.6e-36;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY      226  SEKSEINEKDLRKSELOQTALGNLKOIYYNYSKAITSEKSDAQFLNTNLLFKGFFTG 285
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1  SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFFTD 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      286  HPWYNLLVDLGSSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  HSWYNLLVDVDFSKDIDVKYKGVLDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      346  EEKVPINLWIDGKQTTVPIDKVTSSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVK 405
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  HSWYNLLVDVDFSKDIDVKYKGVLDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      406  EEKVPINLWIDGKQTTVPIDKVTSSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVK 458
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Db 181 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNKTINSENMHIDIYLYTS 233

RESULT 68

US-10-267-682-113

; Sequence 113, Application US/10267682

; Publication No. US20040033235A1

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

Matthews, Thomas J.

Wild, Carl T.

Barney, Shawn O.

Lambert, Dennis M.

Petteway, Stephen R.

Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/10/267,682

APPLICATION NUMBER: US/10/267,682

FILING DATE: 08-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223A

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 113:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 113:

US-10-267-682-113

Query Match 26.9%; Score 948; DB 4; Length 257;

Best Local Similarity 76.4%; Pred. No. 9.4e-36;

Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTG 285

DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFFTD 84

QY 286 HPWYNDLLVDLSTATSEYEGSSVDLYGAYGYQCAGTGNKTAQMGVTLHNNRLT 345

DB 85 HSWYNDLLVDFDSKOIVDKYKGVLDLYGAYGYQCAGTGNKTAQMGVTLHNNRLT 144

QY 346 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405

DB 145 EEKKVPINLWIDGKQNTVPLETVTKNKNVTVPQELDLQARRYLQEKYINLYNSDVFQGVQ 204

QY 406 RGLIVFHSSEGTSVSYDLFDAQQGYPTLLRIYRDNTTISSTLSISLYLYTT 458

Db 205 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNKTINSENMHIDIYLYTS 257

RESULT 69

US-10-267-748-113

; Sequence 113, Application US/10267748

; Publication No. US20040052820A1

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

Matthews, Thomas J.

Wild, Carl T.

Barney, Shawn O.

Lambert, Dennis M.

Petteway, Stephen R.

Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/10/267,748

APPLICATION NUMBER: US/10/267,748

FILING DATE: 08-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223A

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 113:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 113:

US-10-267-748-113

Query Match 26.9%; Score 948; DB 4; Length 257;

Best Local Similarity 76.4%; Pred. No. 9.4e-36;

Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTG 285

DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFFTD 84

QY 286 HPWYNDLLVDLSTATSEYEGSSVDLYGAYGYQCAGTGNKTAQMGVTLHNNRLT 345

DB 85 HSWYNDLLVDFDSKOIVDKYKGVLDLYGAYGYQCAGTGNKTAQMGVTLHNNRLT 144

QY 346 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405

DB 145 EEKKVPINLWIDGKQNTVPLETVTKNKNVTVPQELDLQARRYLQEKYINLYNSDVFQGVQ 204


```

; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-354-948-4

Query Match      26.8%; Score 944; DB 4; Length 233;
Best Local Similarity 76.3%; Pred. No. 1.3e-35;
Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 227 EKSEEEINEKDLRKKSELOQTALGNLQIYYYNKSKAITSSSEKADQFLTNTLLFKGPFTH 286
Db 2 EKSEEEINEKDLRKKSELOQTALGNLQIYYYNKSKAITSSSEKADQFLTNTLLFKGPFTH 61

QY 287 PWYNDLLVDLGGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLLHNNRLTE 346
Db 62 SWYNDLLVDFDSKDIVDKYGKKVDLYGAYGYQCAGGTPNKTCMYGGVTLLHNNRLTE 121

QY 347 EKKVPINLWIDGQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGCKVOR 406
Db 122 EKKVPINLWIDGQNTVPLETVTKNKNVTVOELDLQARRYLQEKYLYNSDVFDGKVOR 181

QY 407 GLIVFHSSEGSTVSYDLFDAOGQYPTLLRIYRDNTTISSTLSISLYLYTT 458
Db 182 GLIVFHTSTEPSVNYDLFGAGQYNTLLRIYRDNKTINSENNHIDIYLYTS 233
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Search completed: February 15, 2006, 20:38:30
Job time : 186.042 secs

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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:34:56 ; Search time 16.3359 Seconds
(without alignments)
584.618 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522

Sequence: 1 EVLOQSGDLVKPGASVKI.....EATHKTSPIVKSFRNRES 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 107799 seqs, 14211699 residues

Total number of hits satisfying chosen parameters: 107799

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA_New.*

1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1069	30.4	592	6	US-10-016-686-4
2	972.5	27.6	243	6	US-10-016-686-1
3	967.5	27.5	488	6	US-10-016-686-3
4	944	26.8	233	7	US-11-022-562-226
5	885	25.1	363	7	US-11-000-463-335
6	855.5	24.3	666	6	US-10-981-356A-29
7	855.5	24.3	667	7	US-11-096-046-29
8	852.5	24.2	462	7	US-11-177-648-9
9	850.5	24.1	451	7	US-11-124-620-7
10	849	24.1	446	7	US-11-102-621-119
11	846	24.0	446	7	US-11-102-621-120
12	846	24.0	446	7	US-11-102-621-122
13	845.5	24.0	451	7	US-11-124-620-5
14	845	24.0	446	7	US-11-102-621-123
15	844.5	24.0	462	7	US-11-177-648-33
16	844	24.0	446	7	US-11-102-621-121
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					Sequence 120, Appl
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					Sequence 31, Appl
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Sequence 124, Appl
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Sequence 127, Appl
Sequence 29, Appl
Sequence 128, Appl
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100	779.5	22.1	667	7	US-11-096-046-30	Sequence 30, Appl	173	702.5	19.9	451	6	US-10-923-327-7	Sequence 7, Appl
101	776.5	22.0	232	7	US-11-173-564-2	Sequence 2, Appl	174	702.5	19.9	451	6	US-10-923-327-9	Sequence 9, Appl
102	775.5	22.0	253	7	US-11-106-820-20	Sequence 20, Appl	175	702.5	19.9	464	7	US-11-128-900-2	Sequence 2, Appl
103	775.5	22.0	253	7	US-11-190-364-18	Sequence 18, Appl	176	702.5	19.9	464	7	US-11-128-900-66	Sequence 66, Appl
104	774.5	22.0	666	6	US-10-981-356A-25	Sequence 25, Appl	177	702	19.9	473	7	US-11-144-248-50	Sequence 50, Appl
105	774.5	22.0	667	7	US-11-096-046-25	Sequence 25, Appl	178	702	19.9	473	7	US-11-144-223-50	Sequence 50, Appl
106	779	21.6	449	7	US-11-154-337-15	Sequence 15, Appl	179	702	19.9	473	7	US-11-182-343-50	Sequence 50, Appl
107	759	21.6	449	7	US-11-182-908-14	Sequence 14, Appl	180	702	19.9	524	7	US-11-041-095-58	Sequence 58, Appl
108	757	21.5	489	7	US-11-072-512-3329	Sequence 3329, App	181	701.5	19.9	449	7	US-11-080-587-6	Sequence 6, Appl
109	756.5	21.5	447	7	US-11-004-590-230	Sequence 230, App	182	701	19.9	214	7	US-11-173-564-1	Sequence 1, Appl
110	756	21.5	450	7	US-11-025-712-12	Sequence 12, Appl	183	701	19.9	214	7	US-11-049-536-700	Sequence 700, App
111	749.5	21.3	447	7	US-11-004-590-231	Sequence 231, App	184	701	19.9	236	7	US-11-144-248-48	Sequence 48, Appl
112	749	21.3	444	7	US-11-004-590-232	Sequence 232, App	185	701	19.9	236	7	US-11-144-222-48	Sequence 48, Appl
113	747	21.2	444	7	US-11-004-590-233	Sequence 233, App	186	701	19.9	236	7	US-11-182-343-48	Sequence 49, Appl
114	738.5	21.0	474	7	US-11-000-463-284	Sequence 284, App	187	698.5	19.8	470	7	US-11-144-248-49	Sequence 49, Appl
115	737	20.9	238	7	US-11-158-505-1	Sequence 1, Appl	188	698.5	19.8	470	7	US-11-144-222-49	Sequence 49, Appl
116	737	20.9	238	7	US-11-158-505-3	Sequence 3, Appl	189	698.5	19.8	470	7	US-11-182-343-49	Sequence 49, Appl
117	737	20.9	238	7	US-11-158-505-25	Sequence 25, Appl	190	697.5	19.8	213	7	US-11-158-505-34	Sequence 34, Appl
118	737	20.9	238	7	US-11-158-505-27	Sequence 27, Appl	191	697	19.8	236	7	US-11-144-248-52	Sequence 52, Appl
119	734	20.8	218	7	US-11-158-505-4	Sequence 4, Appl	192	697	19.8	236	7	US-11-144-222-52	Sequence 52, Appl
120	734	20.8	218	7	US-11-158-505-28	Sequence 28, Appl	193	697	19.8	236	7	US-11-182-343-52	Sequence 52, Appl
121	734	20.8	579	4	US-11-174-186-41	Sequence 41, Appl	194	696.5	19.8	235	7	US-11-128-900-14	Sequence 14, Appl
122	731	20.8	233	7	US-11-182-908-17	Sequence 17, Appl	195	696.5	19.8	235	7	US-11-128-900-65	Sequence 65, Appl
123	730	20.7	450	7	US-11-049-536-701	Sequence 701, App	196	696.5	19.8	307	7	US-11-000-463-332	Sequence 332, App
124	727	20.6	217	7	US-11-182-908-23	Sequence 23, Appl	197	695	19.7	218	7	US-11-084-554-11	Sequence 11, Appl
125	727	20.6	238	7	US-11-158-505-9	Sequence 9, Appl	198	695	19.7	218	7	US-11-136-250-11	Sequence 11, Appl
126	727	20.6	238	7	US-11-158-505-11	Sequence 11, Appl	199	695	19.7	234	7	US-11-128-900-17	Sequence 17, Appl
127	727	20.6	238	7	US-11-158-505-17	Sequence 17, Appl	200	695	19.7	234	7	US-11-128-900-69	Sequence 69, Appl
128	727	20.6	238	7	US-11-158-505-19	Sequence 19, Appl	201	694	19.7	463	7	US-11-128-900-4	Sequence 4, Appl
129	727	20.6	238	7	US-11-158-505-74	Sequence 74, Appl	202	694	19.7	463	7	US-11-128-900-68	Sequence 68, Appl
130	726	20.6	214	7	US-11-025-712-11	Sequence 11, Appl	203	693.5	19.7	291	7	US-11-041-095-60	Sequence 60, Appl
131	726	20.6	214	7	US-11-094-625-9	Sequence 9, Appl	204	693.5	19.7	468	7	US-11-086-289-22	Sequence 22, Appl
132	726	20.6	214	7	US-11-154-337-14	Sequence 14, Appl	205	693.5	19.7	472	7	US-11-086-289-2	Sequence 2, Appl
133	726	20.6	214	7	US-11-154-337-16	Sequence 16, Appl	206	693	19.7	236	7	US-11-086-289-4	Sequence 4, Appl
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135	726	20.6	214	7	US-11-182-908-15	Sequence 15, Appl	208	692.5	19.7	232	7	US-11-190-364-21	Sequence 21, Appl
136	724	20.6	218	7	US-11-158-505-12	Sequence 12, Appl	209	692.5	19.7	451	7	US-11-128-900-70	Sequence 70, Appl
137	724	20.6	218	7	US-11-158-505-20	Sequence 20, Appl	210	691.5	19.6	239	7	US-11-139-499-6	Sequence 6, Appl
138	722	20.5	477	7	US-11-000-463-395	Sequence 395, App	211	690.5	19.6	235	7	US-11-166-994-2	Sequence 2, Appl
139	719	20.4	444	7	US-11-172-320-6	Sequence 6, Appl	212	690	19.6	236	7	US-11-144-248-47	Sequence 47, Appl
140	719	20.4	444	7	US-11-173-969-6	Sequence 6, Appl	213	690	19.6	236	7	US-11-144-222-47	Sequence 47, Appl
141	718.5	20.4	232	7	US-11-025-712-10	Sequence 10, Appl	214	690	19.6	236	7	US-11-182-343-47	Sequence 47, Appl
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147	717	20.4	236	7	US-11-221-900-2	Sequence 2, Appl	220	689	19.6	312	7	US-11-000-463-334	Sequence 334, App
148	715	20.3	234	7	US-11-041-095-25	Sequence 25, Appl	221	688.5	19.5	235	7	US-11-086-289-16	Sequence 16, Appl
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152	711	20.2	214	7	US-11-183-205-55	Sequence 55, Appl	225	687.5	19.5	213	7	US-11-107-028-44	Sequence 44, Appl
153	709	20.1	239	7	US-11-041-095-19	Sequence 19, App	226	687.5	19.5	213	7	US-11-106-820-24	Sequence 24, Appl
154	706.5	20.1	451	7	US-11-102-621-142	Sequence 142, App	227	687.5	19.5	213	7	US-11-106-820-29	Sequence 29, Appl
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156	706.5	20.1	451	7	US-11-102-621-145	Sequence 145, App	229	687.5	19.5	213	7	US-11-143-077-13	Sequence 13, Appl
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158	706.5	20.1	470	7	US-11-144-222-46	Sequence 46, App	231	687.5	19.5	233	7	US-11-128-900-15	Sequence 15, Appl
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160	706	20.0	241	7	US-11-106-820-15	Sequence 15, Appl	233	687	19.5	218	6	US-10-923-327-6	Sequence 6, Appl
161	706	20.0	241	7	US-11-190-364-14	Sequence 14, Appl	234	686.5	19.5	468	7	US-11-086-289-14	Sequence 14, Appl
162	706	20.0	248	7	US-11-106-820-16	Sequence 16, Appl	235	686.5	19.5	472	7	US-11-086-289-10	Sequence 10, Appl
163	706	20.0	248	7	US-11-190-364-15	Sequence 15, Appl	236	686	19.5	471	7	US-11-086-289-6	Sequence 6, Appl
164	706	20.0	450	7	US-11-005-726-161	Sequence 161, App	237	684	19.4	218	6	US-10-923-327-8	Sequence 8, Appl
165	705.5	20.0	451	7	US-11-102-621-146	Sequence 146, App	238	684	19.4	218	6	US-10-923-327-10	Sequence 10, Appl
166	705.5	20.0	478	7	US-11-139-499-8	Sequence 8, Appl	239	684	19.4	218	6	US-10-923-327-12	Sequence 12, Appl
167	703.5	20.0	451	6	US-10-923-327-11	Sequence 11, Appl	240	684	19.4	218	6	US-10-923-327-17	Sequence 17, Appl
168	703.5	20.0	451	7	US-11-102-621-144	Sequence 144, App	241	683.5	19.4	215	7	US-11-102-621-141	Sequence 141, App
169	703.5	20.0	451	7	US-11-166-906-1	Sequence 1, Appl	242	683.5	19.4	215	7	US-11-166-906-2	Sequence 2, Appl
170	703	20.0	218	7	US-11-004-590-229	Sequence 229, App	243	681.5	19.3	213	7	US-11-172-320-4	Sequence 4, Appl
171	703	20.0	237	7	US-11-054-669-109	Sequence 109, App	244	681.5	19.3	213	7	US-11-173-969-4	Sequence 4, Appl

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249	678	19.3	463	7	US-11-128-900-63
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255	671.5	19.1	213	7	US-11-172-320-8
256	671.5	19.1	213	7	US-11-173-969-8
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262	664.5	18.9	319	7	US-11-032-773-955
263	663	18.8	214	7	US-11-005-726-163
264	661.5	18.8	238	7	US-11-177-648-35
265	661.5	18.8	478	7	US-11-072-512-3812
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268	660.5	18.8	236	7	US-11-190-364-17
269	660.5	18.8	476	7	US-11-139-499-4
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279	645.5	18.3	238	7	US-11-177-648-40
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283	636	18.1	233	6	US-10-923-327-19
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285	635	18.0	233	6	US-10-923-327-18
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292	609.5	17.3	251	7	US-11-054-515-1921
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297	602.5	17.1	248	6	US-10-512-184-36
298	602	17.1	248	7	US-11-054-515-1446
299	600.5	17.0	247	7	US-11-054-515-3240
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ALIGNMENTS

RESULT 1	
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; Sequence 4, Application US/10016686	
; Publication No. US20060014222A1	
; GENERAL INFORMATION:	
; APPLICANT: Oxford Biomedica (UK) Limited	
; APPLICANT: Kingman, Alan	
; APPLICANT: Kingman, Susan Mary	
; APPLICANT: Bebbington, Christopher Robert	
; APPLICANT: Carrol, Miles William	
; APPLICANT: Ellard, Fiona Margaret	
; APPLICANT: Myers, Kevin Alan	
; TITLE OF INVENTION: Antibodies	
; FILE REFERENCE: 674523-2012	
; CURRENT APPLICATION NUMBER: US/10/016,686	
; PRIOR FILING DATE: 2002-11-02	
; PRIOR APPLICATION NUMBER: PCT/GB00/04317	
; PRIOR FILING DATE: 2000-11-13	
; NUMBER OF SEQ ID NOS: 37	
; SOFTWARE: PatentIn version 3.1	
; SEQ ID NO 4	
; LENGTH: 592	
; TYPE: PRT	
; ORGANISM: Artificial Sequence	
; FEATURE:	
; OTHER INFORMATION: deduced amino acid sequence for the Ig-574 fusion protein	
US-10-016-686-4	
Query Match 30.4%; Score 1069; DB 6; Length 592;	
Best Local Similarity 37.9%; Pred. No. 9.5e-49;	
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DB	20 EVQLQSGPDLVKPGASVKISKASGYFTGYIMHWVKSHGKSLIEWIGRINENGVTLV 79
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DB	139 -----SGL----- 141
QY	241 SELQGTALGNLKOIYYNKAITSSEKSAQDLTNTLLPKGFTGHPWYNDLLVDLGSTA 300
DB	142 ----- 141
QY	301 ATSEYEGSSVDLYGAYGYQCAGGTGPKTACMYGGVTLHDNNRLTEKKVPINLWDGKQ 360
DB	142 -----GGSGGGT-----GG----- 151
QY	361 TTVPIDKVTSKKEVTVQELDLQARHYLHGKFLGYNDSDFGKVGQRLIVFHSSEGSTVS 420
DB	152 -----GG----- 153
QY	421 YDLFDAQQQVPTLLRIYRDNTTISSTLSISLYLTTSIVMTQTPTSLVLSAGDRVIT 480
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DB	297 EPTVTSWNSGALTSGVHTTTPAVLQS-----SGLYSLSVVTVPSSSLGT-QTYICNVN 348
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RESULT 2

US-10-016-686-1
; Sequence 1, Application US/10016686
; Publication No. US20060014222A1

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; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; APPLICANT: Kingeman, Alan
; APPLICANT: Kingeman, Susan Mary
; APPLICANT: Bebbington, Christopher Robert
; APPLICANT: Carroll, Miles William
; APPLICANT: Ellard, Fiona Margaret
; APPLICANT: Myers, Kevin Alan
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 674523-2012
; CURRENT APPLICATION NUMBER: US/10/016,686
; CURRENT FILING DATE: 2002-11-02
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of the mature secreted protein
US-10-016-686-1

Query Match      27.6%; Score 972.5; DB 6; Length 243;
Best Local Similarity 40.1%; Pred. No. 3.9e-44;
Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

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QY 121 AKTTPSPVYPLAPGSAQTNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTPPAVLQSD 180
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QY 181 LYTSSSVTPSPSTWPSSETVTCNVAHPASSTKVDDKIIPRDGGPSEKSEINEKDLRKK 240
Db 120 -----SGG----- 122
QY 241 SELQGTALGNLKOIYYNSKAITSSSEKSAQDQFLTNLLFKGFTGHPWYNDLLVDLGSTA 300
Db 123 ----- 122
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPINLWIDGKQ 360
Db 123 -----GGSGGGGT-----GG----- 132
QY 361 TTVPIDKVKTSKEVTVQELDLOARHYLHGKFLGYNDSFGGKVQKGLIVFHSSEGSTVS 420
Db 133 -----GG----- 134
QY 421 YDLFDAQGOQYPTDLLRIYRDNTTISSTLSISLYLTTSIVMTQTPTSLVNSAGDRVIT 480
Db 135 -----SSIVMTQTPTFLVNSAGDRVIT 157
QY 481 CKASQSVNDVAVYQKPGSKLLISYTSRRYAGVDPDRFSGSGYGTDFTLTISVQAE 540
Db 158 CKASQSVNDVAVYQKPGSKPFLLLISYTSRRYAGVDPDRFIGSGYGTDFTLTISLQAE 217
QY 541 AAVYFCQDYNSPPTFGGGTKLEIKR 566
Db 218 LAVYFCQDYNSPPTFGGGTKLEIKR 243

RESULT 3
US-10-016-686-3
; Sequence 3, Application US/10016686
; Publication No. US20060014222A1

; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; APPLICANT: Kingeman, Alan
; APPLICANT: Kingeman, Susan Mary
; APPLICANT: Bebbington, Christopher Robert
; APPLICANT: Carroll, Miles William
; APPLICANT: Ellard, Fiona Margaret
; APPLICANT: Myers, Kevin Alan
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 674523-2012
; CURRENT APPLICATION NUMBER: US/10/016,686
; CURRENT FILING DATE: 2002-11-02
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deduced amino acid sequence for the B7-1.5T4.1 fusion protein
US-10-016-686-3

Query Match      27.5%; Score 967.5; DB 6; Length 488;
Best Local Similarity 40.0%; Pred. No. 1.4e-43;
Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWKSPGKGLWIGRIINPNNGVTL 60
Db 247 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWKSPGKGLWIGRIINPNNGVTL 306
QY 61 NQKFKDKAILTVDKSSTTAYMELRLSTSDSAVYYCARSTMITNYVMDYWGQTSVTSS 120
Db 307 NQKFKDKAILTVDKSSTTAYMELRLSTSDSAVYYCARSTMITNYVMDYWGQTSVTSS- 365
QY 121 AKTTPSPVYPLAPGSAQTNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTPPAVLQSD 180
Db 366 ----- 365
QY 181 LYTSSSVTPSPSTWPSSETVTCNVAHPASSTKVDDKIIPRDGGPSEKSEINEKDLRKK 240
Db 366 -----SGG----- 368
QY 241 SELQGTALGNLKOIYYNSKAITSSSEKSAQDQFLTNLLFKGFTGHPWYNDLLVDLGSTA 300
Db 369 ----- 368
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPINLWIDGKQ 360
Db 369 -----GGSGGGGT-----GG----- 378
QY 361 TTVPIDKVKTSKEVTVQELDLOARHYLHGKFLGYNDSFGGKVQKGLIVFHSSEGSTVS 420
Db 379 -----GG----- 380
QY 421 YDLFDAQGOQYPTDLLRIYRDNTTISSTLSISLYLTTSIVMTQTPTSLVNSAGDRVIT 480
Db 381 -----SSIVMTQTPTFLVNSAGDRVIT 403
QY 481 CKASQSVNDVAVYQKPGSKLLISYTSRRYAGVDPDRFSGSGYGTDFTLTISVQAE 540
Db 404 CKASQSVNDVAVYQKPGSKPFLLLISYTSRRYAGVDPDRFIGSGYGTDFTLTISLQAE 463
QY 541 AAVYFCQDYNSPPTFGGGTKLEIK 565
Db 464 LAVYFCQDYNSPPTFGGGTKLEIK 488

RESULT 4
US-11-022-562-226
; Sequence 226, Application US/11022562
; Publication No. US20050249742A1
```

GENERAL INFORMATION:
APPLICANT: Ruprecht, Ruth M.
APPLICANT: Shisong, Jiang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
FILE REFERENCE: DFN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: PCT/US03/20322
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 60/392718
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 226
LENGTH: 233
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-11-022-562-226

Query Match 26.8%; Score 944; DB 7; Length 233;
Best Local Similarity 76.0%; Pred. No. 1.le-42;
Matches 177; Conservative 22; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLKKSELOQTALGNLKOIYYNSKAITSEKSAQDQFLTNLLFKGFFTG 285
Db 1 SEKSEINEKDLKKSELOQTALGNLKOIYYNEKAKTENKESHDQFLOHTILFKGFFTD 60

QY 286 HPMYNLLVLDLSTAAITSEVEGSDVLYGAYGVCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 61 HSWYNLLVDFDSKQIDVKYKGGKVDLYGAYGYQACAGGTPNKTACMYGGVTLHDNNRLT 120

QY 346 EEKVPINLWIDGKQITVPIDKVKTSKEVTQELDLQARHYLHGKFGLYNSDSFGKQV 405
Db 121 EEKVPINLWIDGKQITVPIDKVKTSKEVTQELDLQARHYLHGKFGLYNSDSFGKQV 180

QY 406 RGLIVFHSSEGSTSVSDLDFAQGYQDPTLLRIYRDNTTISSTLSLSLYTT 458
Db 181 RGLIVFHSSEGSTSVSDLDFAQGYQDPTLLRIYRDNTTISSTLSLSLYTT 233

RESULT 5
US-11-000-463-335
Sequence 335, Application US/11000463
Publication No. US20050266423A1
GENERAL INFORMATION:
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rui-hong
APPLICANT: Qian, Xiaohong B.
APPLICANT: Wang, Zhiwei
APPLICANT: Wehrman, Tom
APPLICANT: Zhang, Jie
APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Dmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIP4CN
CURRENT APPLICATION NUMBER: US/11/000,463
CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 335
LENGTH: 363
TYPE: PRT
ORGANISM: Homo sapiens
US-11-000-463-335

Query Match 25.1%; Score 885; DB 7; Length 363;
Best Local Similarity 30.8%; Pred. No. 1.9e-39;
Matches 205; Conservative 56; Mismatches 82; Indels 328; Gaps 5;

QY 1 EVOLQOQPDVLPKPGASVKISKASGYSTGYVMHVKQSPGKGLWIGWIRNPNNGVTLY 60
Db 20 EVQLLESGGGLVQPGGSLRLSCAASGFTPSFSMSVVRQAPGKGLWVSSISGSGTYY 79

QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYYCARSTMTIYNYVNDYWGQGTSTVTS 120
Db 80 ADSVKGRTISRDNKNTLYLQWNSLRABDTAVYCAKPP-----YFDYWGQGTSTVTS 135

QY 121 AKTTPSVVPLAPGSAQAQTNMVTGLCLVKGYPPEVPTVTWNSGSLSSGVHTTFAVLQSD 180
Db 136 G----- 136

QY 181 LYTSSSVTPSSSTWSETVTCNVAHPASSTKVDKIVPRDGGPSEKSEINEKDLRKK 240
Db 137 ----- 136

QY 241 SELQGTALGNLKOIYYNSKAITSEKSAQDQFLTNLLFKGFTGHPWYNLLVLDLSTA 300
Db 137 ----- 136

QY 301 ATSEYEGSSVDLYGAYGYQACAGGTPNKTACMYGGVTLHDNNRLTEKKVPIINLWIDGK 360
Db 137 -----GGS----- 143

QY 361 TTVPIDKVKTSKEVTQELDLQARHYLHGKFGLYNSDSFGKQVORGLIVFHSSEGSTVS 420
Db 144 -----VTVSSSDIQ----- 152

QY 421 YDLFDAQGYQDPTLLRIYRDNTTISSTLSLSLYTTISVMTQTPTSLVSGADRVIT 480
Db 153 -----MTQSPSTLSASVGDRTIT 171

QY 481 CKASQSVNDVAVYQKPGQSKLLISYTTSSRYAGVDRPSGSGYGTDTFTLTSSVQAE 540
Db 172 CRASQSIISLAWYQKPGKAPKLLIYKASSUESGVPSPSGSGGTFDTLTSSVQPD 231

QY 541 AAVYFCQDYNSPPTFGGKTKLEIKRADAAPTYSIFPPSSEQLTSGASVVCFLNNFPK 600
Db 232 FAYYCOQVYVYPLTFEGGKTKLEIKRADAAPTYSIFPPSSEQLTSGASVVCFLNNFPK 291

QY 601 DINVKWKIDGSEKQNGVLSWTDQDSKDYNSMSTLTLTCKDYERHNSVTCATHKTST 660
Db 292 EAKVQWQVNDALQSGNSQESVTEQDSKDYNSMSTLTLTCKDYERHNSVTCATHKTST 351

QY 661 SPIVKSFNENE 671
Db 352 SPVTKSFNRGE 362

RESULT 6
US-10-981-356A-29
Sequence 29, Application US/10981356A
Publication No. US20060015952A1
GENERAL INFORMATION:
APPLICANT: FILVAROFF, ELLEN H.
TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
FILE REFERENCE: P2068R1
CURRENT APPLICATION NUMBER: US/10/981,356A
CURRENT FILING DATE: 2004-11-04

; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 29
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-29

Query Match 24.3%; Score 855.5; DB 6; Length 666;
Best Local Similarity 33.5%; Pred. No. 1.1e-37;
Matches 222; Conservative 60; Mismatches 142; Indels 239; Gaps 17;

Qy	1	EVQLQSGDPLVKPGASVKISKASGYFTGYMHVWKSPGKGLIEWIGRINPNNGVTLY	60
Db	220	EVQLQSGAELVRPGTSVKVSKASGYAFTNLIENWKORPGQGLEWIGVNNPGSGSNY	279
Qy	61	NQKFKDKATLVDKSGSTTAYMELRSLTSDSAVYYCARSTMITNYVMDYWGQGSTVTSS	120
Db	280	NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARS---GGFYFDYWGQGSTVTSS	336
Qy	121	AKTTSPSVVPLAPGSAQTNSMVTGLCLVKGYFPEPTVTWNSGSLSSGVHTFPFVQLQSD	180
Db	337	AKTTGPSVFLAPSSKSTSGGTAALGCLVKDFPEPTVTWNSGALTSGVHTFPFVQLQSS	396
Qy	181	-LYTLSSSVTPSSSTWPSSTVTCNVAHPASSTKVKDKIVPRDSGGPSEKSEINEKDLRK	239
Db	397	GLYSLSVVTPSSSLGTQYICNVNHPKSNFKVDKKEPKSC-----	439
Qy	240	KSELQGTALGNLKQIYYNSKAITSEKSAOFLNTLLFKGFFTGHPWYNLLVDLGST	299
Db	440	-----DKHTCCPCPAPPELLGGPSVF--LFPPKP--KDTLM-----	471
Qy	300	AATSEYSGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWDGK	359
Db	472	-----ISRTPEVT-CVVVDVS-----HEDPEVKFNWVDG-	500
Qy	360	QTTVPIDKVKTSKEVTQELDQARHYLHGKFGLYNSDSFGGKVQRGILVPHSSSEGSTV	419
Db	501	---VEVHNAKTPREBQ-----YNSTY---RVVSVLTVLHQDWLNGK	536
Qy	420	SYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYLYTTSIVMTQPTSLLSAGDRVTI	479
Db	537	EY-----	538
Qy	480	TKKASQSVNDVAVYQQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTLTISVQAE	539
Db	539	KCKVS-----NKALPAP---IEKTSKAKGQP-----	562
Qy	540	DAAVYFCQDQYNSPPTFGGQTKLEIKRAADAAPTVISIFPPSSSEQLTSGGASVVCFLNFPY	599
Db	563	-----REPQVYTLPPSREEMTKNQVSLTCLVKGFYP	593
Qy	600	KDINVKWKIDGSEQRQ-----GVLSNWTQDQSKDSTYSMSSTLTLTCKDEYERHNSYTCEA	654
Db	594	SDIAVEWESNGQPPENNYKTTTPVLDSE-----DGSFFLYSKLTVDKSRWQOQGNVFCSV	646
Qy	655	THK 657	
Db	647	MHE 649	

RESULT 7

US-11-096-046-29
; Sequence 29, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE

; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954RIUS
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 29
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 220
; OTHER INFORMATION: Unknown amino acid
US-11-096-046-29

Query Match 24.3%; Score 855.5; DB 7; Length 667;
Best Local Similarity 33.5%; Pred. No. 1.1e-37;
Matches 222; Conservative 60; Mismatches 142; Indels 239; Gaps 17;

Qy	1	EVQLQSGDPLVKPGASVKISKASGYFTGYMHVWKSPGKGLIEWIGRINPNNGVTLY	60
Db	221	EVQLQSGAELVRPGTSVKVSKASGYAFTNLIENWKORPGQGLEWIGVNNPGSGSNY	280
Qy	61	NQKFKDKATLVDKSGSTTAYMELRSLTSDSAVYYCARSTMITNYVMDYWGQGSTVTSS	120
Db	281	NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARS---GGFYFDYWGQGSTVTSS	337
Qy	121	AKTTSPSVVPLAPGSAQTNSMVTGLCLVKGYFPEPTVTWNSGSLSSGVHTFPFVQLQSD	180
Db	338	AKTTGPSVFLAPSSKSTSGGTAALGCLVKDFPEPTVTWNSGALTSGVHTFPFVQLQSS	397
Qy	181	-LYTLSSSVTPSSSTWPSSTVTCNVAHPASSTKVKDKIVPRDSGGPSEKSEINEKDLRK	239
Db	398	GLYSLSVVTPSSSLGTQYICNVNHPKSNFKVDKKEPKSC-----	440
Qy	240	KSELQGTALGNLKQIYYNSKAITSEKSAOFLNTLLFKGFFTGHPWYNLLVDLGST	299
Db	441	-----DKHTCCPCPAPPELLGGPSVF--LFPPKP--KDTLM-----	472
Qy	300	AATSEYSGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWDGK	359
Db	473	-----ISRTPEVT-CVVVDVS-----HEDPEVKFNWVDG-	501
Qy	360	QTTVPIDKVKTSKEVTQELDQARHYLHGKFGLYNSDSFGGKVQRGILVPHSSSEGSTV	419
Db	502	---VEVHNAKTPREBQ-----YNSTY---RVVSVLTVLHQDWLNGK	537
Qy	420	SYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYLYTTSIVMTQPTSLLSAGDRVTI	479
Db	538	EY-----	539
Qy	480	TKKASQSVNDVAVYQQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTLTISVQAE	539
Db	540	KCKVS-----NKALPAP---IEKTSKAKGQP-----	563
Qy	540	DAAVYFCQDQYNSPPTFGGQTKLEIKRAADAAPTVISIFPPSSSEQLTSGGASVVCFLNFPY	599
Db	564	-----REPQVYTLPPSREEMTKNQVSLTCLVKGFYP	594
Qy	600	KDINVKWKIDGSEQRQ-----GVLSNWTQDQSKDSTYSMSSTLTLTCKDEYERHNSYTCEA	654
Db	595	SDIAVEWESNGQPPENNYKTTTPVLDSE-----DGSFFLYSKLTVDKSRWQOQGNVFCSV	647
Qy	655	THK 657	

```
Db          648 MHE 650
RESULT 8
US-11-177-648-9
; Sequence 9, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMELIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; PRIOR FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-177-648-9

Query Match          24.2%; Score 852.5; DB 7; Length 462;
Best Local Similarity 32.4%; Pred. No. 1.1e-37;
Matches 220; Conservative 59; Mismatches 126; Indels 273; Gaps 17;

QY      1 EVOLQSGDPLVKPGASVKLSCKASGYSFTGYVHWVWKSPGKLEWIGRINPVGVTLY 60
Db      20 QVQLQPGTGLVLPFGASVKLSCKASGYSFTGYVHWVWKSPGKLEWIGRINPVGVTLY 79
QY      61 NQKFKDKATLVDSSTTAYMELSLTSEDVAVYCARSTMITNYVMDYWGQGTSTVTS 120
Db      80 NEAFKSKATLVDSSTTAYMELSLTSEDVAVYCARSTMITNYVMDYWGQGTSTVTS 132
QY      121 AKTTPSVVPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGHTFPAVLQSD 180
Db      133 ASTKGPSVFPPLAPSGKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 192
QY      181 -LYTLSSVTVPSSTWPSSETVTCNVAHPASSTKVDDKIIPRD-----SGG 224
Db      193 GLYSLSVTVPSSTWPSSETVTCNVAHPASSTKVDDKIIPRD-----SGG 252
QY      225 PSEKSEINEKOLRKSELSQGTALGNLQIYYNSKAITSSSEKSAQDQFLNTLLFKGFFT 284
Db      253 PS-----VLPFPKP-----KDTLM----- 268
QY      285 GHPWYNDLLVDLSTAATSEYEGSSVDLYGAYGYQCAGTTPNKATCMYGGVTLHDNRL 344
Db      269 -----SRTPEVT-CVVVDVS----- 282
QY      345 TEKKVPINLWIDGKQTTPIDVKTSKKEVTVQELDLQARHLHGKFGLYNSDSFGKV 404
Db      283 HEDPEVKFNWYDQ-----VEVHNAKTPREQ-----YNSTY---RV 317
QY      405 QRLGIVFHSSEGSTVSYDLFDQAQQYDPTLLRIYRDNTTISSTLSLSLYLTTSIVMTQ 464
Db      318 VSVLTVLHQDWLNGKEY----- 334
QY      465 TPTSLVAGDRVITTCASQSVSNVAVYQQKPGSPKLLISYTSRYAGVDPDRFSGG 524
Db      335 -----KCKVS-----NKALPAP-----IEKTISKAKGP----- 358
QY      525 YGTDFTLTISVQAEDNAVYFCQDYNPSPTFGGKTKLEIKRADAAPTVSIFFPSSEQLT 584
Db      359 -----REFQVYTLPPSRDEL----- 374
```

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QY      585 SGCASVVCFLNFPKDIINVKIDGSERON-----GVLSWTDQDSKDSYSTMSSTLT 639
Db      375 KNQVSLTCLVKGYFSPSDIAVWESNGPENNYTKTPVLDL-----DGSFFLYSKLT 427
QY      640 TKDEYERHNSYTCETHK 657
Db      428 DKSRWQQGNVFCSCVMHE 445

RESULT 9
US-11-124-620-7
; Sequence 7, Application US/11124620
; Publication No. US20060024298A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Dang, Wei
; APPLICANT: Desjarlais, John R.
; APPLICANT: Karki, Sher Bahadur
; APPLICANT: Vafa, Omid
; APPLICANT: Hayes, Robert
; TITLE OF INVENTION: OPTIMIZED PC VARIANTS
; FILE REFERENCE: A-71386-9
; CURRENT APPLICATION NUMBER: US/11/124,620
; PRIOR FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US 60/568,440
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/589,906
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/627,026
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 60/626,991
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/627,774
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 10/822,231
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 10/672,280
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US 10/379,392
; PRIOR FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 7
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-620-7

Query Match          24.1%; Score 850.5; DB 7; Length 451;
Best Local Similarity 33.6%; Pred. No. 1.4e-37;
Matches 223; Conservative 58; Mismatches 146; Indels 237; Gaps 17;

QY      1 EVOLQSGDPLVKPGASVKLSCKASGYSFTGYVHWVWKSPGKLEWIGRINPVGVTLY 60
Db      1 QVQLQPGTGLVLPFGASVKLSCKASGYSFTGYVHWVWKSPGKLEWIGRINPVGVTLY 60
QY      61 NQKFKDKATLVDSSTTAYMELSLTSEDVAVYCARSTMITNYVMDYWGQGTSTVTS 119
Db      61 NQKFKDKATLVDSSTTAYMELSLTSEDVAVYCARSTMITNYVMDYWGQGTSTVTS 120
QY      120 SAKTTPSVVPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGHTFPAVLQ 179
Db      121 AASTKGPSVFPPLAPSGKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180
QY      180 D-LYTLSSVTVPSSTWPSSETVTCNVAHPASSTKVDDKIIPRDSSGGPSEKSEINEKDLR 238
Db      181 SGLYSLSSVTVPSSTWPSSETVTCNVAHPASSTKVDDKIIPRDSSGGPSEKSEINEKDLR 224
QY      239 KSELOQTALGNLQIYYNSKAITSSSEKSAQDQFLNTLLFKGFFTGHWPYNDLLVDLGS 298
Db      225 -----DKHTTCCPPAPBLGGPSVF--LFPKP--KDTLM----- 256
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QY 299 TAATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEKKVPIINLWIDG 358
Db 257 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVDG 285
QY 359 KQTTVPIDKVTSKKEVTVQELDQARHYLHGKFGLYNSDSFGKVKQORGLIVFHSSEGST 418
Db 286 ----VEVHNAKTKPREEQ-----YNSTY---RVVSVLTVLHQDWLNG 320
QY 419 VSYDLFDAQOQYPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQPTSLLSVAGDRV 478
Db 321 KEY----- 323
QY 479 ITCKASQSVNDVAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTISVQA 538
Db 324 -KCKVS-----NKALPAP---IEKTISKAKGQP----- 347
QY 539 EDAAVYFCQDYNSPPTFGGGTKLEIKRADAAPTVISFPPSSBQLTSGGASVVCFLNPFY 598
Db 348 -----REPQVYTLPPSRDELTKNQVSLTCLVKGFY 377
QY 599 PKDINVWKIDGSERON-----GVLSNSWTDQDSKDYSSMSSTLTLTQDEYERHNSYTCB 653
Db 378 PSDIAVEWESNGQPENNYKTPPVLDs-----DGSFFLYSKLTVDKSRWQQGNVFSCS 430
QY 654 ATHK 657
Db 431 VMHE 434

RESULT 10
US-11-102-621-119
; Sequence 119, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tseo, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 119
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-119
```

Query Match 24.1%; Score 849; DB 7; Length 446;
Best Local Similarity 33.0%; Pred. No. 1.6e-37;
Matches 219; Conservative 62; Mismatches 142; Indels 240; Gaps 17;

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QY 1 EVLOQSGDPLVKPGASVKISKASGYSTGYMHVWKSPGKGLWIGRIINPNNGVTLY 60
Db 1 QVQLVQSGAEVKKPGSVKVCCKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSEDSAVYYCARSTMTITNYVMDYWGQSTSTVSS 120
Db 61 NQKFKDKATITADESTNTAYMELSLRSEDYAVYYCARG-----GGVFDYWGQSTLTVSS 116
QY 121 AKTTPPSVPLAPGSAQNTSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
Db 117 ASTKGFSPVPLAPSSKTSQGTALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 176
QY 181 -LYTSSSVTPSPSTWSPETVTCNVAHPASSTKVDKKIIPRDSGGPSEKSEINEKDLRK 239
Db 177 GLYSLSVTVTPSSSLGTQYICNVNHPKSTNKKVPEPKSC----- 219
```

```
QY 240 KSELQGTALGNLKQIYYNSKAITSEKSADQFLTNLLPKGFETGHPWVNDLLVDLGST 299
Db 220 -----DKTHTPCCPAPPELLGGPSVF--LFPPKP-KDDLMI----- 252
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEKKVPIINLWIDGK 359
Db 253 -----SRTPEVT-CVVVDVS-----HEDPEVKFNWYVDG- 280
QY 360 QTTVPIDKVTSKKEVTVQELDQARHYLHGKFGLYNSDSFGKVKQORGLIVFHSSEGSTV 419
Db 281 ----VEVHNAKTKPREEQ-----YNSTY---RVVSVLTVLHQDWLNGK 316
QY 420 SYDLFDAQOQYPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQPTSLLSVAGDRV 479
Db 317 EY----- 318
QY 480 TCKASQSVNDVAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTISVQA 539
Db 319 KCKVS-----NKALPAP---IEKTISKAKGQP----- 342
QY 540 DAAVYFCQDYNSPPTFGGGTKLEIKRADAAPTVISFPPSSBQLTSGGASVVCFLNPFY 599
Db 343 -----REPQVYTLPPSRDELTKNQVSLTCLVKGFY 373
QY 600 KDINVWKIDGSERON-----GVLSNSWTDQDSKDYSSMSSTLTLTQDEYERHNSYTC 654
Db 374 SDIAVEWESNGQPENNYKTPPVLDs-----DGSFFLYSKLTVDKSRWQQGNVFSCSV 426
QY 655 THK 657
Db 427 MHE 429
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RESULT 11
US-11-102-621-120
; Sequence 120, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tseo, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-120
```

Query Match 24.0%; Score 846; DB 7; Length 446;
Best Local Similarity 32.0%; Pred. No. 2.3e-37;
Matches 217; Conservative 62; Mismatches 129; Indels 270; Gaps 17;

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QY 1 EVLOQSGDPLVKPGASVKISKASGYSTGYMHVWKSPGKGLWIGRIINPNNGVTLY 60
Db 1 QVQLVQSGAEVKKPGSVKVCCKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSEDSAVYYCARSTMTITNYVMDYWGQSTSTVSS 120
Db 61 NQKFKDKATITADESTNTAYMELSLRSEDYAVYYCARG-----GGVFDYWGQSTLTVSS 116
QY 121 AKTTPPSVPLAPGSAQNTSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
```

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Db 117 ASTKGPVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 176
QY 181 -LYTLSSSVTPSPSTWSETVTCNVAHPASSTKVDKKIVPRDS-----GG 224
Db 177 GLYSLSVTVTPSSSLGTQYICNVNKPSTNTKVKVEPKSCDKTHTCTPCPAPELLGG 236
QY 225 PSKSEINEKDLRKKSSELOGTALGNLQKIYYNSKAITSEKSAQOFLNTLLFKGFFT 284
Db 237 PS-----VFLF-----PPKPKDQLMISR----- 254
QY 285 GHPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGVTLHDNNRL 344
Db 255 -----TPEVT-CVVVDVS----- 266
QY 345 TEEKKVPINLWIDGKOTTPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKV 404
Db 267 HEDPEVKFNWYVDG---VEVHNAKTPREEQ-----YNSTY---RV 301
QY 405 QRLIIVPHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNNTTISLSISLYLTTISVMTQ 464
Db 302 VSVLTVLHQDWLNGKEY-----NKAHPAP-----IEKTISKAKGQP----- 318
QY 465 TPTSLLSVAGSDRVTITCKASQSVSNVAVYQKPGQSPKLLISVTSRYAGVDPDRFSGSG 524
Db 319 -----CKVVS-----NKAHPAP-----IEKTISKAKGQP----- 342
QY 525 YGDTFTLTISVQAEADAAYVFCQDYNSPPTFGGKLEIKRADAAPTIVSIFPPSSSEQLT 584
Db 343 -----REPQVYTLPPSRDELT 358
QY 585 SGGASVVCFLNNFPKDIWVKWIDGSEKRON-----GVLSNWTDDQSKSTYSMSSTLTLL 639
Db 359 KNQVSLTCLVKGYFSPDAVWEESNGQPENNYKTTPPVLDSD-----DGSFPLYSKLTIV 411
QY 640 TKDEYERHNSYTCEATHK 657
Db 412 DKSRWQOQGNVFCSVLHE 429

RESULT 12
US-11-102-621-122
; Sequence 122, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Ito, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-122

Query Match 24.0%; Score 846; DB 7; Length 446;
Best Local Similarity 32.0%; Pred. No. 2.3e-37;
Matches 217; Conservative 62; Mismatches 129; Indels 270; Gaps 17;

QY 1 EVOLQSGDPLVKPGASVKISCKASGYSTFGYGMHWVKQSPGKGLWIGRIINPNNGVTLY 60
Db 1 QVQLVQSGAEVKKPGSSVKVCKASGYTFTSYRMHWVRQAPGQGLEWIGVINFSTGYEY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSEDSAVYYCARSTMTITNYVMDYWGQGTSTVTVSS 120
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Db 61 NQKFKDKATITADESTNTAYMELSSLRSEDTAVYYCARG-----GVFDYWGQGTSTVTVSS 116
QY 121 AKTTPPSVTVPLAPSGAQTNSMVTCLCLVKGYFPEPVTVTWNSGSLSSGVTHTTPAVLQSD 180
Db 117 ASTKGPVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 176
QY 181 -LYTLSSSVTPSPSTWSETVTCNVAHPASSTKVDKKIVPRDS-----GG 224
Db 177 GLYSLSVTVTPSSSLGTQYICNVNKPSTNTKVKVEPKSCDKTHTCTPCPAPELLGG 236
QY 225 PSKSEINEKDLRKKSSELOGTALGNLQKIYYNSKAITSEKSAQOFLNTLLFKGFFT 284
Db 237 PS-----VFLF-----PPKPKDQLMISR----- 254
QY 285 GHPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGVTLHDNNRL 344
Db 255 -----TPEVT-CVVVDVS----- 266
QY 345 TEEKKVPINLWIDGKOTTPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKV 404
Db 267 HEDPEVKFNWYVDG---VEVHNAKTPREEQ-----YNSTY---RV 301
QY 405 QRLIIVPHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNNTTISLSISLYLTTISVMTQ 464
Db 302 VSVLTVLHQDWLNGKEY-----NKAHPAP-----IEKTISKAKGQP----- 318
QY 465 TPTSLLSVAGSDRVTITCKASQSVSNVAVYQKPGQSPKLLISVTSRYAGVDPDRFSGSG 524
Db 319 -----CKVVS-----NKAHPAP-----IEKTISKAKGQP----- 342
QY 525 YGDTFTLTISVQAEADAAYVFCQDYNSPPTFGGKLEIKRADAAPTIVSIFPPSSSEQLT 584
Db 343 -----REPQVYTLPPSRDELT 358
QY 585 SGGASVVCFLNNFPKDIWVKWIDGSEKRON-----GVLSNWTDDQSKSTYSMSSTLTLL 639
Db 359 KNQVSLTCLVKGYFSPDAVWEESNGQPENNYKTTPPVLDSD-----DGSFPLYSKLTIV 411
QY 640 TKDEYERHNSYTCEATHK 657
Db 412 DKSRWQOQGNVFCSVLHE 429

RESULT 13
US-11-124-620-5
; Sequence 5, Application US/11124620
; Publication No. US20060024298A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Dang, Wei
; APPLICANT: Desjarlais, John R.
; APPLICANT: Karki, Sher Bahadur
; APPLICANT: Vafa, Omid
; APPLICANT: Hayes, Robert
; TITLE OF INVENTION: OPTIMIZED FC VARIANTS
; FILE REFERENCE: A-71386-9
; CURRENT APPLICATION NUMBER: US/11/124,620
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US 60/568,440
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/589,906
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/627,026
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 60/626,991
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/627,774
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 10/822,231
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 10/672,280
; PRIOR FILING DATE: 2003-09-26
```


Db 61 NQPKDKATITADRESTNTAYNELSLRSEDATVYICARG-----GGVFDYMGQGGFLVTVSS 116
Qy 121 AKTTPSPVYPLAPGSAQAQTNMTVLGCLVKGYPPEPVTVTWNSGSLSSGVHTFPVAVLQSD 180
Db 117 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPPEPVTVSWNSGALTSGVHTFPVAVLQSS 176
Qy 181 -LYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKKIVPRDS-----GG 224
Db 177 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKEPKSCDKTHTCCPCPAPELGG 236
Qy 225 PSEKSEBINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLNTLLFKGFFT 284
Db 237 PS-----VFLP-----PPKPKDQLMISR----- 254
Qy 285 GHPWYNDLLVDLSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRL 344
Db 255 -----TPEVT-CVVVDVS----- 266
Qy 345 TEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDSFGKV 404
Db 267 HEDPEVKFNWYDQ-----VEVHNAKTPREEQ-----YNSTY---RV 301
Qy 405 QRGILVPHSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYLTTSIIVMTQ 464
Db 302 VSVLTVLHQDLNGKEY----- 318
Qy 465 TPTSLVLSAGDRVTITCKASQSVSNVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSG 524
Db 319 -----KCKVS-----NKALPAP-----IEKTISKAKGQP----- 342
Qy 525 YGTDFTLTISVQAEDAAVYFCQDYNSPPTFGGGTKLEIKRADAAPTISIFPPSSSEQLT 584
Db 343 -----REPQVYTLPPSRDELT----- 358
Qy 585 SGGASVVCFLNNFYPKDINVKWKIDGSERON-----GVLSWTDQDSKDSYMSSTLTL 639
Db 359 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSE-----DGSFFLYSKLTV 411
Qy 640 TKDEYERHNSYTCETHK 657
Db 412 DKSRWQOGNVFSCSVFHE 429

RESULT 15
US-11-177-648-33
; Sequence 33, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMELIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR FILING DATE: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H18
US-11-177-648-33

Query Match

24.0%; Score 844.5; DB 7; Length 462;

Best Local Similarity 32.3%; Pred. No. 2.9e-37;
Matches 219; Conservative 59; Mismatches 127; Indels 273; Gaps 17;
Qy 1 EVOLQSGGPDLPKPGASVKISCKASGYSTFGYYHHWKQSPGKGLEWIGRINPNNGVTLY 60
Db 20 QVQLVQSGAEVFPKASVKLSCKASGYTFTSYHHWKQSPGQGLEWIGINPNPSGGTNY 79
Qy 61 NQPKDKATITVDKSTTAYMELRSLTSDSAVYICARSTMI TNYVMDYMGQGGSTVTVSS 120
Db 80 NEKPKSKATITVDKSSSTAYMELSLRSDSAVYICELG-----QGYMGQGGFLVTVSS 132
Qy 121 AKTTPSPVYPLAPGSAQAQTNMTVLGCLVKGYPPEPVTVTWNSGSLSSGVHTFPVAVLQSD 180
Db 133 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPPEPVTVSWNSGALTSGVHTFPVAVLQSS 192
Qy 181 -LYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKKIVPRD-----SGG 224
Db 193 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKEPKSCDKTHTCCPCPAPELAGA 252
Qy 225 PSEKSEBINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLNTLLFKGFFT 284
Db 253 PS-----VFLP-----KDTLMI----- 268
Qy 285 GHPWYNDLLVDLSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRL 344
Db 269 -----SRTPEVT-CVVVDVS----- 282
Qy 345 TEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDSFGKV 404
Db 283 HEDPEVKFNWYDQ-----VEVHNAKTPREEQ-----YNSTY---RV 317
Qy 405 QRGILVPHSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYLTTSIIVMTQ 464
Db 318 VSVLTVLHQDLNGKEY----- 334
Qy 465 TPTSLVLSAGDRVTITCKASQSVSNVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSG 524
Db 335 -----KCKVS-----NKALPAP-----IEKTISKAKGQP----- 358
Qy 525 YGTDFTLTISVQAEDAAVYFCQDYNSPPTFGGGTKLEIKRADAAPTISIFPPSSSEQLT 584
Db 359 -----REPQVYTLPPSRDELT----- 374
Qy 585 SGGASVVCFLNNFYPKDINVKWKIDGSERON-----GVLSWTDQDSKDSYMSSTLTL 639
Db 375 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSE-----DGSFFLYSKLTV 427
Qy 640 TKDEYERHNSYTCETHK 657
Db 428 DKSRWQOGNVFSCSVFHE 445

RESULT 16
US-11-102-621-121
; Sequence 121, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882, 0039, 00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 121
; LENGTH: 446

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-121

Query Match      24.0%; Score 844; DB 7; Length 446;
Best Local Similarity 33.0%; Pred. No. 3e-37;
Matches 219; Conservative 60; Mismatches 144; Indels 240; Gaps 17;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYVMHWKSPGKGLWIGRINPNNGVTLY 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 QVLVQSGAEVKKPGSSVKSCASGYSTGYVMHWVRQAPGKGLWIGVYINPSTGYTEY 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NQKFKDKATLVDSKSTTAYMELRSITSDSAVYVCARSTMTITNYMDYWGQSTVTVSS 120
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NQKFKDKATITADESTNTAYMELSLRSEDATVYICARG-----GGVFDYWGQSTLVTVSS 116
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 AKTTTPSVVPLAPGSAQAQNSMTWLGCLVKGPPEPTVTWNSGSLSSGVHTFPFVQLQSD 180
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 117 ASTKGSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPFVQLQSS 176
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 -LYTLSSVTVPSSTWPSSTVTCNVAHPASSTKVDKKIIPRDSGGPSEKSEINEKDLRK 239
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 177 GLYSLSVTVPSLSLGTQYICNNVHKPSNTKVDKKVEPKSC----- 219
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 KSELOQTALGNLKQIYYNKAITSSEKSAQDQFLNTLLFKGFTTGHMPWINDLLVDLGS 299
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 220 -----DKTHTCPPCPAPPELLGSPVF--LFPKP--KDTLM----- 251
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPINLWIDGK 359
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 252 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVDG- 280
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 360 QTTVPIDKVKTSKEVTVOELDQARHYLHGKFLGYNLSDSFGKVGQGLIVFHSSSEGSTV 419
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 281 ---VEVHNAKTPREBQ-----YNSTY---RVSVSLTVLHQDWLNGK 316
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 420 SYDLFDAQOQPDTLRIYRDNTTISSTLSISLYLYTTSIVMTQPTSLIVSAGDRVIT 479
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 317 EY----- 318
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 480 TKCASQSVNDVAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTFTLTISVQAE 539
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 319 KCKVS-----NKALPAP---IETISKAKGP----- 342
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 540 DAAVYFCQDYNSSPPTFGGKTKLEIKRADAAAPTVISIFPPSSSEQLTSGGASVVCFLNFP 599
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 343 -----REPQVYTLPPSRDELTKNQVSLTCLVKGFY 373
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 600 KDINVKWKIDGSRQN-----GVLSNWTQDQSKDSTYSMSSTLTLTCKDEYERHNSYTCEA 654
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 374 SDIAVWESNGQPNENYKTPPVLDSE-----DGSFFLYSKLTVDKSRWQGNVFCSV 426
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 655 THK 657
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 427 LHE 429
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 17
US-11-000-463-804
; Sequence 804, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
```

```
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 804
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-804

Query Match      23.9%; Score 841.5; DB 7; Length 384;
Best Local Similarity 30.2%; Pred. No. 3.5e-37;
Matches 203; Conservative 64; Mismatches 95; Indels 311; Gaps 10;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYVMHWKSPGKGLWIGRINPNNG-VTL 59
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 20 EVLVESGGLVQPGSLRLSCAAGFTFSSVAMSVRQAPGKGLWVSGLSGSGSSTY 79
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 YNQKFKDKATLVDSKSTTAYMELRSITSDSAVYVCARSTMTITNYMDYWGQSTVTVSS 119
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 80 YADSVKGRFTISRDNSKGTLYLQMNSLRADDTARYYCAKG-----GVELA 124
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 SAKTTPSVVPLAPGSAQAQNSMTWLGCLVKGPPEPTVTWNSGSLSSGVHTFPVQLQ 179
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 125 STK----- 127
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 DLYTLSSVTVPSSTWPSSTVTCNVAHPASSTKVDKKIIPRDSGGPSEKSEINEKDLRK 239
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 128 -----PSSIW----- 132
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 KSELOQTALGNLKQIYYNKAITSSEKSAQDQFLNTLLFKGFTTGHMPWINDLLVDLGS 299
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 133 -----RLNPIRY-----WYFDLW-QQGTL 150
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPINLWIDGK 359
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 151 VTVSGDGS-----GGAS----- 167
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 360 QTTVPIDKVKTSKEVTVOELDQARHYLHGKFLGYNLSDSFGKVGQGLIVFHSSSEGSTV 419
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 168 ----- 167
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 420 SYDLFDAQOQPDTLRIYRDNTTISSTLSISLYLYTTSIVMTQPTSLIVSAGDRVIT 479
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 168 -----TGEIVLTQSPFTLSLSPGERATL 190
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 480 TKCASQSVND-VAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTFTLTISVQAE 538
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 191 SCRASQSVSSSYLAWYQKPGQAPRLIYIGASSRATGIPDRFSGSGSGGTFTLTISRLEP 250
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 539 EDAAVYFCQDYNSSPPTFGGKTKLEIKRADAAAPTVISIFPPSSSEQLTSGGASVVCFLNFP 598
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 251 EDFAVYVCOQYGSPTTFGGTKVDIKRTVAAPSVEIFPPSDDEQLKSGTASVVCFLNFP 310
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 599 PKDINVKWKIDGSRONGVLSNWTQDQSKDSTYSMSSTLTLTCKDEYERHNSYTCEATHKT 658
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 311 BREAKVQWVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG 370
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```


Qy	1	EVQLQQSGPDLVVKPGASVKISKCKASGYFTGYIMHWVQSPQKGLIEWIGRINPNNG-VTL	59
Db	20	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMGSWVRQAPGKGLIEWVSGLSGSGSGSY	79
Qy	60	YNQKPKDKATLTVDKSSSTAYMELRSLTSEDSAVVYCARSTMIINVVMDYQGQTSVTVS	119
Db	80	YADSVKGRFTISRDNKSGTGLYQMNSLRADDTARYYCAKG-----GVELA	124
Qy	120	SAKTTTPSVVYFLAPGSAAGTNSMVTGLCLVKGYPPEPVTVTWNSGSLSSGVHTFPAVLQS	179
Db	125	STK-----	127
Qy	180	DLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKYVDKKI VPRDSGSPSEKSEBINEKLRK	239
Db	128	-----PSGIW-----	132
Qy	240	KSELTGALGNLKOIYYNYSKAITSSSEKSAQFLNTLLFKGFTGHPMYNDLLVDLQST	299
Db	133	-----RLNPIRY-----WYFLW-QGGTL	150
Qy	300	AATSEYEGSSVDLYGAYYGYOCAGGTPNKTCMCGVTLHDNRLTEKKVPINLWDGK	359
Db	151	VTVSSGDGSS-----GGAS-----	167
Qy	360	QTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGCKVQRGILVPHSSEGSTV	419
Db	168	-----	167
Qy	420	SYDLFDAQQGYPDTLRIYRDNNTTISSTLSISLYLTTSI VMTQTPTSLLVSAGDRVTI	479
Db	168	-----TGEIVLTQSPGTLSPGERATL	190
Qy	480	TKCASQSVND-VAMVYQKPGQPKLLISYTSRRYAGVPDRFGSGYGFDTLTSSVQA	538
Db	191	SCRASQSVSSSLAWYQKPGQAPRLLIYGASSRATGIPDRFGSGSGGDTLTISRLEP	250
Qy	539	EDAAVYFCQDYNSPPTFGGKTLEIKRADAAPTYSIIPPPSEQLTSGASVVCFINNEY	598
Db	251	EDFAVYVYQQYSGSPPTFGQGTVDIKRTVAAPSFI PPSDSQLKSGTASVVCLLNNEY	310
Qy	599	PKDINVKWIKDGSERONGVLNSWTDQDSKDSYMSSTLTLTKDVERHNSYTCBATHKT	658
Db	311	PREAKVQWKVDNALQSGNSQESVTEQDSKDSIYSLSSLTLTLSKADYKHKVYACEVTHQG	370
Qy	659	STSPIVKSFNRNE	671
Db	371	LSSPVTKSFNRGE	383

```

RESULT 20
US-11-000-463-807
; Sequence 807, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radjef T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785C1P4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623

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; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 807
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-807

Query Match      23.9%; Score 841.5; DB 7; Length 384;
Best Local Similarity 30.2%; Pred. No. 3.5e-37;
Matches 203; Conservative 64; Mismatches 95; Indels 311; Gaps 10;

Qy 1 EVLQQSGPDLVKPGASVKISCKASGYSGFYGMHWVKQSPGKLEWIGRINPNNG-VTL 59
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 20 EVLVSGGGLVQPGGSLRLSCAASGFTSSYAMSVMVRQAPGKLEWVSLGSGSGSTY 79
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 60 YNQKFKDKATLTVDKSSITAYMELRSITSDSAVYICARSTMITNVMYMGQGTSTVTS 119
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 80 YADSVKGRFTISRDNSKGTLYLQWNSLRADDTARYVCAG- 124
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 120 SAKTTPPSVYPLAPGSAAQTNMVTGLCVKGYFPBPVTVTNWNSGSLSSGVHTFPAVLQS 179
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 125 STK- 127
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 180 DLYTLSSVTVPSSTWPESETVTCNVAHPASSTKVKDKIVPRDSGSPKSEINEKDLRK 239
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 128 -PSSIW- 132
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 240 KSELQGTALGNLKQIYYYNASKAITSSEKSAQDQFLTNTLLFKGFTGHPWYNLLVDLGST 299
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 133 -----RLNPIRY- 150
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 300 AATSEYEGSSVDLYGAYGYQCAGGTGPNKTACHMYGGVTLHDNNRLTEKKVPLNLWDGK 359
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 151 VTVSSGDGSS- 167
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 360 QTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLYNSDSFGGKVGQGLIVFHSSSEGSTV 419
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 168 ----- 167
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 420 SYDLFDLQGGYPDTLLRIYRDNTTISTSLISLYLTTISVMTQTPTSLLSAGDRVTI 479
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 168 -----TGEIVLTQSFGTSLSPGERATL 190
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 480 TCKASQSVND-VAWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTLTITISVQA 538
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 191 SCRASQSVSSYLANWQKFGQAPRLLIYCASSRATGIPDRFSGSGSGTDTLTISRLEP 250
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 539 EDAAVYPCQDYNSSPPTFGGGTKLEIKRADAAPTVSIFFPSSSQTSGGASVVCFLNNFY 598
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 251 EDEFAVYCCQYSGSPPTFGGQTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCFLNNFY 310
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 599 PKDINVKWKIDGSRQNGVLNSMTDQSDKSTYSMSSTLTLTDEYERHNSYCEATHKT 658
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 311 PREAKVQKVDNALQSGNSQESVTEQDSKDSTLSLSSTLTLSKADYEKKHKVYACEVTHQ 370
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 659 STSPIVKSFNRNE 671
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 371 LSSPVTKSFNRGE 383
Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

```

RESULT 21

```
US-11-177-648-30
; Sequence 30, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLEN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H15
US-11-177-648-30

Query Match      23.8%; Score 838.5; DB 7; Length 462;
Best Local Similarity 32.2%; Pred. No. 5.9e-37;
Matches 218; Conservative 59; Mismatches 128; Indels 273; Gaps 17;

QY 1 EVLOQSGDPLVPGASVKLSCKASGYFTSYGMHWVKQPGKGLWIGINPNNGVTLY 60
DB 20 QVQLVQSGAEVVPFGASVKLSCKASGYFTSYGMHWVKQPGQGLEWIGINPNNGVTNY 79

QY 61 NQPKDKATLTVDKSTTAYMELRSLSLTSSEDSAVVYCARSTMTITNYMDYQGQSTVTVSS 120
DB 80 NEKFKSKATLTVDKSTTAYMELSSLSLTSSEDSAVVYCELG-----QGYWGQGLTVTVSS 132

QY 121 AKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYPEPVTVTVNSGSLSSGVHTTTPAVLQSD 180
DB 133 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSVNSGALTSGVHTTTPAVLQSS 192

QY 181 -LYTLSSSVTVPSSTWPSSTVTCNVAHPASSTKVDKKIIPRD-----SGG 224
DB 193 GLYSLSSVTVPSSSLGTQYICNVNHPKNTKVDKKVEPKSCDKHTCTCPAPAPLAGA 252

QY 225 PSEKSEINEKDLRKKSSELOQTALGNLKQIYYNNSKAITSSSEKSAQDQFLNTLLFKGFFT 284
DB 253 PS-----VFLPPPKP-----KDTLMI----- 268

QY 285 GHPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRL 344
DB 269 -----SRTPEVT-CVVVDVS----- 282

QY 345 TEKKVPIINLWIDGKQTTPIDIKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKV 404
DB 283 HEDPEVKFNWYVDG-----VEVHNAKTPREEQ-----YNSTY---RV 317

QY 405 QRGLIVPHSSEGSTVSYDLFDQAQGYPTDLLRIYRDNTTISSTLSLSLYLTTSIVMTQ 464
DB 318 VSVLTVLHQPDLNGKEY----- 334

QY 465 TPTSLLSAGDRVITITCKASQSVNSDVAVTQQKPGQPKLLISYTSRYAGVDPDRFSGSG 524
DB 335 -----KCKVS-----NKALPAP-----IEKTSKAGQP----- 358

QY 525 YGDTFTLTISVQAEDAAYVFCQDYNSPTFFGGGTGKLEIKRADAAPTIVSIFPPSSSEQLT 584
DB 359 -----REPQVTLTPSRDEL 374

QY 585 SGGASVVCFLNNFYPKDINVKWIDGSRQN-----GVLSNWTDDQDSKDSYMSSTLTL 639
```

```
US-11-177-648-32
; Sequence 32, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLEN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H17
US-11-177-648-32

Query Match      23.8%; Score 838.5; DB 7; Length 462;
Best Local Similarity 32.0%; Pred. No. 5.9e-37;
Matches 217; Conservative 61; Mismatches 127; Indels 273; Gaps 17;

QY 1 EVLOQSGDPLVPGASVKLSCKASGYFTSYGMHWVKQPGKGLWIGINPNNGVTLY 60
DB 20 QVQLVQSGAEVVPFGASVKLSCKASGYFTSYGMHWVKQPGQGLEWIGINPNNGVTNY 79

QY 61 NQPKDKATLTVDKSTTAYMELRSLSLTSSEDSAVVYCARSTMTITNYMDYQGQSTVTVSS 120
DB 80 NEKFKSKATLTVDKSTTAYMELSSLSLTSSEDSAVVYCELG-----QGYWGQGLTVTVSS 132

QY 121 AKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYPEPVTVTVNSGSLSSGVHTTTPAVLQSD 180
DB 133 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSVNSGALTSGVHTTTPAVLQSS 192

QY 181 -LYTLSSSVTVPSSTWPSSTVTCNVAHPASSTKVDKKIIPRD-----SGG 224
DB 193 GLYSLSSVTVPSSSLGTQYICNVNHPKNTKVDKKVEPKSCDKHTCTCPAPAPLAGA 252

QY 225 PSEKSEINEKDLRKKSSELOQTALGNLKQIYYNNSKAITSSSEKSAQDQFLNTLLFKGFFT 284
DB 253 PS-----VFLPPPKP-----KDTLMI----- 268

QY 285 GHPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRL 344
DB 269 -----SRTPEVT-CVVVDVS----- 282

QY 345 TEKKVPIINLWIDGKQTTPIDIKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKV 404
DB 283 HEDPEVKFNWYVDG-----VEVHNAKTPREEQ-----YNSTY---RV 317

QY 405 QRGLIVPHSSEGSTVSYDLFDQAQGYPTDLLRIYRDNTTISSTLSLSLYLTTSIVMTQ 464
DB 318 VSVLTVLHQPDLNGKEY----- 334
```

```
QY 465 TPTSLVAGDRVTITCKASQSVNDVAVYQOKPGOSP KLLISYTSR YAGVDPDRFSGS 524
Db 335 -----KCKVS-----NKALPAP---TEKTSKAKGP----- 358
QY 525 YGTDFTLTISVQAEDAAYVFCQDYNSPPTFGGKLEIKRADAAPTVSIIFPPSEQLT 584
Db 359 -----REPVVTLPPSRDEL 374
QY 585 SGGASVVCFLNNFPKDI NVKWKIDGSRQN-----GVLSNWTDDQSKDSTYSMSSTLTL 639
Db 375 KQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPPVLD-----DGSFFLYSKLTV 427
QY 640 TKDEYERHNSYTCETHK 657
Db 428 DKSRWQQGNVFCSCVMHE 445

RESULT 23
US-11-177-648-31
; Sequence 31, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBELIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H16
US-11-177-648-31
```

```
Query Match 23.7%; Score 833.5; DB 7; Length 462;
Best Local Similarity 31.9%; Pred. No. 1.1e-36;
Matches 216; Conservative 61; Mismatches 128; Indels 273; Gaps 17;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYTHHWVKSPGKGLWIGRIINPNNGVTL 60
Db 20 QVQLVQSGAEVKPGASVKVSKASGYTFTSYMHVVKRPGQGLEWIGNINPNSGGTNY 79
QY 61 NOKFKDKATLTVDKSTTAYMELRSLTSDSAVYICARSTMITNYMDYWGQGTSTVTVSS 120
Db 80 NEKFKSRATLTVDKSTTAYMELSLRSEDATVYICELG-----QGYWGQGTSTVTVSS 132
QY 121 AKTTPSVVPLAPGSAQAQTNMVTGLCLVKGYFPEPVTVTWNSGSLSSGHHVTPFPAVLQSD 180
Db 133 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 192
QY 181 -LYTLSSSVTPSPSTWPESTVTCNVAHPASSTKVDKKIIPRD-----SGG 224
Db 193 GLYSLSVTVTPSSSLGTQYICNVNHPKSTKVDKKVPEKSDKTHKCPCCAPAPELAGA 252
QY 225 PSEKSEINEKDKRKSELOGTALGNLKOIYYNKAITSSEKSAQDFLNTLLPKGFFT 284
Db 253 PS-----VFLPPPKP-----KDTLMI----- 268
QY 285 GHPWYNDLLVDLGLSTAATSEYEGSSVDLYGAYIGYQCAGGTGPNKTACMGYGVTLHDNRL 344
Db 269 -----SRTPEVT-CVVVDVS----- 282
```

```
QY 345 TBEKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKV 404
Db 283 HEDPEVKFNWYDGG---VEVHNATKPREEQ-----YNSTY---RV 317
QY 405 QRGLIVFHSSEGSTVSYDLFDAQGOVPDTLRIYRDNTTISSTLSISLYLTTSIVMTQ 464
Db 318 VSVLTVLHQDWLNGKEY----- 334
QY 465 TPTSLVAGDRVTITCKASQSVNDVAVYQOKPGOSP KLLISYTSR YAGVDPDRFSGS 524
Db 335 -----KCKVS-----NKALPAP---TEKTSKAKGP----- 358
QY 525 YGTDFTLTISVQAEDAAYVFCQDYNSPPTFGGKLEIKRADAAPTVSIIFPPSEQLT 584
Db 359 -----REPVVTLPPSRDEL 374
QY 585 SGGASVVCFLNNFPKDI NVKWKIDGSRQN-----GVLSNWTDDQSKDSTYSMSSTLTL 639
Db 375 KQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPPVLD-----DGSFFLYSKLTV 427
QY 640 TKDEYERHNSYTCETHK 657
Db 428 DKSRWQQGNVFCSCVMHE 445

RESULT 24
US-11-177-648-28
; Sequence 28, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBELIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H700
US-11-177-648-28
```

```
Query Match 23.6%; Score 829.5; DB 7; Length 462;
Best Local Similarity 31.6%; Pred. No. 1.7e-36;
Matches 214; Conservative 64; Mismatches 127; Indels 273; Gaps 17;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYTHHWVKSPGKGLWIGRIINPNNGVTL 60
Db 20 QVQLVQSGAEVKPGASVKVSKASGYTFTSYMHVVKRPGQGLEWIGNINPNSGGTNY 79
QY 61 NOKFKDKATLTVDKSTTAYMELRSLTSDSAVYICARSTMITNYMDYWGQGTSTVTVSS 120
Db 80 NEKFKSRATLTVDKSTTAYMELSLRSEDATVYICELG-----QGYWGQGTSTVTVSS 132
QY 121 AKTTPSVVPLAPGSAQAQTNMVTGLCLVKGYFPEPVTVTWNSGSLSSGHHVTPFPAVLQSD 180
Db 133 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 192
QY 181 -LYTLSSSVTPSPSTWPESTVTCNVAHPASSTKVDKKIIPRD-----SGG 224
Db 193 GLYSLSVTVTPSSSLGTQYICNVNHPKSTKVDKKVPEKSDKTHKCPCCAPAPELAGA 252
QY 225 PSEKSEINEKDKRKSELOGTALGNLKOIYYNKAITSSEKSAQDFLNTLLPKGFFT 284
Db 253 PS-----VFLPPPKP-----KDTLMI----- 268
QY 285 GHPWYNDLLVDLGLSTAATSEYEGSSVDLYGAYIGYQCAGGTGPNKTACMGYGVTLHDNRL 344
Db 269 -----SRTPEVT-CVVVDVS----- 282
```

Db 193 GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVPEKSCDKTKHTCCPPCAPAPELAGA 252
Qy 225 PSEKSEINEKDLRKKSELOGTALGNLKOIYYNYSKAITSEKSAQDQFLNTLLFKGFFT 284
Db 253 PS-----VFLFPPKP-----KDTLMI----- 268
Qy 285 GHPWYNLLVDLGSTAATSEYEGSSVDLYGAIYGYQCAGGTPNKTACMYGGVTLHDNNRL 344
Db 269 -----SRTPEVT-CVVVDVS----- 282
Qy 345 TEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDQARHYLHGKFLGNSDSFGGKV 404
Db 283 HEDEVKFNWYVDG-----VEVHNAKTPREEQ-----YNSTY---RV 317
Qy 405 QRGILVPHSSEGSTVSVDLFDQAQGYEDTLRLIYRDNNTTISSTLSLSLYLTTSIIVMTQ 464
Db 318 VSVLTVLHQDWLNGKEY-----REQVYVTLPPSRDELT 374
Qy 585 SGGASVVCFLNNFPKIDNVKWKIDGSERON-----GVLSNWTDDQSKDSTYSMSSTLTL 639
Db 375 KNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSD-----DGSFFLYSKLTV 427
Qy 640 TKDEYERHNSYTCETHK 657
Db 428 DKSRWQOGNVFSCVMHE 445

RESULT 25

US-11-177-648-97
; Sequence 97, Application US/11/177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLEN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H24
US-11-177-648-97

Query Match 23.5%; Score 827.5; DB 7; Length 462;
Best Local Similarity 31.7%; Pred. No. 2.2e-36;
Matches 215; Conservative 61; Mismatches 129; Indels 273; Gaps 17;
Qy 1 EVOLQQSGPDLVKPGASVKISCKASGYSTGYVMHWKQSPGKGLWIGRINPNNGVTLY 60
Db 20 QVQLVQSGAEVKPKASVKISCKASGYSTGYVMHWKQSPGKGLWIGRINPNNGVTNY 79
Qy 61 NQPKDKATLTVDKSTTAYMELRSLTSEDSAVYCARSTWITNYVMDYWGQGTSTVTVSS 120

Db 80 NEKFASKATLTVDSTSTAYMELSSLSRSEDATVYICELG-----QGYWQOGLTVTVSS 132
Qy 121 AKTTPPSVYPLAPGSAQTNSMTVTLGCLVAGYRPEPVTVTWNSGSLSGVHTFFPAVLQSD 180
Db 133 ASTKGPVFPPLAPSSKSTSGTAAALGCLVADYFPPEPVTVSNWNSGALISGVHTFFPAVLQSS 192
Qy 181 -LYTLSSSVTVPSSTWPFSETVTCNVAHPASSTKVDKKIVPRD-----SGG 224
Db 193 GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVPEKSCDKTKHTCCPPCAPAPELAGA 252
Qy 225 PSEKSEINEKDLRKKSELOGTALGNLKOIYYNYSKAITSEKSAQDQFLNTLLFKGFFT 284
Db 253 PS-----VFLFPPKP-----KDTLMI----- 268
Qy 285 GHPWYNLLVDLGSTAATSEYEGSSVDLYGAIYGYQCAGGTPNKTACMYGGVTLHDNNRL 344
Db 269 -----SRTPEVT-CVVVDVS----- 282
Qy 345 TEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDQARHYLHGKFLGNSDSFGGKV 404
Db 283 HEDEVKFNWYVDG-----VEVHNAKTPREEQ-----YNSTY---RV 317
Qy 405 QRGILVPHSSEGSTVSVDLFDQAQGYEDTLRLIYRDNNTTISSTLSLSLYLTTSIIVMTQ 464
Db 318 VSVLTVLHQDWLNGKEY-----REQVYVTLPPSRDELT 374
Qy 585 SGGASVVCFLNNFPKIDNVKWKIDGSERON-----GVLSNWTDDQSKDSTYSMSSTLTL 639
Db 375 KNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSD-----DGSFFLYSKLTV 427
Qy 640 TKDEYERHNSYTCETHK 657
Db 428 DKSRWQOGNVFSCVMHE 445

RESULT 26

US-11-177-648-96
; Sequence 96, Application US/11/177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLEN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H23
US-11-177-648-96

; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 125
; LENGTH: 442
; TYPE: PRP
; ORGANISM: Homo sapiens
US-11-102-621-125

Query Match 23.4%; Score 825; DB 7; Length 442;
Best Local Similarity 30.6%; Pred. No. 2.8e-36;
Matches 206; Conservative 71; Mismatches 131; Indels 266; Gaps 15;

QY 1 EVOLQSGDPLVKPGASVKISKASGYSTGYTHMHWKQSPGKLEWIGRINPNNGVTLY 60
DB 1 QVQLVQSGAEVKPGSSVKVCKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
QY 61 NQKPKDKATLVTKDSSTAYMELRLSTSEDAVYYCARSTMTINYYMDYWGQGTSTVTVSS 120
DB 61 NQKPKDKATITADESTNTAYMELSLRSEDAVYYCARG---GGVFDYWGQGTSLTVTVSS 116
QY 121 AKTTPPSVPLAPGSAQTNSMTVTLGCLVKGYPEPEVPTVWNSGSLSSGVHTTTPAVLQSD 180
DB 117 ASKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 176
QY 181 -LYTSSSVTPSPSTWPESTVTCNVAHPASSTKVDKKIVPR-----DSGGPSEK 228
DB 177 GLYSLSVTVTPSSNFGTQYTCNVDPKPSNTKVDKVERKCCVPCPAPAAAPS-- 234
QY 229 SEINEKDLRKSELOGTALGNLKQIYYNKAITSSEKADQFLNTLLFKGFFTGHPW 288
DB 235 ---VFLF-----PPKPKDQLMISR-----HEDP 266
QY 289 YNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMGVTLHDNNRLTEEK 348
DB 251 ---TPEVT-CVVVDVS-----HEDP 266
QY 349 KVPINLWIDGKQTTPIDKVTSKKEVTQELDLQARHYLHGKFGLYNSDSFGKVRQGL 408
DB 267 EVQFNWYVDG---VEVHNAKTKPRE-----HEDP 266
QY 409 IVFHSSEGSTVSDLDFAQGYPTDLLRIYRDNTTISTSLSLSLYLYTTSIVMTQTPTS 468
DB 289 ---EQFNSTFRVSVLTVVHOD-----HEDP 266
QY 469 LLVSGADRVITITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGT 528
DB 308 ---WLNKEYKC-----KVSNGKGLPAP 326
QY 529 FTLTISVQAEADAAYFCQDYNPPTFGGKLEIKRADAAPTYSIFPPSSQLTSGGA 588
DB 327 IEKTIKTKGQ-----PREQVYTLPPSREMTKNQV 358
QY 589 SVVCFLLNFPKPDINVKWKIDGSEKRON-----GVLSWTDQDSKSTYSMSLTITKDE 643
DB 359 SLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDS-----DGSFFLYSLKLTVDKSR 411
QY 644 YERHNSYTCEATHK 657
DB 412 WQGNVFCVSMHE 425

RESULT 29
US-11-102-621-127
; Sequence 127, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano

; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
; LENGTH: 442
; TYPE: PRP
; ORGANISM: Homo sapiens
US-11-102-621-127

Query Match 23.4%; Score 825; DB 7; Length 442;
Best Local Similarity 30.6%; Pred. No. 2.8e-36;
Matches 206; Conservative 71; Mismatches 131; Indels 266; Gaps 15;

QY 1 EVOLQSGDPLVKPGASVKISKASGYSTGYTHMHWKQSPGKLEWIGRINPNNGVTLY 60
DB 1 QVQLVQSGAEVKPGSSVKVCKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
QY 61 NQKPKDKATLVTKDSSTAYMELRLSTSEDAVYYCARSTMTINYYMDYWGQGTSTVTVSS 120
DB 61 NQKPKDKATITADESTNTAYMELSLRSEDAVYYCARG---GGVFDYWGQGTSLTVTVSS 116
QY 121 AKTTPPSVPLAPGSAQTNSMTVTLGCLVKGYPEPEVPTVWNSGSLSSGVHTTTPAVLQSD 180
DB 117 ASKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 176
QY 181 -LYTSSSVTPSPSTWPESTVTCNVAHPASSTKVDKKIVPR-----DSGGPSEK 228
DB 177 GLYSLSVTVTPSSNFGTQYTCNVDPKPSNTKVDKVERKCCVPCPAPAAAPS-- 234
QY 229 SEINEKDLRKSELOGTALGNLKQIYYNKAITSSEKADQFLNTLLFKGFFTGHPW 288
DB 235 ---VFLF-----PPKPKDQLMISR-----HEDP 266
QY 289 YNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMGVTLHDNNRLTEEK 348
DB 251 ---TPEVT-CVVVDVS-----HEDP 266
QY 349 KVPINLWIDGKQTTPIDKVTSKKEVTQELDLQARHYLHGKFGLYNSDSFGKVRQGL 408
DB 267 EVQFNWYVDG---VEVHNAKTKPRE-----HEDP 266
QY 409 IVFHSSEGSTVSDLDFAQGYPTDLLRIYRDNTTISTSLSLSLYLYTTSIVMTQTPTS 468
DB 289 ---EQFNSTFRVSVLTVVHOD-----HEDP 266
QY 469 LLVSGADRVITITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGT 528
DB 308 ---WLNKEYKC-----KVSNGKGLPAP 326
QY 529 FTLTISVQAEADAAYFCQDYNPPTFGGKLEIKRADAAPTYSIFPPSSQLTSGGA 588
DB 327 IEKTIKTKGQ-----PREQVYTLPPSREMTKNQV 358
QY 589 SVVCFLLNFPKPDINVKWKIDGSEKRON-----GVLSWTDQDSKSTYSMSLTITKDE 643
DB 359 SLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDS-----DGSFFLYSLKLTVDKSR 411
QY 644 YERHNSYTCEATHK 657
DB 412 WQGNVFCVSMHE 425

RESULT 30
US-11-177-648-29
; Sequence 29, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:


```
QY 589 SVVCFLLNNFYPKDINVWKIDGSRQN-----GVLNSWTDQDSDKDYSSMSTLTLTKE 643
Db 359 SLTCLVKGFYPSDIAVWESNGQPNKYKTPPMLDS-----DGSFFLYSKLTVDKSR 411
QY 644 YERHNSVTCEATHK 657
Db 412 WQGNVFCVSFVHE 425

RESULT 32
US-11-102-621-126
; Sequence 126, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsuruhita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102.621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-126

Query Match 23.3%; Score 822; DB 7; Length 442;
Best Local Similarity 30.6%; Pred. No. 4e-36;
Matches 206; Conservative 71; Mismatches 131; Indels 266; Gaps 15;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYFTGYIMHWVKQSPGKLEWIGRIINPNNGVTLY 60
Db 1 QVQLVQSGAEVKPGSSVKVCKASGYFTSYRMHWVRQAPGQGLEWIGVINSTGYTEY 60
QY 61 NQPKFKDKATLVTKGSTTAYMELRLTSEDSAVYICARSTMTIYNYVNDYQGQTSVTSS 120
Db 61 NQPKFKDKATITADESTNTAYMELSSRLSEDAVYICARG-----GGVFDYMGQGLTVTSS 116
QY 121 AKTTPSPVYPLAPCSAAQTSMVTGLCLVKGYGPEPTVTNNSGLSGGVHTPFAVLQSD 180
Db 117 ASTKGPSPVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 176
QY 181 -LYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKIVPR-----DSGGPSEK 228
Db 177 GLYSLSGVVTPSPSNFTQYTCNVDRKPSNTKVDKIVPRKCCVCPCPAPPAAPS-- 234
QY 229 SEBINEKDLRKKSELOQTALGNLKIYYIYNSKAITSEKSAQDQLTNTLLFKGFTGHPW 288
Db 235 -----VLFPPPKP-----KDTLMI----- 248
QY 289 YNDLLVDLGSATSEYEGSSVDLYGAYYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 348
Db 249 -----SRTPVET-CVVVDVS-----HEDP 266
QY 349 KVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQGR 408
Db 267 EVQFNWYVDG-----VEVHNKATKPRE----- 288
QY 409 IVFHSSEGSSTVSDFLDPAQOQYPTDLLRIYRDNTTISTSLSLXLYTTSIVMTQPTS 468
Db 289 -----EQFNSTFRVSVLTVHQD----- 307
QY 469 LLVSAGDRVTITCKASQSVNDVAWYQKQSPKLLISYTSRYAGVPRFSGSGYGTD 528
Db 308 -----WLNGKEYKC-----KVSNNKGLPAP 326
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QY 529 FTLTISVQAEADAAYFCQDYNSPPTFGGGTKLEIKRADAAPTVAFTSIFPPSSBQLTSGGA 588
Db 327 IEKTIKTKGQ-----PREQVYTLPPSREEMTKNQV 358
QY 589 SVVCFLLNNFYPKDINVWKIDGSRQN-----GVLNSWTDQDSDKDYSSMSTLTLTKE 643
Db 359 SLTCLVKGFYPSDIAVWESNGQPNKYKTPPMLDS-----DGSFFLYSKLTVDKSR 411
QY 644 YERHNSVTCEATHK 657
Db 412 WQGNVFCVSFVHE 425

RESULT 33
US-11-000-463-899
; Sequence 899, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 899
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-899

Query Match 23.3%; Score 821; DB 7; Length 367;
Best Local Similarity 28.2%; Pred. No. 3.8e-16;
Matches 193; Conservative 56; Mismatches 85; Indels 350; Gaps 4;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYFTGYIMHWVKQSPGKLEWIGRIINPNNGV 57
Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMSVWRQAPGKLEWVSGFTSGSGSGS 79
QY 58 TLYNQPKDKATLVTKGSTTAYMELRLTSEDSAVYICARSTMTIYNYV-----M 107
Db 80 TYVADSVKGRFTISRDNSKNTLFLQMNSLRADETAVYCAKGLLPPRWAYRVYEDSGIFF 139
QY 108 DWGQGTSTVTSSAKTTPPSVYPLAPGSAQTSMVTGLCLVKGYGPEPTVTWNSGSL 167
Db 140 DWGQGTSTVTSS----- 153
QY 168 SGVHTFPAVLQSDLYTLSSSVTPSPSTVTCNVAHPASSTKVDKIVPRDSGPFSE 227
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Db 154 ----- 153
QY 228 KSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSAQDFTNLLFKGFTGHP 287
Db 154 ----- 153
QY 288 WYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRLTEE 347
Db 154 ----- 153
QY 348 KKVPIINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQRG 407
Db 154 ----- 156
QY 408 LIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNTTISSTLSISLYLTTTSIVMTQPT 467
Db 157 ----- 162
QY 468 SLLVSAGDRVTITCKASQSVNDVAVYQKPGOSPKLLISYTSRRVAGVDPDRFSGSGYCT 527
Db 163 TLASVGDRTVITCRASQSISSWLAWYQKPGKPKLLIYKASSLQSGVPSRPSGSGGT 222
QY 528 DFTLTSSVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRAADAAPTYSIIPPSSSEQLTSGG 587
Db 223 DFTLTSSLOPDDFATYYCQQLSTYVYTFGQGTQVDIKRTVAAPSVFIIPPSSDEQLKSGT 282
QY 588 ASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSKDSTYSMSSTLTITKDYERH 647
Db 283 ASVVCFLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEXH 342
QY 648 NSYTCEATHKTSPIVKSFNRNE 671
Db 343 KVVACEVTHQGLSSPVTKSFNRGE 366
RESULT 34
US-11-177-648-95
; Sequence 95, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLEN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; PRIOR FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H22
US-11-177-648-95

Query Match 23.2%; Score 818.5; DB 7; Length 462;
Best Local Similarity 31.4%; Pred. No. 6.3e-36;
Matches 213; Conservative 62; Mismatches 130; Indels 273; Gaps 17;
QY 1 EVOLQSGDPLVKPGASVKISKASGYSFTGYGYNHVVKQSPGKLEWIGRINPNNGVTLY 60
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGVTFTSYNHWVVKQRPQGQLEWIGNINPSNGGTNY 79

QY 61 NOKFKDKATLTVDKSTTAYMELSLTSDSAVYVCARSTMITNYYMDYWGQTSVTSS 120
Db 80 NEKFSKATMTDSTSTAYMELSLRSDTAVYICELG-----QGWGQGLTVTSS 132
QY 121 AKTTPPSVYPLAPGAAQTNSMVTLCGLVKGYFPBPVTVWNSGSLSSGVHTFPFVQLQSD 180
Db 133 ASTKGPSVFPAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 192
QY 181 -LYTSSSVTPSSWSPSETVTCNAHPASSTKDKKIVPRD-----SGG 224
Db 193 GLYSVVTVPSSSLGQTQYICNVNHPSPNTKDKKPEPKSCDTHTCPPCPAPPLAGA 252
QY 225 PEEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSAQDFTNLLFKGFTT 284
Db 253 PS-----VLPFPPKP-----KDTLMI----- 268
QY 285 GHPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRL 344
Db 269 -----SRTPEVT-CVVVDVS----- 282
QY 345 TEEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKV 404
Db 283 HEDPEVKFNWYDGG-----VEVHNAKTKPREQ-----YNSTY---RV 317
QY 405 QRGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNTTISSTLSISLYLTTTSIVMTQ 464
Db 318 VSVLTVLHQDWLNGKEY----- 334
QY 465 TPTSLLLVSAGDRVTITCKASQSVNDVAVYQKPGOSPKLLISYTSRRVAGVDPDRFSGSG 524
Db 335 -----KCKVS-----NKALPAP---IEKTISKAGQP----- 358
QY 525 YGTDFTLTSSVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRAADAAPTYSIIPPSSSEQLT 584
Db 359 -----REFQVYTLPPSRDEL 374
QY 585 SGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSKDSTYSMSSTLT 639
Db 375 KQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD-----DGSFELYSLKLT 427
QY 640 TKDEYERHNSYTCEATHK 657
Db 428 DKSRWQQNGVFCSCVMHE 445
RESULT 35
US-11-102-621-130
; Sequence 130, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-130

Query Match 23.2%; Score 817.5; DB 7; Length 447;
Best Local Similarity 32.7%; Pred. No. 6.9e-36;
Matches 217; Conservative 64; Mismatches 143; Indels 239; Gaps 18;

; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 136
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-136

Query Match 23.2%; Score 816; DB 7; Length 446;
Best Local Similarity 30.4%; Pred. No. 8.3e-36;
Matches 205; Conservative 71; Mismatches 136; Indels 262; Gaps 14;

```
QY 1 EVQLQSGDPLVKPGASVKISKASGYFTGYGMHVKQSPGKLEWIGRINPNNGVTLY 60
   :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFISYTMHWVRQAPGQGLEWMGYNPRSGYTH 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 NQFKDKATLTVDKSTTAYMELRSLTSDSAVYYCARSTMTITNYVMDYWGQGTSTVTS 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 NQKLDKATLTADKASTAYMELSLRSEDATVYYCARSAAYDYDGFAYWGQGTSLTVSS 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 AKTTPPSVPLAPGSAAOQNSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 ASTKGSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 -LYTSSSVTPSPSTPSETVTCNVAHPASSSTKVDKIVPR-----DSGGPSEK 228
   :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 181 GLYSLSVTPSPSSNFGTQYTCNVDPKPSNTKVDKVERKCCVECPCPAPPAAPAS-- 238
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 229 SEINEKDLRKSELOQTALGNLKOIYYNYSKAITSSSEKSAQDFLNTLLFKGFFTGHPW 288
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 239 -----VFLPPPKP----- 246
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 289 YNDLLVDLGSTAATSEYSGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 348
   :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 247 KDDLMI-----SRTPEVT-CVVVDVS-----HEDP 270
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 349 KVPINLWIDGKQTTVPIDKVTSKKEVTYVQELDLQARHYLHGKFGLYNSDSFGGKVQRL 408
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 271 EVQFNMYVDG----VEVHNAKTKPRE----- 292
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 409 IVFHSSEGTSVSDLDFAQOQYPTLLRIYRDNNTTISSTLSLSLYLYTTSIVMTQTPTS 468
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 293 -----EQFNSTFRVVSVLTVVHQD----- 311
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 469 LLVSAGDRVITTCASQSVNDVAMVYQKPGQSPKLLISYTSRSYAGVDPDRFSGSGYTD 528
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 312 -----WLNKEYKC-----KVNKGLPAP 330
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 529 FTLTSSVQAEADAAYFCQDYNPSPTFGGKTKLEIKRADAAPTYSIFPPSSQLTSGGA 588
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 331 IEKTIKTKGQ-----PREQVTVTLPPSREEMTKNOV 362
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 589 SVVCFLLNFPYKIDINVKWKIDGSEKQ-----GVLSNWTDDQSDKSTYSMSSTLTITKDE 643
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 363 SLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDS-----DGSFFLYSKLTVDKSR 415
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 644 YERHNSYTCEATHK 657
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 416 WQQGNVFSCSVMHE 429
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
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RESULT 38
US-11-102-621-137
; Sequence 137, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Teurushita, Naoya
; APPLICANT: Tso, J. Yun

; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCGR BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-137

Query Match 23.2%; Score 816; DB 7; Length 446;
Best Local Similarity 30.4%; Pred. No. 8.3e-36;
Matches 205; Conservative 70; Mismatches 137; Indels 262; Gaps 14;

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QY 1 EVQLQSGDPLVKPGASVKISKASGYFTGYGMHVKQSPGKLEWIGRINPNNGVTLY 60
   :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFISYTMHWVRQAPGQGLEWMGYNPRSGYTH 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 NQFKDKATLTVDKSTTAYMELRSLTSDSAVYYCARSTMTITNYVMDYWGQGTSTVTS 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 NQKLDKATLTADKASTAYMELSLRSEDATVYYCARSAAYDYDGFAYWGQGTSLTVSS 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 AKTTPPSVPLAPGSAAOQNSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 ASTKGSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 -LYTSSSVTPSPSTPSETVTCNVAHPASSSTKVDKIVPR-----DSGGPSEK 228
   :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 181 GLYSLSVTPSPSSNFGTQYTCNVDPKPSNTKVDKVERKCCVECPCPAPPAAPAS-- 238
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 229 SEINEKDLRKSELOQTALGNLKOIYYNYSKAITSSSEKSAQDFLNTLLFKGFFTGHPW 288
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 239 -----VFLF-----PPKDKQLMISR----- 254
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 289 YNDLLVDLGSTAATSEYSGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 348
   :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 255 -----TPEVT-CVVVDVS-----HEDP 270
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 349 KVPINLWIDGKQTTVPIDKVTSKKEVTYVQELDLQARHYLHGKFGLYNSDSFGGKVQRL 408
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 271 EVQFNMYVDG----VEVHNAKTKPRE----- 292
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 409 IVFHSSEGTSVSDLDFAQOQYPTLLRIYRDNNTTISSTLSLSLYLYTTSIVMTQTPTS 468
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 293 -----EQFNSTFRVVSVLTVVHQD----- 311
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 469 LLVSAGDRVITTCASQSVNDVAMVYQKPGQSPKLLISYTSRSYAGVDPDRFSGSGYTD 528
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 312 -----WLNKEYKC-----KVNKGLPAP 330
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 529 FTLTSSVQAEADAAYFCQDYNPSPTFGGKTKLEIKRADAAPTYSIFPPSSQLTSGGA 588
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 331 IEKTIKTKGQ-----PREQVTVTLPPSREEMTKNOV 362
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 589 SVVCFLLNFPYKIDINVKWKIDGSEKQ-----GVLSNWTDDQSDKSTYSMSSTLTITKDE 643
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 363 SLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDS-----DGSFFLYSKLTVDKSR 415
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 644 YERHNSYTCEATHK 657
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 416 WQQGNVFSCSVMHE 429
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
```

RESULT 39
US-11-102-621-139
; Sequence 139, Application US/11102621
; Publication No. US20050276799A1

QY 585 SGASVVCFLNNFPKIDNVKWKIDGSRQN-----GVLSNWTDDQSDKSTYSMSSTLT 639
DB 375 KQVSLTCLVKGFYPSDIAVWESNGQPNYKTTTPVLDS-----DGSFFLYSKLTV 427
QY 640 TKDEYERHNSYTCEATHK 657
DB 428 DKSRWQGNVFCSCVMHE 445

RESULT 41
US-11-102-621-140
; Sequence 140, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 140
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-140

Query Match 23.1%; Score 815; DB 7; Length 446;
Best Local Similarity 30.4%; Pred. No. 9.3e-36;
Matches 205; Conservative 70; Mismatches 137; Indels 262; Gaps 14;

QY 1 EVLOQSGDPLVKPGASVKISKASGYFTGYMHVVKSPGKGLWIGRIINPNNGVTLY 60
DB 1 QVOLVQSGAEVKKPGASVKVSKASGYFTSYTMHWVRQAPGQGLEWMGVINPRSGYTH 60
QY 61 NQKFKDKATLTVDKSTTAYMELRLSITSDSAVYYCARSTMITNYVMDYWGQTSVTSS 120
DB 61 NQKLDKATLTADKASTAYMELSLRSEDTAVYYCARSAAYDYDGFAYWGQTLTVSS 120
QY 121 AKTTPPSVPLAPGSAQAQNSMVTLCGLVKGFPEPVTTCNVAHPASSTKVDKIVPR 180
DB 121 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPVTVSNWNSGALTSVGHVTFPAVLQSS 180
QY 181 -LYTLSSSVTPSSSTWSPSETVTCNVAHPASSTKVDKIVPR-----DSGGPSEK 228
DB 181 GLYSLSVVTPSSNFGTQTYTCNVDPKPSNTKVDKVERKCCVCEPCPCPAPPAAPAS-- 238
QY 229 SEINEKDLRKSELQGTALGNLKOIYYNNSKAITTSSEKSAQDLNTLLFKGFFTGHPW 288
DB 239 -----VFLF-----PPPKDQLMISR----- 254
QY 289 YNDLLVDLGSTAATSEYEGSSVDLYGAYGYCAGGTGPNKTACMYGGVTLHDNNRLTEBK 348
DB 255 -----TPEVT-CVVVDVS-----HEDP 270
QY 349 KVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQRL 408
DB 271 EVQFNWYVDG-----VEVHNAKTKPRE----- 292
QY 409 IVPHSSEGSTVSVDLFDAGQCYPTLLRIYRDNNTTISSTLSLSLYLYTTSIVMTQPTS 468
DB 293 -----EQFNSTFRVVSVLTVVHQD----- 311
QY 469 LLVSAGDRVITITKASQGSVNSDVAMWYQKPGQSKLLIISYTSRAGYVDPDRFSGSGYGT 528

DB 312 -----WLNKEYKC-----KVSNGKGLPAP 330
QY 529 FTLTISVQAEADAAVYFCQDYNSPPTFGGKTLBIKRADAAPTYSIFPSPSEQLTSGGA 588
DB 331 IEKTIKTKGQ-----PRBPQVVTLPSPSREEMTKNQV 362
QY 589 SVVCFLLNNFPKIDNVKWKIDGSRQN-----GVLSNWTDDQSDKSTYSMSSTLT 643
DB 363 SLTCLVKGFYPSDIAVWESNGQPNYKTTTPMLDS-----DGSFFLYSKLTVDKSR 415
QY 644 YERHNSYTCEATHK 657
DB 416 WQGNVFCSCVPE 429

RESULT 42
US-11-102-621-131
; Sequence 131, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 131
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-131

Query Match 23.1%; Score 814.5; DB 7; Length 447;
Best Local Similarity 31.7%; Pred. No. 9.9e-36;
Matches 215; Conservative 64; Mismatches 130; Indels 269; Gaps 18;

QY 1 EVLOQSGDPLVKPGASVKISKASGYFTGYMHVVKSPGKGLWIGRIINPNNGVTLY 60
DB 1 QVOLVQSGAEVKKPGSSVVKVSKASGYFTSSWINVWVRQAPGQGLEWIGRIDPSGEVHY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRLSITSDSAVYYCARSTMITNYVMDYWGQTSVTSS 120
DB 61 NQDFKDKATLTVDKSTNTAYMELSLRSEDTAVYYCARGFL--PWPAD-WGQGLTVTVSS 117
QY 121 AKTTPPSVPLAPGSAQAQNSMVTLCGLVKGFPEPVTTCNVAHPASSTKVDKIVPR 180
DB 118 ASTKGPSVFLAPSSKSTSGTAALGCLVKDYFPEPVTVSNWNSGALTSVGHVTFPAVLQSS 177
QY 181 -LYTLSSSVTPSSSTWSPSETVTCNVAHPASSTKVDKIVPRDS-----GG 224
DB 178 GLYSLSVVTPSSSLGTLQTYTCNVNHPKSNKVDKVERKCCVCEPCPCPAPPAELLGG 237
QY 225 PSEKSEINEKDLRKSELQGTALGNLKOIYYNNSKAITTSSEKSAQDLNTLLFKGFFT 284
DB 238 PS-----VFLF-----PPPKDQLMISR----- 255
QY 285 GHPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYCAGGTGPNKTACMYGGVTLHDNNRL 344
DB 256 -----TPEVT-CVVVDVS----- 267
QY 345 TREKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGK 404
DB 268 HEDPEKFNWYVDG-----VEVHNAKTKPREQ-----YNSY---RV 302
QY 405 QRGLIVFHSSEGSTVSVDLFDAGQCYPTLLRIYRDNNTTISSTLSLSLYLYTTSIVMTQ 464


```
Db 303 VSVLTVLHQDWLNGKEY----- 319
QY 465 TPTSLVLSAGDRVTITCKASQSVSNDVAVYQKPGQSPKLLISYTSRVAGVDFRFGSG 524
Db 320 -----KCKVS-----NKALPAP-----IEKTIKAKGP----- 343
QY 525 YGTDFTLTISVQAEDAAYVFCQDYNSPPTFGGGTKEIKRADAAPTIVSIFPPSSEQLT 584
Db 344 -----KCKVS-----NKALPAP-----IEKTIKAKGP----- 359
QY 585 SGGASVVCFLNNFYPKDINVKWKIDGSERON-----GVLNSWTDQDQSKDSTYMSSTLT 639
Db 360 KNQVSLTCLVKGFPYPSDIAVWESNGQPNENYKTPPVLDSD-----DGSFFLYSKLTV 412
QY 640 TKDEYERHNSYTCEATHK 657
Db 413 DKSRWQOQGNVFCSCVLMHE 430

RESULT 43
US-11-102-621-133
; Sequence 133, Application US/11102621
; Publication No. US2005027699A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tsao, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 133
; TYPE: PRT
; LENGTH: 447
; ORGANISM: Homo sapiens
US-11-102-621-133

Query Match 23.1%; Score 814.5; DB 7; Length 447;
Best Local Similarity 31.7%; Pred. No. 9.9e-36;
Matches 215; Conservative 64; Mismatches 130; Indels 269; Gaps 18;

QY 1 EVQLQSGDPLVKPGASVKISKASGYFTGYMHVWKQSPGKGLWIGRIINPNNGVTL 60
Db 1 QVQLVQSGAELEKPGSSVKVSKASGYFTFTSSMINVWKQAPQGQGLEWIGRIDPSDGEVHY 60
QY 61 NQKFKDKATLTVDKSSSTAYMELRSLTSDSAVYYCARSTMTITNYMDYWGQGSTVTSS 120
Db 61 NQDFKDKATLTVDKSTNTAYMELSLRSDTAVYYCARGFL--PWFAD-WGQGLTVTVSS 117
QY 121 AKTTPPSVPLAPGSAQNTSMVTLGCLVKGYPEPPTVTVNWSGSLSSGGVHTFPVQLQSD 180
Db 118 ASTKGSPVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWSGALTSGVHTFPVQLQSS 177
QY 181 -LYLTSSSVTVPSSTWSPSETVTCNVAHPASSTKVDKKIVPRDS-----GG 224
Db 178 GLYSLSVTVTPSSSLGTQYICNVNHPKSNTKVDKKVBPCKDTHCTCPPCAPPELLGG 237
QY 225 PSEKSEINEKDKLRKSEELQGTALGNLKOIYYNKAITSSEKSAQDQFLNTTLFKGFFT 284
Db 238 PS-----VFLF-----PPKPKDQLMISR----- 255
QY 285 GHPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPTNKTAACMGVGLHDNRL 344
Db 256 -----TPEVT-CVVVDVS----- 267
```

```
QY 345 TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDQARHYLHGKFGLYNSDSFGKV 404
Db 268 HEDPEVKFNWYVDG---VEVHNAKTKPREQ-----YNSTY---RV 302
QY 405 QRGLIVFHSESEGSVSYDLFDAQGOYPTLLRLIYRDNNTTISSTLSLSLTYTTSVMTQ 464
Db 303 VSVLTVLHQDWLNGKEY----- 319
QY 465 TPTSLVLSAGDRVTITCKASQSVSNDVAVYQKPGQSPKLLISYTSRVAGVDFRFGSG 524
Db 320 -----KCKVS-----NKALPAP-----IEKTIKAKGP----- 343
QY 525 YGTDFTLTISVQAEDAAYVFCQDYNSPPTFGGGTKEIKRADAAPTIVSIFPPSSEQLT 584
Db 344 -----KCKVS-----NKALPAP-----IEKTIKAKGP----- 359
QY 585 SGGASVVCFLNNFYPKDINVKWKIDGSERON-----GVLNSWTDQDQSKDSTYMSSTLT 639
Db 360 KNQVSLTCLVKGFPYPSDIAVWESNGQPNENYKTPPVLDSD-----DGSFFLYSKLTV 412
QY 640 TKDEYERHNSYTCEATHK 657
Db 413 DKSRWQOQGNVFCSCVLMHE 430

RESULT 44
US-11-177-648-27
; Sequence 27, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLEN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; TYPE: PRT
; LENGTH: 462
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H6
US-11-177-648-27

Query Match 23.1%; Score 814.5; DB 7; Length 462;
Best Local Similarity 31.1%; Pred. No. 1e-35;
Matches 211; Conservative 65; Mismatches 129; Indels 273; Gaps 17;

QY 1 EVQLQSGDPLVKPGASVKISKASGYFTGYMHVWKQSPGKGLWIGRIINPNNGVTL 60
Db 20 QVQLVQSGAEVKKPGASVKVSKASGYFTTSYMHVWRQAPQGQLEWIGNINFGGTNY 79
QY 61 NQKFKDKATLTVDKSSSTAYMELRSLTSDSAVYYCARSTMTITNYMDYWGQGSTVTSS 120
Db 80 NEKFKSRATWTRDTSTSTAYMELSLRSDTAVYYCELG-----QGYWGQGLTVTVSS 132
QY 121 AKTTPPSVPLAPGSAQNTSMVTLGCLVKGYPEPPTVTVNWSGSLSSGGVHTFPVQLQSD 180
Db 133 ASTKGSPVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWSGALTSGVHTFPVQLQSS 192
QY 181 -LYLTSSSVTVPSSTWSPSETVTCNVAHPASSTKVDKKIVPRD-----SGG 224
Db 193 GLYSLSVTVTPSSSLGTQYICNVNHPKSNTKVDKKVBPCKDTHCTCPPCAPPELLAGA 252
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QY 225 PSEKSEINEKDLKKSELOQTALGNLKOIYYNKAITSSEKSAQDLTNTLLPKGFFT 284
Db 253 PS-----VFUFPKPB-----KDTLMI-----268
QY 285 GHPWYNLLVLDLSTAAATSEYEGSSVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRL 344
Db 269 -----SRTPEVT-CVVVDVS-----282
QY 345 TEEKKVPINLWIDGKOTTPIDKVKTSKEVTVQELDLQARHYLHGKFLGYNDSDFGGKV 404
Db 283 HEDPEVKFNWYDVG---VEVHNKTKPREEQ-----YNSTY---RV 317
QY 405 QRGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNNTTISSTLSLSLYLTTISIVMTQ 464
Db 318 VSVLTVLHQDWLNGKEY-----334
QY 465 TPTSLLSVAGDRVTITCKASQSVSNDAVYQKPGQSPKLLISYTSRVRAGVDPDRPSGSG 524
Db 335 -----KCKVS-----NKALPAP---TEKTISKAKGP-----358
QY 525 YGTDFTLTISVQAEDAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTYSIIPPPSEQLT 584
Db 359 -----REPOVYTLPPSRDEL 374
QY 585 SGGASVVCFLNNFYPKDINVWKIDGSRQN-----GVLSNWTDDQSKDSTYSMSSTLTL 639
Db 375 KNOVSLTCLVKGFPSPDI AVEWESNGQPNYKTTTPVLDS-----DGSFFLYSKLTV 427
QY 640 TKDEYERHNSYTCEATHK 657
Db 428 DKSRWQOQGNVFCSSVWHE 445

RESULT 45
US-11-102-621-134
; Sequence 134, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 134
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-134

Query Match 23.1%; Score 813.5; DB 7; Length 447;
Best Local Similarity 31.7%; Pred. No. 1.1e-35;
Matches 215; Conservative 64; Mismatches 130; Indels 269; Gaps 18;

QY 1 EVLOQSGPDLVKPGASVKISCKASGYFTGYMHVWKSPGKGLWIGRIINPNNGVTLY 60
Db 1 QVQLVQSGAELKKPGSSVKVSKASGYFTSSMINVWKQAPGQGLEWIGRIDPDSGEVHY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRLSTSEDAVYYCARSTMTITNYMDYWGQGSTVTVSS 120
Db 61 NQDFKDKATLTVDKSTNTAYMELSLRSEDAVYYCARGFL--PWFAF-WGQGLTVTVSS 117
QY 121 AKTTPPSVPLAPGSAQNTNSMVTLCGLVKGYPEPPTVTWNSGSLSSGSGVTFPPAYLQSD 180

Db 118 ASTKGSPVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSMNSGALTSGVHTFPAVLQSS 177
QY 181 -LYTILSSSVTPSSSTWSPSETVTCNVAHPASSTKVDKKIVPRDS-----GG 224
Db 178 GLYSLSVVTVSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCTCPCPAPPELLGG 237
QY 225 PEKSEINEKDLKKSELOQTALGNLKOIYYNKAITSSEKSAQDLTNTLLPKGFFT 284
Db 238 PS-----VFUFP-----PPKPKDQLMISR-----255
QY 285 GHPWYNLLVLDLSTAAATSEYEGSSVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRL 344
Db 256 -----TPEVT-CVVVDVS-----267
QY 345 TEEKKVPINLWIDGKOTTPIDKVKTSKEVTVQELDLQARHYLHGKFLGYNDSDFGGKV 404
Db 268 HEDPEVKFNWYDVG---VEVHNKTKPREEQ-----YNSTY---RV 302
QY 405 QRGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNNTTISSTLSLSLYLTTISIVMTQ 464
Db 303 VSVLTVLHQDWLNGKEY-----319
QY 465 TPTSLLSVAGDRVTITCKASQSVSNDAVYQKPGQSPKLLISYTSRVRAGVDPDRPSGSG 524
Db 320 -----KCKVS-----NKALPAP---TEKTISKAKGP-----343
QY 525 YGTDFTLTISVQAEDAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTYSIIPPPSEQLT 584
Db 344 -----REPOVYTLPPSRDEL 359
QY 585 SGGASVVCFLNNFYPKDINVWKIDGSRQN-----GVLSNWTDDQSKDSTYSMSSTLTL 639
Db 360 KNOVSLTCLVKGFPSPDI AVEWESNGQPNYKTTTPVLDS-----DGSFFLYSKLTV 412
QY 640 TKDEYERHNSYTCEATHK 657
Db 413 DKSRWQOQGNVFCSSVWHE 430

RESULT 46
US-11-102-621-138
; Sequence 138, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 138
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-138

Query Match 23.1%; Score 813; DB 7; Length 446;
Best Local Similarity 30.4%; Pred. No. 1.2e-35;
Matches 205; Conservative 70; Mismatches 137; Indels 262; Gaps 14;

QY 1 EVLOQSGPDLVKPGASVKISCKASGYFTGYMHVWKSPGKGLWIGRIINPNNGVTLY 60
Db 1 QVQLVQSGAELKKPGSSVKVSKASGYFTISYMHVWRQAPGQGLEWIGVINPRSGTHY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRLSTSEDAVYYCARSTMTITNYMDYWGQGSTVTVSS 120

Db 61 NOKLKD KATLTADKSASTAYMELSSLRSEDATVYCARSAAYDYDGFAYWQGTTLTVSS 120
Qy 121 AKTTPPSVYPLAPGSAAOQNSMVTGLCKVKGYPEPVTWNSGSLSSGVHTTFAVLQSD 180
Db 121 ASTKGSVFLAPLCSSTSESTALGCLVKDYFPEPVTWNSGALTSGVHTTFAVLQSS 180
Qy 181 -LYTSSSVTPSSTWPSSTVTCNVAHPASSTKVDKXIVPR-----DSGGPSEK 228
Db 181 GLYLSVSVTPSSTWPSSTVTCNVAHPASSTKVDKXIVPR-----VFLPFPKP 238
Qy 229 SEBINEKDLKXSELQALGNLKOIYYNSKAITSSSEKSAQDLTNTLLFKGFFTHPW 288
Db 239 -----VFLPFPKP-----KDTLMI----- 252
Qy 289 YNDLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMGVTLHDNNRLTEEK 348
Db 253 -----SRTPVT-CVVVDVS-----HEDP 270
Qy 349 KVPINLWIDKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLGNSDSFGKVGQRL 408
Db 271 EVQFNWYVDG-----VEVHNAKTPRE----- 292
Qy 409 IVPHSSEGSTVSDLDFAQOQYPTDLRIYRDNTTISSTLSLSLYLYTTSIVMTQTPS 468
Db 293 -----EQFNSTFRVSVLTVHQD----- 311
Qy 469 LTVSAGDRVTITCKASQSVNDVAVYQKQSPKLLISYTSRYAGVDPDRFSGSGVGD 528
Db 312 -----WLNKGEYK-----KVNKGLPAP 330
Qy 529 FTLTSSVQAEADAAYVFCQDYNPSPTFGGKTKLEIKRADAAPTIFPPSSQLTSGGA 588
Db 331 IEKTISSKTKGQ-----PREQVTVLTPSREEMTKNQV 362
Qy 589 SVVCFPLNFPKQINVKWKIDGSRQN-----GVLSWTDQDSKDYSSMSTLTITKDE 643
Db 363 SLTCLVKGFYPSDIAVEWESNGQPPENNYKTPPMLDS-----DGSFFLYSKLTVDKSR 415
Qy 644 YERHNSVTCETHK 657
Db 416 WQGNVFCSVLHE 429

RESULT 47
US-11-102-621-132
; Sequence 132, Application US/11102621
; Publication No. US2005027679A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tsao, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 132
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-132

Query Match 23.1%; Score 812.5; DB 7; Length 447;
Best Local Similarity 22.7%; Pred. No. 1.3e-35;
Matches 217; Conservative 62; Mismatches 145; Indels 239; Gaps 18;

Qy 1 EVOLQSGPDLVKPGASVKISKASGYSTGYTHMHWKSPGKGLWIGRINPNNGVTLY 60
Db 1 QVQLVQSGAELKKPGSSVKVCKASGYFTSTSWINWVKQAPGQGLEWIGRIPDSGEVHY 60

Qy 61 NQFKDKATLTVDKSSSTTAYMELSLTSDSAVYCARSTMTITNYVMDYWGQGTSTVSS 120
Db 61 NQFKDKATLTVDKSSSTTAYMELSLTSDSAVYCARSTMTITNYVMDYWGQGTSTVSS 117

Qy 121 AKTTPPSVYPLAPGSAAOQNSMVTGLCKVKGYPEPVTWNSGSLSSGVHTTFAVLQSD 180
Db 118 ASTKGSVFLAPLCSSTSESTALGCLVKDYFPEPVTWNSGALTSGVHTTFAVLQSS 177

Qy 181 -LYTSSSVTPSSTWPSSTVTCNVAHPASSTKVDKXIVPRDSGSPSEKSENEKDLRK 239
Db 178 GLYLSVSVTPSSTWPSSTVTCNVAHPASSTKVDKXIVPRDSGSPSEKSENEKDLRK 220

Qy 240 KSELQGTALGNLKOIYYNSKAITSSSEKSAQDLTNTLLFKGFFTHPWINDLLVDLST 299
Db 221 -----DKHTCPKPAPELLGGPSVF--LFPKPP--KDTLM----- 252

Qy 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMGVTLHDNNRLTEKKVPINLWIDGK 359
Db 253 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVDG- 281

Qy 360 QTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLGNSDSFGKVGQRLIVFHSSEGSTV 419
Db 282 ---VEVHNAKTPRE---YNSTY---RVSVLTVLHQDWLNGK 317

Qy 420 SYDLFDAQOQYPTDLRIYRDNTTISSTLSLSLYLYTTSIVMTQTPSLTVSAGDRVTI 479
Db 318 EY----- 319

Qy 480 TKCASQSVNDVAVYQKQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTSSVQAE 539
Db 320 KCKVS-----NKALPAP--IEKTISSKAKGP----- 343

Qy 540 DAAVYFCQDYNPSPTFGGKTKLEIKRADAAPTIFPPSSQLTSGGASVWVCFLNFPY 599
Db 344 -----REPOVYTLPPSRDELTKNQVSLTCLVKGFY 374

Qy 600 KOINVKWKIDGSRQN-----GVLSWTDQDSKDYSSMSTLTITKDEYERHNSVTC 654
Db 375 SDIAVEWESNGQPPENNYKTPPMLDS-----DGSFFLYSKLTVDKSRWQGNVFCSV 427

Qy 655 THK 657
Db 428 LHE 430

RESULT 48
US-11-177-648-92
; Sequence 92, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLEN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; PRIOR FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 462
; TYPE: PRT

Db 428 DKSRWQQGNVFCSCVMHE 445

RESULT 51

US-11-177-648-79

; Sequence 79, Application US/11177648

; Publication No. US20060029603A1

; GENERAL INFORMATION:

; APPLICANT: Jonathon Henry ELLIS

; APPLICANT: Paul Andrew HAMBLIN

; APPLICANT: Paul Alexander WILSON

; APPLICANT: Alan Peter LEWIS

; TITLE OF INVENTION: IMMUNOGLOBULINS

; FILE REFERENCE: PB60608-2

; CURRENT APPLICATION NUMBER: US/11/177,648

; CURRENT FILING DATE: 2005-07-06

; PRIOR APPLICATION NUMBER: PCT/GB2004/005325

; PRIOR FILING DATE: 2004-12-20

; PRIOR APPLICATION NUMBER: GB0329711.6

; PRIOR FILING DATE: 2003-12-22

; PRIOR APPLICATION NUMBER: GB0329684.5

; PRIOR FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 113

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 79

; LENGTH: 462

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: 2A10 heavy chain humanised construct H1

US-11-177-648-79

Query Match 22.8%; Score 803.5; DB 7; Length 462;

Best Local Similarity 30.7%; Pred. No. 3.8e-35;

Matches 208; Conservative 66; Mismatches 131; Indels 273; Gaps 17;

Qy 1 EVQLQGGPDLVPKASVKISKASGYSTFGYVMHWKQSPGKLEWIGRINPNNGVTLY 60

Db 20 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYVMHWVRAQPGQGKLEWIGRINPNNGVTNY 79

Qy 61 NQPKDKATLTVDKSSSTAWEIERSLTSDSAVYVCARSTMITNYMDYKGGTSTVTSS 120

Db 80 NEPKGRVMTROTSTSTVMEUSSRSEDTAVYCELG-----QYWGQGLVTVSS 132

Qy 121 AKTTTPSVYPLAPGSAAQTNMSWVTLGCLVKGYFPEPVTVTWNSGSLSSGVHPTFPVILQSD 180

Db 133 ASTKGFSVPFLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 192

Qy 181 -LYTLSSSVTPGSTWPFSEFTVCNVAHPASTKVDKKIIPRD-----SGG 224

Db 193 GLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTKCPCPAPELAGA 252

Qy 225 PSEKSEINEKDLRKSELOGTALGNLKOIYYVNSKAITSSSEKSAQDPLTNTLLFKGFFT 284

Db 253 PS-----VFLPFPKP-----KDTLMI----- 268

Qy 285 GHPWYNDLLVDLGSTAATSEYEGSSVDLYGAYYGYQCAGGTPNKTAQMGVTLHDNRL 344

Db 269 -----SETPEVT-CVVVDVS----- 282

Qy 345 TEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKV 404

Db 283 HEDPEVKFNWYVDG---VEVHNAKTKPREQ-----YNSTY---RV 317

Qy 405 QRGLIVFHSSEGSTVSVDLEDAQGVPTDLLRIYRDNRTTISSTLSLSLYLYTTSIVMTQ 464

Db 318 VSVLTVLHQLWLNKKEY----- 334

Qy 465 TPTSLLSVAGDRVITTCIKASQSVNDVAMVQQKPGOSPKLLISYTSRVRAGVDRFSGSG 524

Db 335 -----KCKVS-----NKALPAP-----IEKTSIKAKQGP----- 358

Qy 525 YGTDFTLTISGVQAEDAAVYFCQDDVNSPPTFGGKTKLEIKRADAAPTVAIFPPPSSEQLT 584

Qy 478 TITCKASQSVNDVAMVYQKPGOSPKLLISYTSRYAGVDPDRFSGSGYGTDLTTLTSSVQ 537
Db 325 --KCKV5-----NKALPAP---IEKTISKAKGP----- 348
Qy 538 AEDAAVYFCOODYNSPPTFGGKLEIKRADAAPTUSIFPPPSSEQLTSGGASVVCFLNNF 597
Db 349 -----REPOVYTLPPSREEMTKNQVSLTCLVKGF 377
Qy 598 YPKDINVKWIDGERON-----GVLNSWTDQDSKOSTYSMSSTLTTLTKDEYERHNSYTC 652
Db 378 YPSDIAVWESNGQPNENYKTPPVLD5-----DGSFFLYSKLTVDKSRWQGNVFSC 430
Qy 653 EATHK 657
Db 431 SVMHE 435

RESULT 54
US-11-107-028-32
; Sequence 32, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 32
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-32

Query Match 22.7%; Score 800; DB 7; Length 452;
Best Local Similarity 31.4%; Pred. No. 5.6e-35;
Matches 209; Conservative 65; Mismatches 153; Indels 238; Gaps 17;

Qy 1 EVOLQSGPDLVKPGASVKISKASGYSTGYTMHWKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAASGYFTSYNNHWVRQAPGKLEWVGAIYPGNGDTSY 60
Qy 61 NQKFKDKATLTVDKSSSTAYMELRSLTSDSAVYICARSTMTN--YVMDYWGQGTSTV 118
Db 61 NQKFKGRFTISVDKSKNTLYLQMSLRAEDTAVYICARVVYSNSYWFYDVGQGLTV 120
Qy 119 SSAKTPPSPVYPLAPGSAATNSMTLGLVKGYFPPEPTVTWNSGSLSGVHTFPAVLQ 178
Db 121 SSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPPEPTVSWNSGALTSGVHTFPAVLQ 180
Qy 179 SD-LYTLSSSVTPSSSLGQTQYICNVNHPKSNKVDKVPKSC----- 225
Db 181 SSGLYSLSSVTPSSSLGQTQYICNVNHPKSNKVDKVPKSC----- 225
Qy 238 RKSELOQTALGNLKOIYYNSKAITSSSEKSAQDLTNTLLFKGFTFGHPWYNDLLVDLG 297
Db 226 -----DKHTCTPCCPAPPELLGGPSVF--LFPKP--KDTLM-- 257
Qy 298 STAATSEYEGSSVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRLTEBKKVPINLWID 357
Db 258 -----ISRTPEVT--CVVVDVS-----HEDPEVKFNWYVD 285
Qy 358 GKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGQGLVPHSSEGS 417
Db 286 G-----VEVHNAKTPREEQ-----INSTY---RVVSVLTVLHQDLN 320

Qy 418 TVSYDLFDAQQGVYDPTLLRIYRDNMTTISSTLSISLYLTYTTSIVMTQTPTSLLSVAGDRV 477
Db 321 GKEY----- 324
Qy 478 TITCKASQSVNDVAMVYQKPGOSPKLLISYTSRYAGVDPDRFSGSGYGTDLTTLTSSVQ 537
Db 325 --KCKV5-----NKALPAP---IEKTISKAKGP----- 348
Qy 538 AEDAAVYFCOODYNSPPTFGGKLEIKRADAAPTUSIFPPPSSEQLTSGGASVVCFLNNF 597
Db 349 -----REPOVYTLPPSREEMTKNQVSLTCLVKGF 377
Qy 598 YPKDINVKWIDGERON-----GVLNSWTDQDSKOSTYSMSSTLTTLTKDEYERHNSYTC 652
Db 378 YPSDIAVWESNGQPNENYKTPPVLD5-----DGSFFLYSKLTVDKSRWQGNVFSC 430
Qy 653 EATHK 657
Db 431 SVMHE 435

RESULT 55
US-11-106-820-26
; Sequence 26, Application US/11106820
; Publication No. US20060002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 26
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-106-820-26

Query Match 22.7%; Score 800; DB 7; Length 452;
Best Local Similarity 31.4%; Pred. No. 5.6e-35;
Matches 209; Conservative 65; Mismatches 153; Indels 238; Gaps 17;

Qy 1 EVOLQSGPDLVKPGASVKISKASGYSTGYTMHWKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAASGYFTSYNNHWVRQAPGKLEWVGAIYPGNGDTSY 60
Qy 61 NQKFKDKATLTVDKSSSTAYMELRSLTSDSAVYICARSTMTN--YVMDYWGQGTSTV 118
Db 61 NQKFKGRFTISVDKSKNTLYLQMSLRAEDTAVYICARVVYSNSYWFYDVGQGLTV 120
Qy 119 SSAKTPPSPVYPLAPGSAATNSMTLGLVKGYFPPEPTVTWNSGSLSGVHTFPAVLQ 178
Db 121 SSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPPEPTVSWNSGALTSGVHTFPAVLQ 180
Qy 179 SD-LYTLSSSVTPSSSLGQTQYICNVNHPKSNKVDKVPKSC----- 225
Db 181 SSGLYSLSSVTPSSSLGQTQYICNVNHPKSNKVDKVPKSC----- 225
Qy 238 RKSELOQTALGNLKOIYYNSKAITSSSEKSAQDLTNTLLFKGFTFGHPWYNDLLVDLG 297
Db 226 -----DKHTCTPCCPAPPELLGGPSVF--LFPKP--KDTLM-- 257
Qy 298 STAATSEYEGSSVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRLTEBKKVPINLWID 357
Db 258 -----ISRTPEVT--CVVVDVS-----HEDPEVKFNWYVD 285

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QY 358 GKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQGRGLIVFHSSEGS 417
Db 286 G-----VEVHNAKTKPREQ-----YNSTY-----RVSVLTVLHQDWLN 320
QY 418 TVSYDLFDAQGOVPTDLLRIYRDNNTTSSLSLSISLYLTTISVMTQTPTSLVASGDRV 477
Db 321 GKEY-----324
QY 478 TITCKASQSVSNDAVYQKPGSPKLLISYTSRRYAGVDPDRFSGSGYGTDFLTITSSVQ 537
Db 325 --KCKVS-----NKALPAP---IEKTIKAKGQP-----348
QY 538 AEDAAVYFCQDYNPSPTFGGKLEIKRADAAPTVSIIRPPSSEQLTSGASVVCFLNPF 597
Db 349 -----REPQVYTLPPSREEMTKNQVSLTCLVKGF 377
QY 598 YPKDINVKWKIDGSRQN-----GVLNSWTDQDSKDYSTYSMSSTLTLTCKDEYERHNSYTC 652
Db 378 YPSDIAVESNGQPNENYKTTTPPVLDS-----DGSFPLYSKLTVDKSRWQGNVFSC 430
QY 653 EATHK 657
Db 431 SVMHE 435

RESULT 56
US-11-143-077-14
; Sequence 14, Application US/11143077
; Publication No. US20060024295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/617,997
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 14
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-143-077-14

Query Match 22.7%; Score 800; DB 7; Length 452;
Best Local Similarity 31.4%; Pred. No. 5.6e-35;
Matches 209; Conservative 65; Mismatches 153; Indels 238; Gaps 17;

QY 1 EVOLQSGPDLVKPGASVKISKASGYSTGYGMHWKQSPGKLEWIGRIINPNNGVTL 60
Db 1 EVOLVESGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKLEWVGAIYFGNGDTSY 60
QY 61 NQKFKDKATLVDSKSTTAYMELRSLTSDSAVYICARSTMITN--YVMDYWGQGTSTV 118
Db 61 NQKFKGRFTISVDKSKNTLYLQWNSLRAEDTAVYICARVYVYNSYMYFDVWGQGLTV 120
QY 119 SSAKTTTPPSVYPLAPGSAQTNSMVTLCGLVKGYFPPEPTVTWNSSGSLSGVHTFPVLQ 178
Db 121 SSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 180
QY 179 SD--LYTLSSSVTPPSWTPSETVTCNVAHPASSTKVDKIKIVPRDSGGPSEKSEINEKOL 237
Db 181 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKVKPEKSC-----225
QY 238 RKKSELOQTALGNLKOIYYNSKAITSEKSAQDQFLNTLLFKGFTTGHWPYNDLLVDLG 297
Db 226 -----DKTHTCPPCPAPELLGGPSVF--LPFPKP--KDTLM---257
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNRLTEKKVPINLWID 357

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Db 258 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 285
QY 358 GKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQGRGLIVFHSSEGS 417
Db 286 G-----VEVHNAKTKPREQ-----YNSTY-----RVSVLTVLHQDWLN 320
QY 418 TVSYDLFDAQGOVPTDLLRIYRDNNTTSSLSLSISLYLTTISVMTQTPTSLVASGDRV 477
Db 321 GKEY-----324
QY 478 TITCKASQSVSNDAVYQKPGSPKLLISYTSRRYAGVDPDRFSGSGYGTDFLTITSSVQ 537
Db 325 --KCKVS-----NKALPAP---IEKTIKAKGQP-----348
QY 538 AEDAAVYFCQDYNPSPTFGGKLEIKRADAAPTVSIIRPPSSEQLTSGASVVCFLNPF 597
Db 349 -----REPQVYTLPPSREEMTKNQVSLTCLVKGF 377
QY 598 YPKDINVKWKIDGSRQN-----GVLNSWTDQDSKDYSTYSMSSTLTLTCKDEYERHNSYTC 652
Db 378 YPSDIAVESNGQPNENYKTTTPPVLDS-----DGSFPLYSKLTVDKSRWQGNVFSC 430
QY 653 EATHK 657
Db 431 SVMHE 435

RESULT 57
US-11-106-820-25
; Sequence 25, Application US/11106820
; Publication No. US20060002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 25
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-106-820-25

Query Match 22.7%; Score 800; DB 7; Length 471;
Best Local Similarity 31.4%; Pred. No. 5.8e-35;
Matches 209; Conservative 65; Mismatches 153; Indels 238; Gaps 17;

QY 1 EVOLQSGPDLVKPGASVKISKASGYSTGYGMHWKQSPGKLEWIGRIINPNNGVTL 60
Db 20 EVOLVESGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKLEWVGAIYFGNGDTSY 79
QY 61 NQKFKDKATLVDSKSTTAYMELRSLTSDSAVYICARSTMITN--YVMDYWGQGTSTV 118
Db 80 NQKFKGRFTISVDKSKNTLYLQWNSLRAEDTAVYICARVYVYNSYMYFDVWGQGLTV 139
QY 119 SSAKTTTPPSVYPLAPGSAQTNSMVTLCGLVKGYFPPEPTVTWNSSGSLSGVHTFPVLQ 178
Db 140 SSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 199
QY 179 SD--LYTLSSSVTPPSWTPSETVTCNVAHPASSTKVDKIKIVPRDSGGPSEKSEINEKOL 237
Db 200 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKVKPEKSC-----244
QY 238 RKKSELOQTALGNLKOIYYNSKAITSEKSAQDQFLNTLLFKGFTTGHWPYNDLLVDLG 297

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Db 245 -----DKTHTCPAPPELLGSPV--LPPPKP--KDTLM-- 276
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTGNKTKACMYGGVTLHDNNRLTEKKVPIINLWID 357
Db 277 -----ISRTPEVT--CVVVDVS-----HEDPEVKFNWYVD 304
QY 358 GKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLGYNDSFGGKVQVGLIIVFHSSEGS 417
Db 305 G-----VEVHNAKTKPREEQ-----YNSTY---RVVSVLTVLHQDWLNL 339
QY 418 TVSYDLFDAAGQVPTDLLRIYRDNNTTSSLSLSLYLTTSIVMTQTPTSLLSVAGDRV 477
Db 340 GKEY-----ISRTPEVT--CVVVDVS-----HEDPEVKFNWYVD 343
QY 478 TITCKASQSVNDVAMVYQKPGOSPKLLISYTSRVRAGVDPDRFSGSGYGTDTLTITSSVQ 537
Db 344 --KCKVS-----NKALPAP---IEKTLISKAKGP----- 367
QY 538 AEDAAVYFCQDYNPPTFGGKTKLEIKRADAAPTYSIFPPPSSEQLTSGGASVVCFLNPF 597
Db 368 -----REPQVYTLPPSREEMTKNQVSLTCLVKGF 396
QY 598 YPKDINVKWKIDGSEKON-----GVLSNWTDDQSKDSTYSMSSTLTILTKDEYERHNSYTC 652
Db 397 YPSDIAVEWESNGQPENNYKTPPPVLDS-----DGSFFLYSKLTVDKSRWQGNVFSC 449
QY 653 EATHK 657
Db 450 SVMHE 454

RESULT 58
US-11-190-364-22
; Sequence 22, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1P1
; CURRENT APPLICATION NUMBER: US/11/190,364
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 11/147,780
; PRIOR FILING DATE: 2005-06-07
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 22
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-190-364-22

Query Match 22.7%; Score 800; DB 7; Length 471;
Best Local Similarity 31.4%; Pred. No. 5.8e-35;
Matches 209; Conservative 65; Mismatches 153; Indels 238; Gaps 17;

QY 1 EVOLQSGDPLVKPGASVKISCKASGYSTGYIMHWVKQSPGKGLIEWIGRINPNNGVTLY 60
Db 20 EVQLVESGGGLVPGGSLRLSCAASGYTFYSYNHWVRQAPGKLEWVGAIYPNGDTSY 79
QY 61 NQPKDKATLTVDKSTTAYMELRSITSDSAVYICARSTMITN--YVMDYWGQGTSTVTV 118
Db 80 NQKFKGRFTISVDKSKNTLYLQMSLRAEDTAVYICARVYVYSNSYWFYFVWGQGLTVTV 139
QY 119 SSATKTPPSVPLAPGSAATNSMTLGLCLVKKYFPPEPTVTVWNSGSLSSGVHTFFPAVLQ 178
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Db 140 SSASTKGPSVFPPLAPSPKSTSGGTAALGCLVKKDYFPPEPTVTVWNSGALTSGGVHTFFPAVLQ 199
QY 179 SD--LYTLSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIKIVPRDSDGGPSEKSEINEKDL 237
Db 200 SSGLYSLSSVTVTPSSSLGTQTIVCNVHKPSNTKVDKKVEPKSC----- 244
QY 238 RKKSELQGTALGNLKOIYYNSKAITSSSEKSAQDLTNLLFFKGFTTGHWPYNDLLVDLG 297
Db 245 -----DKTHTCPAPPELLGSPV--LPPPKP--KDTLM-- 276
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTGNKTKACMYGGVTLHDNNRLTEKKVPIINLWID 357
Db 277 -----ISRTPEVT--CVVVDVS-----HEDPEVKFNWYVD 304
QY 358 GKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLGYNDSFGGKVQVGLIIVFHSSEGS 417
Db 305 G-----VEVHNAKTKPREEQ-----YNSTY---RVVSVLTVLHQDWLNL 339
QY 418 TVSYDLFDAAGQVPTDLLRIYRDNNTTSSLSLSLYLTTSIVMTQTPTSLLSVAGDRV 477
Db 340 GKEY-----ISRTPEVT--CVVVDVS-----HEDPEVKFNWYVD 343
QY 478 TITCKASQSVNDVAMVYQKPGOSPKLLISYTSRVRAGVDPDRFSGSGYGTDTLTITSSVQ 537
Db 344 --KCKVS-----NKALPAP---IEKTLISKAKGP----- 367
QY 538 AEDAAVYFCQDYNPPTFGGKTKLEIKRADAAPTYSIFPPPSSEQLTSGGASVVCFLNPF 597
Db 368 -----REPQVYTLPPSREEMTKNQVSLTCLVKGF 396
QY 598 YPKDINVKWKIDGSEKON-----GVLSNWTDDQSKDSTYSMSSTLTILTKDEYERHNSYTC 652
Db 397 YPSDIAVEWESNGQPENNYKTPPPVLDS-----DGSFFLYSKLTVDKSRWQGNVFSC 449
QY 653 EATHK 657
Db 450 SVMHE 454

RESULT 59
US-11-120-338-15
; Sequence 15, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IOBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 15
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-15

Query Match 22.7%; Score 798; DB 7; Length 452;
Best Local Similarity 30.8%; Pred. No. 7.1e-35;
Matches 207; Conservative 69; Mismatches 144; Indels 252; Gaps 17;

QY 1 EVOLQSGDPLVKPGASVKISCKASGYSTGYIMHWVKQSPGKGLIEWIGRINPNNGVTLY 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGYTFYSYNHWVRQAPGKLEWVGAIYPNGDTSY 60
QY 61 NQPKDKATLTVDKSTTAYMELRSITSDSAVYICARSTMITN--YVMDYWGQGTSTVTV 118
Db 61 NQKFKGRFTISVDKSKNTLYLQMSLRAEDTAVYICARVYVYSNSYWFYFVWGQGLTVTV 120
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QY 119 SAKTTPSVYPLAPGSAQAQTNMWTLCGLVKGYPPEPVTVTWNSGSLSSGSHHTPPAVLQ 178
Db 121 SASTKGPVFPPLAPSSKSTSGTAAALGCLVXDYFPEPVTVSWNSGALTSGVHTPPAVLQ 180
QY 179 SD-LYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDDKIVPRDSCGPGSEKSEINEKDL 237
Db 181 SGLVSLSSVTVPSSSLGTQYICNVNHPKPNKVDKVEPKSC----- 225
QY 238 RKKSELQGTALGNLQIYYYNKAITSSSEKSDQFLNTLLFKGFFTHGHPWYNDLLVDLG 297
Db 226 -----DKTHTCPPCPAPPELLGGPSVF--LPPKP--KDTLM--- 257
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTPNKACTMYGGVTLHDNNRLTEKKVPIINLWID 357
Db 258 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 285
QY 411 FHSSEGSTVSYDLFDAQGYQYPTDLLRIYRDNTTISSTLSISLYLYTTTSIVMTQTPTSL 470
Db 323 -----EY----- 324
QY 471 VSAGDRVTTCASQSVNDVAWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFT 530
Db 325 -----KCKVS-----NKALPAP---IAATISKAKGQP----- 348
QY 531 LTISVQAEDAAYVFCQDYNSPPTFGGKLEIKRADAAPTIVSIPPPSEQLTSGGASV 590
Db 349 -----REPQYVTLPPBREEMTKNOVSL 370
QY 591 VCFLNFPYKIDINVKWKIDGSRQN-----GVLSNMTDQDSKDYMSSTLTLTKEDEYE 645
Db 371 TCLVKGFPYSDIAVESNGQPNVYKTPPVLDL-----DGSFFLYSKLTVDKSRWQ 423
QY 646 RHNSYTCETHK 657
Db 424 QGNVFCSCVMHE 435

RESULT 60
US-11-107-028-33
; Sequence 33, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 33
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-33

Query Match 22.7%; Score 798; DB 7; Length 452;
Best Local Similarity 30.8%; Pred. No. 7.1e-35;
Matches 207; Conservative 69; Mismatches 144; Indels 252; Gaps 17;

QY 1 EVQLQQSGPDLVRPGASVKISKASGYSTFGYYMHVWKQSPGKLEWIGRINPNNGVTLV 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNNHVRQAPGKLEWVGAIYPCNGDTSY 60

QY 61 NOKFKDKATLTVDKSGSTTAYMELRSLTSEDSAVVYCARSTMITN--YVMDYMGQGTSTV 118
Db 61 NOKFKGRFTISVDKSKNTLYLQMNLSRAEDTAVYCARVVYSNSWYEDVNGQGLTIV 120
QY 119 SAKTTPSVYPLAPGSAQAQTNMWTLCGLVKGYPPEPVTVTWNSGSLSSGSHHTPPAVLQ 178
Db 121 SASTKGPVFPPLAPSSKSTSGTAAALGCLVXDYFPEPVTVSWNSGALTSGVHTPPAVLQ 180
QY 179 SD-LYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDDKIVPRDSCGPGSEKSEINEKDL 237
Db 181 SGLVSLSSVTVPSSSLGTQYICNVNHPKPNKVDKVEPKSC----- 225
QY 238 RKKSELQGTALGNLQIYYYNKAITSSSEKSDQFLNTLLFKGFFTHGHPWYNDLLVDLG 297
Db 226 -----DKTHTCPPCPAPPELLGGPSVF--LPPKP--KDTLM--- 257
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTPNKACTMYGGVTLHDNNRLTEKKVPIINLWID 357
Db 258 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 285
QY 358 GKQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGKFGLYNSDSFGGKVQORGLIV 410
Db 286 G-----VEVHNKTKPREEQYNATYRVVSVLTVLHQDWLNGK----- 322
QY 411 FHSSEGSTVSYDLFDAQGYQYPTDLLRIYRDNTTISSTLSISLYLYTTTSIVMTQTPTSL 470
Db 323 -----EY----- 324
QY 471 VSAGDRVTTCASQSVNDVAWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFT 530
Db 325 -----KCKVS-----NKALPAP---IAATISKAKGQP----- 348
QY 531 LTISVQAEDAAYVFCQDYNSPPTFGGKLEIKRADAAPTIVSIPPPSEQLTSGGASV 590
Db 349 -----REPQYVTLPPBREEMTKNOVSL 370
QY 591 VCFLNFPYKIDINVKWKIDGSRQN-----GVLSNMTDQDSKDYMSSTLTLTKEDEYE 645
Db 371 TCLVKGFPYSDIAVESNGQPNVYKTPPVLDL-----DGSFFLYSKLTVDKSRWQ 423
QY 646 RHNSYTCETHK 657
Db 424 QGNVFCSCVMHE 435

RESULT 61
US-11-106-820-28
; Sequence 28, Application US/11106820
; Publication No. US20060002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 28
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-106-820-28

Query Match 22.7%; Score 798; DB 7; Length 452;
Best Local Similarity 30.8%; Pred. No. 7.1e-35;
Matches 207; Conservative 69; Mismatches 144; Indels 252; Gaps 17;

[illegible]

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RESULT 62
US-11-143-077-15
; Sequence 15, Application US/11143077
; Publication No. US20060024295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/617,997
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 15
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-143-077-15

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Query Match

22.7%; Score 798; DB 7; Length 452;

Best Local Similarity 30.8%; Pred: No. 7.1e-35;	
Matches 207; Conservative 69; Mismatches 144; Indels 252; Gaps 17;	
Qy	1 EVLOQSGPDLVKPGASVKISKASGYSEFTGYMHVVKOSPGKGLEWIGRINPNNGVTLY 60
Db	1 EVLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHVVRQAPGKGLEWGAIFYPGNGDTSY 60
Qy	61 NQFKPKALITVDKSTTAYMEURSLTSEDSAVVYCARSTMITN--YVMDYWGQGSVTV 118
Db	61 NQFKGRFTISVDKSKNTLYLQMSLRAEDTAVVYCARVVVYSNSYWFYFDVMGQGLTVT 120
Qy	119 SSATKTPPSVYPLAPGSAQTNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTEPAVLQ 178
Db	121 SSASTKGPSVFPPLAPSGKSTGGTAALGCLLVKDYFPEPVTVSNWNSGALTSGVHTEPAVLQ 180
Qy	179 SD-LYTLSSSVTVPPSSVTPSETVTCNVAHPASSTKYDKKIVPRDSGSGPSEKSEINEKDL 237
Db	181 SSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSC-----225
Qy	238 RKKSELQGTALGNLKOIYYNSKAITSSEKSAQDFLTNTLLFKGFTGHPWYNDLLVLDL 297
Db	226 -----DKTHCTPCPCAPPELLGGPSVF--LPPPKP--KDTLM---257
Qy	298 STAATSEYEGSSVDLYGAYGYOCAGTGNKTCACMGVYTLHDNNRLTEKKYPINLWID 357
Db	258 -----ISRTPEVT--CVVDVDS-----HEDPEYKFNMYVD 285
Qy	358 GKQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGKFGLYNSDSFGGKVQGRGLV 410
Db	286 G-----VEVHNATKPREQYNATYRVSVULTVLHQDLNKG-----322
Qy	411 FHSSEGSTVSYDLFDAGQGYPDTLRLRIYRDNTTISSTSLISLYLYTTSIVMTQTPTSLL 470
Db	323 -----EY-----324
Qy	471 VSGDRVITTCASQSVSNVDVAWYQQKPGQSPKLLISYTSRRYAGVDPDRFSGSGYGTDF 530
Db	325 -----KCKVS-----NKALPAP--IAATISKAKGQF-----348
Qy	531 LTISVQAEDAAYVFCQDYNSPPTFGGKTLEIKRADAAPTYSIFPPSEQLTSGASV 590
Db	349 -----REPQVYTLPPSREEMTKNQVSL 370
Qy	591 VCFLNPFYPRDINVKWKIDGSEKQN-----GVLSNWTQDQSKDSTYSMSSTLTLTDEYE 645
Db	371 TCLVKGFYPSDIAVESNGSQPNKYKTPPVLDSE-----DGSFFLYSKLTVDKSRWQ 423
Qy	646 RHNSYTCETHK 657
Db	424 QGNVFSQSVNME 435
RESULT 63	
US-11-106-820-27	
; Sequence 27, Application US/11106820	
; Publication No. US20060002930A1	
; GENERAL INFORMATION:	
; APPLICANT: BRUNETTA, PAUL G	
; APPLICANT: SEWELL, KATHRYN L.	
; TITLE OF INVENTION: Treatment of Disorders	
; FILE REFERENCE: P2102R1	
; CURRENT APPLICATION NUMBER: US/11/106,820	
; CURRENT FILING DATE: 2005-04-15	
; PRIOR APPLICATION NUMBER: US 60/563,227	
; PRIOR FILING DATE: 2004-04-16	
; PRIOR APPLICATION NUMBER: US 60/565,098	
; PRIOR FILING DATE: 2004-04-22	
; NUMBER OF SEQ ID NOS: 45	
; SEQ ID NO 27	
; LENGTH: 471	
; TYPE: PRT	
; ORGANISM: Artificial sequence	
; FEATURE:	

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; OTHER INFORMATION: sequence is synthesized
US-11-106-820-27

Query Match      22.7%; Score 798; DB 7; Length 471;
Best Local Similarity 30.8%; Pred. No. 7.4e-35;
Matches 207; Conservative 69; Mismatches 144; Indels 252; Gaps 17;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHVWVQSPGKGLEWIGRIINPNNGVTLV 60
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVROAPGKGLEWGAIIYPNGDTSY 79
QY 61 NQKFKDKATLTVDKSTTAYMELRLSDSAVYICARSTMITN--YVMDYWGQGSVTV 118
DB 80 NQKFKGRFTISVDKSKNTLYLQWNSLRADTAIVYICARVVYSNSYWFYDVMGQGLTVV 139
QY 119 SSAKTTTPSVYPLAPGSAATQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVTHTPPAVLQ 178
DB 140 SSAATKGPSVFPPLAPGSKTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQ 199
QY 179 SD-LYTLSSVTVPSSTWPSSETVTCNVAPASSTKVDKIVPRDSGGPSEKSEINEKDL 237
DB 200 SSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSC----- 244
QY 238 RKKSELQGTALGNLQIYYVNSKAITSEKSDAQFLTNTLLFKGFTGHPVNDLLVDLG 297
DB 245 -----DKTHTCPPCPAPPELLGGPSV--LPFPKP--KDTLM--- 276
QY 298 STAATSEYEGSSVDLYGAYGYQCAGTPNKTACMYGGVTLHDNNRLTBEKKVPINLWID 357
DB 277 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 304
QY 358 GKQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGKFGLYNSDSFGGKVGQGLIV 410
DB 305 G-----VEVHNAKTKEEQYNATYRVVSVLTVLHQDWLNGK----- 341
QY 411 FHSSEGSTVSYDLFDAQGYQPDTLRLIYRDNTTISSTLSLSILYLTYSIVMTQTPTSL 470
DB 342 -----EY----- 343
QY 471 VSAGDRVTITCKASQSVNDVAWYQKPGQSKLLISYTSRYAGVDPDRFSGSGYGTDTFT 530
DB 344 -----KCKVS-----NKALPAP---IAATISKAKGP----- 367
QY 531 LTISSVQAEDAAYVFCQDYNSPPTFGGGTKLEIKRADAAPTYSIFPPSSEQLTSGASV 590
DB 368 -----REPQVYTLPPSREEMTKNQVSL 389
QY 591 VCFLNPFYPKDINVKWKIDGSRQN-----GVLSNMTDQDSKDYSMSTLTLTCKDEYE 645
DB 390 TCLVKGFPYSDIAVENESNGQPNYKTTTPVLDS-----DGSFFLYSKLTVDKSRWQ 442
QY 646 RHNSYTCETHK 657
DB 443 QGNVFSCSVME 454

RESULT 64
US-11-190-364-23
; Sequence 23, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P19903C1P1
; CURRENT APPLICATION NUMBER: US/11/190,364
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 11/147,780
;

; PRIOR FILING DATE: 2005-06-07
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 23
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-190-364-23

Query Match      22.7%; Score 798; DB 7; Length 471;
Best Local Similarity 30.8%; Pred. No. 7.4e-35;
Matches 207; Conservative 69; Mismatches 144; Indels 252; Gaps 17;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHVWVQSPGKGLEWIGRIINPNNGVTLV 60
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVROAPGKGLEWGAIIYPNGDTSY 79
QY 61 NQKFKDKATLTVDKSTTAYMELRLSDSAVYICARSTMITN--YVMDYWGQGSVTV 118
DB 80 NQKFKGRFTISVDKSKNTLYLQWNSLRADTAIVYICARVVYSNSYWFYDVMGQGLTVV 139
QY 119 SSAKTTTPSVYPLAPGSAATQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVTHTPPAVLQ 178
DB 140 SSAATKGPSVFPPLAPGSKTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQ 199
QY 179 SD-LYTLSSVTVPSSTWPSSETVTCNVAPASSTKVDKIVPRDSGGPSEKSEINEKDL 237
DB 200 SSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSC----- 244
QY 238 RKKSELQGTALGNLQIYYVNSKAITSEKSDAQFLTNTLLFKGFTGHPVNDLLVDLG 297
DB 245 -----DKTHTCPPCPAPPELLGGPSV--LPFPKP--KDTLM--- 276
QY 298 STAATSEYEGSSVDLYGAYGYQCAGTPNKTACMYGGVTLHDNNRLTBEKKVPINLWID 357
DB 277 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 304
QY 358 GKQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGKFGLYNSDSFGGKVGQGLIV 410
DB 305 G-----VEVHNAKTKEEQYNATYRVVSVLTVLHQDWLNGK----- 341
QY 411 FHSSEGSTVSYDLFDAQGYQPDTLRLIYRDNTTISSTLSLSILYLTYSIVMTQTPTSL 470
DB 342 -----EY----- 343
QY 471 VSAGDRVTITCKASQSVNDVAWYQKPGQSKLLISYTSRYAGVDPDRFSGSGYGTDTFT 530
DB 344 -----KCKVS-----NKALPAP---IAATISKAKGP----- 367
QY 531 LTISSVQAEDAAYVFCQDYNSPPTFGGGTKLEIKRADAAPTYSIFPPSSEQLTSGASV 590
DB 368 -----REPQVYTLPPSREEMTKNQVSL 389
QY 591 VCFLNPFYPKDINVKWKIDGSRQN-----GVLSNMTDQDSKDYSMSTLTLTCKDEYE 645
DB 390 TCLVKGFPYSDIAVENESNGQPNYKTTTPVLDS-----DGSFFLYSKLTVDKSRWQ 442
QY 646 RHNSYTCETHK 657
DB 443 QGNVFSCSVME 454

RESULT 65
US-11-183-205-56
; Sequence 56, Application US/11183205
; Publication No. US20060030521A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bowe, Caryn
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QY 471 VSAGDRVTITCKASQSVNDVAVYQKPGQPKLLISYTSRRYAGVDPDRFGSGGYGTDFT 530
Db 325 -----KCKVS-----NKALPAP-----IAATISKAKGP----- 348
QY 531 LTISSVQAEADAAYFYCQDYNSPPTFGGKTLEIKRAADAAPTYSIFPPSSQELTSGGASV 590
Db 349 -----EQYAST-YRVVSVLTVLHQDWLNGKEY----- 320
QY 591 VCFLNPFYPKDINVWKIDGSRQN-----GVLSNWTQDQSKDSTYSMSSTLTLTXYDEYR 645
Db 371 TCLVKGFPSPDIAVEWESNGQPNKYKTPPVLDSE-----DGSFFLYSKLTVDKSRMQ 423
QY 646 RNSYTCETHK 657
Db 424 QGNVFCSCVMHE 435

RESULT 67
US-11-158-505-16
; Sequence 16, Application US/111158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; PRIOR FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 16
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody heavy chain construct
US-11-158-505-16

Query Match 22.5%; Score 792; DB 7; Length 448;
Best Local Similarity 31.5%; Pred. No. 1.4e-34;
Matches 209; Conservative 67; Mismatches 149; Indels 238; Gaps 17;

QY 1 EVOLQSGPDLVKPGASVKISKASGYSTGYVMHWKSPGKGLWIGRINPNNGVTLY 60
Db 1 QVOLVSGAEVKKPGASVKSKASGYTTAYVISWRQAPGQGLEWMGEIYFGSSSY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRSLSSEDSAYVYCARSTMTITNYVMDYWGQTSVTSS 120
Db 61 NEKFKGRVTWTRDTSTSTVMELSLRSEDTAVVYCARSGDGRFV--YWGQGLTVTVSS 118
QY 121 AKTTPSPVPLAPGSAQAQNSMTVLGCLVKGYPPEPVTVTNWNSGSLSSGVHTFPVLQSD 180
Db 119 ASTKGPSVPLAPSSKTSGGTAAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPVLQSS 178
QY 181 -LYTLSSSVTVPSSTWPSSTVTCNVAHPASSTKVDKKIIPRDSGGPSEKSEENEDLRK 239
Db 179 GLYSLSVTVTPSSSLGTQYICNVNHPKSNKTKVDKKEPKSC----- 221
QY 240 KSELOGTALGNLKIQIYYNSKAITSEKSDAQDFLTNTLTFKGPFTGHPWYNLDLLVGLST 299
Db 222 -----DKHTCCPCAPPELLGGPSVF--LFPKPK--KDTLM----- 253
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPTNKATCMYGVGTLHDNRLTEKKVPINLMDGK 359
Db 254 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVDG-- 282
QY 360 QTTVPIDKVKTSKEVTVQBELDQARHLYHGKFLYNSDSFGKVGQRGLIVFHSSEGSTV 419
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Db 283 -----VEVHNAKTPRE----- 294
QY 420 SYDLFDAQOQYPTDLLRIYRDNTTISSTLSLSLYLYTTSIVMTQPTSLLSVAGDRVTI 479
Db 295 -----EQYAST-YRVVSVLTVLHQDWLNGKEY----- 320
QY 480 TCKASQSVNDVAVYQKPGQPKLLISYTSRRYAGVDPDRFGSGGYGTDFTLTSSVQAE 539
Db 321 KCKVS-----NKALPAP-----IEKTSKAKGP----- 344
QY 540 DAAVFCQDYNSPPTFGGKTLEIKRAADAAPTYSIFPPSSQELTSGGASVVCFLNNFYP 599
Db 345 -----REQVYTLPPSRDELTKNOVSLTCLVKGFPY 375
QY 600 KDINVWKIDGSRQN-----GVLSNWTQDQSKDSTYSMSSTLTLTXYDEYRINSTCEA 654
Db 376 SDIAVEWESNGQPNKYKTPPVLDSE-----DGSFFLYSKLTVDKSRMQGNVFCSCV 428
QY 655 THK 657
Db 429 MHE 431

RESULT 68
US-11-158-505-32
; Sequence 32, Application US/111158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; PRIOR FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 32
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: heavy chain construct
US-11-158-505-32

Query Match 22.5%; Score 792; DB 7; Length 448;
Best Local Similarity 31.5%; Pred. No. 1.4e-34;
Matches 209; Conservative 67; Mismatches 149; Indels 238; Gaps 17;

QY 1 EVOLQSGPDLVKPGASVKISKASGYSTGYVMHWKSPGKGLWIGRINPNNGVTLY 60
Db 1 QVOLVSGAEVKKPGASVKSKASGYTTAYVISWRQAPGQGLEWMGEIYFGSSSY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRSLSSEDSAYVYCARSTMTITNYVMDYWGQTSVTSS 120
Db 61 NEKFKGRVTWTRDTSTSTVMELSLRSEDTAVVYCARSGDGRFV--YWGQGLTVTVSS 118
QY 121 AKTTPSPVPLAPGSAQAQNSMTVLGCLVKGYPPEPVTVTNWNSGSLSSGVHTFPVLQSD 180
Db 119 ASTKGPSVPLAPSSKTSGGTAAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPVLQSS 178
QY 181 -LYTLSSSVTVPSSTWPSSTVTCNVAHPASSTKVDKKIIPRDSGGPSEKSEENEDLRK 239
Db 179 GLYSLSVTVTPSSSLGTQYICNVNHPKSNKTKVDKKEPKSC----- 221
QY 240 KSELOGTALGNLKIQIYYNSKAITSEKSDAQDFLTNTLTFKGPFTGHPWYNLDLLVGLST 299
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Db 222 -----DKHTCCPPCAPPELLGGPSVF--LPPPKP--KOTLM----- 253
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTGNKTAACMYGGVTLHDNNRLTEKKVPIINLWDGK 359
Db 254 -----DKHTCCPPCAPPELLGGPSVF--LPPPKP--KOTLM----- 257
QY 360 QTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSSEGSTV 419
Db 283 ---VEVHNKTKPRE-----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 285
QY 420 SYDLFDAQGOVPTLLRIYRDNTTISSTLSISLYLYTTTSIVMTQTPSLLVAGDRVTI 470
Db 295 -----EQAST-YRVSVTLVHQDWLNGKEY----- 322
QY 480 TCKASQSVNDVAVYQOQPGQSKLLISYTSRRYAGVDPDRFSGSGYGTDTFTLTISSVQAE 539
Db 321 KCKVS-----NKALPAP--LEKTSKAKGQP----- 324
QY 540 DAAVYFCQDYNPPPTFGGQTKLEIKRADAAPTYSIPPSSEQLTSGGASVVCFLNFPY 599
Db 345 -----REPQVYTLPPSRDELTKNQVSLTCLVRGFPY 375
QY 600 KDINVKWKIDGSRQN-----GVLSNWTDDQSKDSTYSMSLTLTCKDEYERHNSYCEA 654
Db 376 SDIAYVESNGQPNENYKTTTPPVLDL-----DGSFFLYSKLTVDKSRWQGNVFSV 423
QY 655 THK 657
Db 429 MHE 431

RESULT 69
US-11-120-338-25
; Sequence 25, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P20792
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 25
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-25

Query Match 22.5%; Score 792; DB 7; Length 451;
Best Local Similarity 30.5%; Pred. No. 1.4e-34;
Matches 205; Conservative 70; Mismatches 145; Indels 252; Gaps 17;
QY 1 EVOLQSGDPLVKPGASVKISKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVOLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVROAPGKLEWVGAIYFGNGATSY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRSITSEDSAVYYCARSTMIT--NYVMDYWGQGSVTV 118
Db 61 NQKFKGRFTISVDKSKNTLYLQWNSLRABDTAVYCARVYVYRYWYFDVWGQGLTVT 120
QY 119 SSAKTTTPPSVYPLAPGSAQTNSMVTLCGLVKGYFPPEVTVTNWNSGSLSSGVHTTFAVLQ 178
Db 121 SSASTKGPSVFPPLAPSSKTSFGTAALGCLVKDYPPEVTVSNWNSGALTSGVHTTFAVLQ 180
QY 179 SD-LYTLSSSVTVPSSTWSEVTVCNVAHPASTKVDKLVPRDSDGPGSEKSEINEKDL 237
Db 181 SSGLYSLSSVTVPPSSSLGQTQYICNVNHPKSNKTKVDKKEPKSC----- 225

QY 238 RKKSELQGTALGNLKOIYYYNKAITSSSEKSAQDQFLNTLLFKGFFTHGFWYNDLLVLDG 297
Db 226 -----DKHTCCPPCAPPELLGGPSVF--LPPPKP--KOTLM----- 257
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTGNKTAACMYGGVTLHDNNRLTEKKVPIINLWD 357
Db 258 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 285
QY 358 GKQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGKFGLYNSDSFGKVGQGLIV 410
Db 286 G-----VEVHNKTKPREEQYNATYRVSVTLVHQDWLNGK----- 322
QY 411 FHSSEGSTVSYDLFDAQGOVPTLLRIYRDNTTISSTLSISLYLYTTTSIVMTQTPSLL 470
Db 323 -----EY----- 324
QY 471 VSAGDRVTITCKASQSVNDVAVYQOQPGQSKLLISYTSRRYAGVDPDRFSGSGYGTDTFT 530
Db 325 -----KCKVSNAAL-----PAP--IAATISKAKGQP----- 348
QY 531 LTISVQAEADAAVYFCQDYNPPPTFGGQTKLEIKRADAAPTYSIPPSSEQLTSGGASV 590
Db 349 -----REPQVYTLPPSRDELTKNQVSLTCLVRGFPY 375
QY 591 VCFLNFPYKIDINVKWKIDGSRQN-----GVLSNWTDDQSKDSTYSMSLTLTCKDEYE 645
Db 371 TCLVKGFPDIAVWESNGQPNENYKTTTPPVLDL-----DGSFFLYSKLTVDKSRWQ 423
QY 646 RHNSYTCETHK 657
Db 424 QGNVFSVSMHE 435

RESULT 70
US-11-143-077-22
; Sequence 22, Application US/11143077
; Publication No. US20060024295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/617,997
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 22
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-143-077-22

Query Match 22.5%; Score 792; DB 7; Length 451;
Best Local Similarity 30.5%; Pred. No. 1.4e-34;
Matches 205; Conservative 70; Mismatches 145; Indels 252; Gaps 17;
QY 1 EVOLQSGDPLVKPGASVKISKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVOLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVROAPGKLEWVGAIYFGNGATSY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRSITSEDSAVYYCARSTMIT--NYVMDYWGQGSVTV 118
Db 61 NQKFKGRFTISVDKSKNTLYLQWNSLRABDTAVYCARVYVYRYWYFDVWGQGLTVT 120
QY 119 SSAKTTTPPSVYPLAPGSAQTNSMVTLCGLVKGYFPPEVTVTNWNSGSLSSGVHTTFAVLQ 178
Db 121 SSASTKGPSVFPPLAPSSKTSFGTAALGCLVKDYPPEVTVSNWNSGALTSGVHTTFAVLQ 180

Qy	179	SD-LVTLSSVTPSGTWPSEVTVCNVAHPASTKVDDKIVPRDGGPSEKSEENKDL	237
Db	181	SSGLYSLSSVTPVSSSLGTQYICNVNHPKNTKVKKVEPKSC-----	225
Qy	238	RKSELOGTALGNLKQIYYINSKAITSEKSDAQFLTNTLLPKGFETHGWPYNDLLVDLG	297
Db	226	-----DKTHCTPCPAPELLGGPSVF--LFPKP--KDTLM---	257
Qy	298	STAATSEYEGSVDLYGAYGYQCAGGTENKTACWVGVTLHDNNRLTEBKVKPINLMWD	357
Db	258	-----ISRPEVT-CVVVDVS-----HEDPEVKFNWYVD	285
Qy	358	GKQTTVPIDKVKTSKEV-----TVQELDIQARHYLHGKFGLYNSDSFGGKVQRG LIV	410
Db	286	G-----VEVHNAKTKPREEQNATYRVSVLTVLHQDWLNGK-----	322
Qy	411	FHSSGSGSVYDLDPAQOQYPTTLRIYRDNTTISTSTSISLYLYTTSIVMTQPTSL	470
Db	323	-----EY-----	324
Qy	471	VSAGDRVITITCASQSVSNDVAWYQQKPGQSKLLISYTSRVAGVDPDRFSGSGYGTDT	530
Db	325	-----KCKVSNAAAL-----PAP--IAATISKAKGQP-----	348
Qy	531	LTISVQAEADAAYFCQDYNSPPTFGGCTKLEIKRADAAPTYSVIPPPSSEQLTSGGASV	590
Db	349	-----REPQYITLPPREEMTKNOVSL	370
Qy	591	VCFLNFPYKIDINVKWIDGSRQN-----GVLNSWTDQDSKDSYVSMSTLTTLTKDEVE	645
Db	371	TCLVKGFFYPSDIAVWESNGQPNKYKTTFPVLDLS-----DGSPFLYSLKLTVDKSRWQ	423
Qy	646	RHNSVTCETHAK	657
Db	424	OGNVFSCSVMHE	435

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RESULT 71
US-11-120-338-17
; Sequence 17, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 17
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-17

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Db	121	SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDIFPPPEVTVSWNSGALTSGVHPFPAVLQ	180
Qy	179	SD-LYTLSSSVTVPSSSTWSPBETVCNVAHPASSTKDKKIVPRDSGGPSEKSEINEKDL	237
Db	181	SSGLYSLSSVVTVPSSSLGTQYICNVNHKPSNTKVKDKVEPKSC-	225
Qy	238	RKXSELOGTALGNLKQIYYIYNSKAITTSEKSAADQFLNTLLFKGPFTHGHPWYNDLLVDLG	297
Db	226	-----DKTHTCPPCPAPELLGGPSVF--LFPKPK--KDTLM-----	257
Qy	298	STAATSEYEGSSVDLYGAYGYQCAGGTTPNKACMYGGVTLHDNNRLTEKKKVPINLMID	357
Db	258	-----ISRTPEVT-CVVVDVS-----HEDPEVKENWYVD	285
Qy	358	GKQTTVPIDKVKTSKKEV-----TVQELDLQARHYLHGKFGLYNSDSFGKGVGORGLIV	410
Db	286	G-----VEVHNAKTPREBEQYNATYRVVSVLTVLHQDWLNGK-----	322
Qy	411	FHSSEGSTSVSYDLFDAQGYQPDTLRLIRYDRDNTTISSTLSISLYLYTTSIVMTQPTSLI	470
Db	323	-----EY-----	324
Qy	471	VSAGRVTITCKASQSVSNDVAMVYQKPGQSPKLLISYTSRYAGVPPDRFSGSGYGTDTFT	530
Db	325	-----KCKVSNAAAL-----PAP-----IAATISKAKGQP-----	348
Qy	531	LTISVQAEADAANYFCQODYNSPPTFGGTXLEIKRAADAAPTVISIFPPSSQLTSGGASV	590
Db	349	-----REFQVYTLPPSREEMTKNQVSL	370
Qy	591	VCFLNNFPKDIIVKWKIDGSERON-----GVLNSWTDQDSKDSYTSYMSSTLTLPKDEYE	645
Db	371	TCLVKGYFSPSDIAVEWESNGQENPNYKTTTPVLDS-----DGSFFLYSKLTVKDSRWQ	423
Qy	646	RHNSYTCEATHK	657
Db	424	QGNVFSGSVMHE	435

```

RESULT 72
US-11-107-028-43
; Sequence 43, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 43
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-43

```

```

Query Match      22.5%; Score 792; DB 7; Length 452;
Best Local Similarity 30.5%; Pred. No. 1.4e-34;
Matches 205; Conservative 70; Mismatches 145; Indels 252; Gaps 17

Qy 1 EVQLQQSGPDLVPCASVKISCKASGYSTGYMHVHKQSPGKGLEWIGRINPNNGVLT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 EVQLVESGGGLVQPGGSLRLCSAASGYTFTSYMHVWRQAPGKGLEWVGAIPGNGATSY 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 61 NQKPKDKATLTLDKSSITAYNELRLTSEDSAVYYCARST--MITYNYVDYWGQGTSTVTV 118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


Db 61 NQKFKGRFTISVDKSNKNTLYLQNSLRAEDTAVYYCARVYVYASVYFDVWGQGLTVV 120
QY 119 SSAKTTTPSVYPLAPGSAQTNSMTVLGCLVKGYPFPEPTVTWNSSGSLSSGVHTFPAVLQ 178
Db 121 SSAKTTTPSVYPLAPGSAQTNSMTVLGCLVKGYPFPEPTVTWNSSGSLSSGVHTFPAVLQ 180
QY 179 SD-LYTLSSSVTPSPSTWTPSETVTCNVAPASSTKVDKIKVPRDSDGSPSEKSEINEKDL 237
Db 181 SSGLSLSSSVTPSPSTWTPSETVTCNVAPASSTKVDKIKVPRDSDGSPSEKSEINEKDL 225
QY 238 RKSELOQTALGNLKIYYIYNNSKAITSSKSAQDLTNTLLFKGFTGHPWYNDLLVDLG 297
Db 226 -----DKHTCPPCPAPELLGGPSVF--LPPPKP--KDTLM-- 257
QY 298 STAATSEYEGSSVDLYGAYYGQCAGGTGNKTAACMYGGVTLHDNNRLTEKKVPIINLWID 357
Db 258 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 285
QY 358 GKQTTVPIDKVTSSKEV-----TVQELDLQARHYLHGKGLYNSDSFGGKVQVRLIV 410
Db 286 G-----VEVHNATKPREEQYNATYRVVSVLTVLHQDWLNGK----- 322
QY 411 FHSSEGSTVSYDLFDAQGYPDTLRLIYRDNTTISSTLSLSLYLYTTTSIVMTQTPSLL 470
Db 323 -----EY----- 324
QY 471 VSAGDRVTITCKASQSVNDVAVYQKPGSKLLISYTSRYSYAGVDPDRFSGSGYGTDF 530
Db 325 -----KCKVSNAL-----PAP---IAATISKAKGP----- 348
QY 531 LTSSVQAEADAAYVFCQDYNSPPTFGGKTLEIKRADAAPTYSIFPPSSEQLTSGASV 590
Db 349 -----REPQVYTLPPSREEMTKQVSL 370
QY 591 VCFLNFPYKIDINVKWKIDGSRQN-----GVLSNWTDDQSKDSTYSMSSTLTLTDEYE 645
Db 371 TCLVKGFPYSDIAVEWESNGQPNKYKTPPVLDLS-----DGSFFLYSKLTVDKSRWQ 423
QY 646 RHNSYTCETHK 657
Db 424 QGNVFCSCVMHE 435

RESULT 73

US-11-107-028-46
; Sequence 46, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 46
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-46

Query Match 22.5%; Score 792; DB 7; Length 452;
Best Local Similarity 30.5%; Pred. No. 1.4e-34;
Matches 205; Conservative 70; Mismatches 145; Indels 252; Gaps 17;
QY 1 EVLOQSGDPLVKGASVKISCAASGYSTFYGVYHVVKQSPGKLEWIGRINPNNGVTLV 60
Db 1 EVLVESGGGLVQPGGSLRLSCAASGYSTFYGVYHVVKQSPGKLEWIGRINPNNGVTLV 60

QY 61 NQKFKDKATLTVDKSSSTAYMELRSITSEDSAVYYCARST--MITNYVMDYWGQTSVTV 118
Db 61 NQKFKGRFTISVDKSNKNTLYLQNSLRAEDTAVYYCARVYVYASVYFDVWGQGLTVV 120
QY 119 SSAKTTTPSVYPLAPGSAQTNSMTVLGCLVKGYPFPEPTVTWNSSGSLSSGVHTFPAVLQ 178
Db 121 SSAKTTTPSVYPLAPGSAQTNSMTVLGCLVKGYPFPEPTVTWNSSGSLSSGVHTFPAVLQ 180
QY 179 SD-LYTLSSSVTPSPSTWTPSETVTCNVAPASSTKVDKIKVPRDSDGSPSEKSEINEKDL 237
Db 181 SSGLSLSSSVTPSPSTWTPSETVTCNVAPASSTKVDKIKVPRDSDGSPSEKSEINEKDL 225
QY 238 RKSELOQTALGNLKIYYIYNNSKAITSSKSAQDLTNTLLFKGFTGHPWYNDLLVDLG 297
Db 226 -----DKHTCPPCPAPELLGGPSVF--LPPPKP--KDTLM-- 257
QY 298 STAATSEYEGSSVDLYGAYYGQCAGGTGNKTAACMYGGVTLHDNNRLTEKKVPIINLWID 357
Db 258 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 285
QY 358 GKQTTVPIDKVTSSKEV-----TVQELDLQARHYLHGKGLYNSDSFGGKVQVRLIV 410
Db 286 G-----VEVHNATKPREEQYNATYRVVSVLTVLHQDWLNGK----- 322
QY 411 FHSSEGSTVSYDLFDAQGYPDTLRLIYRDNTTISSTLSLSLYLYTTTSIVMTQTPSLL 470
Db 323 -----EY----- 324
QY 471 VSAGDRVTITCKASQSVNDVAVYQKPGSKLLISYTSRYSYAGVDPDRFSGSGYGTDF 530
Db 325 -----KCKVSNAL-----PAP---IAATISKAKGP----- 348
QY 531 LTSSVQAEADAAYVFCQDYNSPPTFGGKTLEIKRADAAPTYSIFPPSSEQLTSGASV 590
Db 349 -----REPQVYTLPPSREEMTKQVSL 370
QY 591 VCFLNFPYKIDINVKWKIDGSRQN-----GVLSNWTDDQSKDSTYSMSSTLTLTDEYE 645
Db 371 TCLVKGFPYSDIAVEWESNGQPNKYKTPPVLDLS-----DGSFFLYSKLTVDKSRWQ 423
QY 646 RHNSYTCETHK 657
Db 424 QGNVFCSCVMHE 435

RESULT 74

US-11-107-028-47
; Sequence 47, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 47
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-47

Query Match 22.5%; Score 792; DB 7; Length 452;
Best Local Similarity 30.5%; Pred. No. 1.4e-34;
Matches 205; Conservative 70; Mismatches 145; Indels 252; Gaps 17;

Qy	1	EVQLQSGPDLVLPKPGASVKISCKASGYFTGYMHMWKQSPGKGLEWIGRINPNNGVTLY	60
Db	1	EVQIVESGGGLVQPGGSLRLSCAASGYFTSYNMHWVRQAPGKGLIEWGAIYFPGNGATSY	60
Qy	61	NQKPKDKATILVDKSSITAYNELSLTSEDSAVVYCARSTMIT--NYVMYDWGQGTSTV	118
Db	61	NQKPKGRTISVDKSKNTLYIQMSLRAEDTAVYICARVYYSRYWYFDVWGQGLTV	120
Qy	119	SSAKTTPPSVYPLAPGSAAOQNSMWTGLCLVKGYFPEPVTVTVMSGSISSGVHITPPAVLQ	178
Db	121	SSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTTTPAVLQ	180
Qy	179	SD-LYTLSSSYTVPSSVTPSETVTCNVAHPASSTKVDKKIIPRDSGGSGSEKSEI	237
Db	181	SSGLYSLSVVTVPSSSLGTQYICNVNHRKPSNTKVDKKVPSKC-----	225
Qy	238	RKSELOQTALGNLKQIYYVNSKAITSSSEKSAQDLTNTLFLKGFFTGHPMYNDLLVDIG	297
Db	226	-----DKTHTCPPCPAPELLGGPSVF--LFPKP--KDTLM--	257
Qy	298	STAATSEVSGSSVDLYGAYGYQCAGGTPTNKTACHYGGVTLLHDNNRLTEEKVPI	357
Db	258	-----ISRTP EVT-CVVVDVS-----HEDPEVKFNWYVD	285
Qy	358	GKQTTVPIDKVKTSKEV-----TVQELDLQARHLYHGKFLYNSDSFGKGQVGRGLIV	410
Db	286	G----VEVHNKTPREQYNATYRVVSVLTVLHQDWLNGK-----	322
Qy	411	PHSSEGSTVSYDLFDAQCQYPTDLLRIYRDNTTISSTLSISLYLYTTSIVMTQPTSL	470
Db	323	-----EY-----	324
Qy	471	VSAGDRVITITCKASQSVSNDVAWYQKPGQSPKLLISYTSRYSAGVDPDRFGSGYGT	530
Db	325	-----KCKVNAAL-----PAP--IAATISKAKGP-----	348
Qy	531	LTISVQAEDAAVYFCQODYNSPPTFGGGTKLEIKRADAAPTVSIPTPSSSEOLTSGGASV	590
Db	349	-----REPOVYTLPPSREEMTKNQVSL	370
Qy	591	VCFLNNFYPKDINVKWKIDGSRQN-----GVLNSWTQDSDKSYTSMSSTLTLT	645
Db	371	TCLVKGYFVPSDIAVEWESNGQPENNYKTPPVLDSE-----DGSEFFLYSKLTIV	423
Qy	646	RHNSYTCETHK	657
Db	424	QGNVFSQSVMEH	435

RESULT 75

```

US-11-106-820-30
; Sequence 30, Application US/11106820
; Publication No. US20060002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIORITY APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 30
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-106-820-30

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[illegible]

Search completed: February 15, 2006, 20:39:04
Job time : 38.3359 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 15, 2006, 20:08:10 ; Search time 69.7713 Seconds
(without alignments)
1467.298 Million cell updates/sec

Title: US-09-900-766-7

Perfect score: 1238

Sequence: 1 SKSEBINEKDLKKSELR.....RDKNKTENSELHLDLYLTT 233.

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 300 summaries

Database :

A_Geneseq_21.*
1: Geneseq1990s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1238	100.0	233	6	ABP58456 Staphyloc
2	1238	100.0	257	4	AAU14103 Peptide s
3	1238	100.0	257	6	ABO10268 S. aureus
4	1238	100.0	257	8	ADF89830 Staphyloc
5	1224	98.9	230	4	AAH67339 Staphyloc
6	1222	98.7	245	2	AAW35374 Staphyloc
7	1210	97.7	233	6	ABP58457 Engineere
8	1202	97.1	245	2	AAW35375 Staphyloc
9	1188	96.0	248	6	ABU79072 S. aureus
10	1188	96.0	248	7	ADF43296 Staphyloc
11	1188	96.0	248	9	AEA02990 Staphyloc
12	1179	95.2	230	2	AAAR45012 Staphyloc
13	1175	94.9	230	5	ABW76235 Staphyloc
14	1156	93.4	230	2	AAAR13204 Staphyloc
15	1107	89.4	233	6	ABP58455 Engineere
16	1107	89.4	672	6	ABP58454 Engineere
17	1035	82.6	233	2	AAAR13203 Staphyloc
18	1023	82.6	233	6	ABP58458 Staphyloc
19	1023	82.6	257	4	AAU14104 Peptide s
20	1023	82.6	257	6	ABO10269 S. aureus
21	1023	82.6	257	7	ADDA4368 Staphyloc
22	1023	82.6	257	8	ADH10956 Enterotox
23	1023	82.6	257	9	ADV11662 Staphyloc
24	1023	82.6	301	9	ABE13483 EGF-SEA f

25	1023	82.6	369	9	ABE13485	Aeb13485 VEGF-SEA
26	1019	82.3	233	2	AAW06738	Aaw06738 Staphyloc
27	1019	82.3	233	8	ADI95318	OSPF-rela
28	1016	82.1	233	2	AAW35373	Staphyloc
29	1016	82.1	233	4	AAW67338	Staphyloc
30	1013	81.8	233	2	AAAR45011	Staphyloc
31	1013	81.8	257	6	ABU79068	S. aureus
32	1013	81.8	257	7	ADF43288	Staphyloc
33	1013	81.8	257	9	AEA02982	Staphyloc
34	1004	81.1	233	5	ABW76234	Staphyloc
35	1000	80.8	257	5	ABW79501	Staphyloc
36	1000	80.8	257	6	ABU10081	Staphyloc
37	1000	80.8	257	7	ABU62324	S. aureus
38	1000	80.8	257	7	AAE37676	Protein #
39	1000	80.8	257	7	ADY93171	Bacterial
40	996	80.5	233	3	AAW54463	Amino aci
41	996	80.5	233	5	ABW79502	Staphyloc
42	996	80.5	233	6	ABU10082	Staphyloc
43	996	80.5	233	7	ABU62325	S. aureus
44	996	80.5	233	7	AAE37677	Protein #
45	996	80.5	233	9	ADY93173	Bacterial
46	992	80.1	233	6	ABU10099	Staphyloc
47	991	80.0	231	8	ADF89824	Staphyloc
48	987	79.7	233	6	ABU10098	Staphyloc
49	983	79.4	257	3	AAW70102	Staphyloc
50	978	79.0	233	3	AAW70103	Mutant St
51	830	67.0	268	8	ADF89835	Staphyloc
52	663	53.6	258	6	ABU79071	S. aureus
53	663	53.6	258	7	ADF43294	Staphyloc
54	663	53.6	258	8	ADF89829	Staphyloc
55	663	53.6	258	9	AEA02988	Staphyloc
56	657	53.1	228	2	AAAR45013	Staphyloc
57	657	53.1	228	5	ABW76236	Staphyloc
58	657	53.1	228	5	ABW76236	Staphyloc
59	649	52.4	228	2	AAAR13205	Staphyloc
60	523	42.2	203	6	ABP58459	Staphyloc
61	492.5	39.8	250	6	ABW70958	Staphyloc
62	457	36.9	82	6	ABU10091	Bacterial
63	457	36.9	82	7	ABU62338	S. aureus
64	457	36.9	82	9	ADY931188	Staphyloc
65	399	32.2	82	6	ABU10089	Bacterial
66	399	32.2	82	7	ABU62336	S. aureus
67	399	32.2	82	9	ADY931186	Staphyloc
68	370	29.9	91	2	AAW242299	Staphyloc
69	366	29.6	217	6	ABP58460	Staphyloc
70	366	29.6	217	8	ADF89833	Staphyloc
71	339.5	27.4	242	8	ADF89834	Staphyloc
72	337	27.2	240	8	ADF89837	Staphyloc
73	336.5	27.2	259	5	ABP29357	Streptoco
74	320	25.8	239	8	ADF89838	Staphyloc
75	319.5	25.8	242	8	ADF89832	Staphyloc
76	310	25.0	242	8	ADF89836	Staphyloc
77	300.5	24.3	266	6	ABU79069	S. aureus
78	300.5	24.3	266	7	ABW75015	S. aureus
79	300.5	24.3	266	7	ADF43290	Staphyloc
80	300.5	24.3	266	9	AEA02984	Staphyloc
81	300	24.2	255	2	AAW06737	Staphyloc
82	299.5	24.2	238	8	ADP98925	Staphyloc
83	299.5	24.2	239	2	AAW64647	Synthetic
84	299.5	24.2	239	4	AAW67341	Staphyloc
85	299.5	24.2	239	7	ABW75016	Unidentifi
86	299.5	24.2	239	8	ADL14247	Wild type
87	297.5	24.0	239	8	ADS87876	Staphyloc
88	297.5	24.0	239	9	ADY63818	Staphyloc
89	297.5	24.0	251	2	AAW12153	Streptoco
90	297.5	24.0	266	7	ABU62455	S. aureus
91	296.5	23.9	221	2	AAAR13209	Staphyloc
92	296.5	23.9	221	2	AAAR45017	Staphyloc
93	296.5	23.9	221	5	ABW76240	Staphyloc
94	296.5	23.9	239	8	ADS87891	Staphyloc
95	296.5	23.9	239	9	ADY63819	S. aureus
96	296.5	23.9	251	2	AAW12151	Streptoco
97	295.5	23.9	239	8	ADS87887	Staphyloc

98	295.5	23.9	251	2	AAW12150	Aaw12150 Streptococ	171	279.5	22.6	238	4	AA567343	Aab67343 Staphyloc
99	295.5	23.9	251	8	ADP89839	Adf89839 Streptococ	172	279.5	22.6	238	5	AB576239	Abb76239 Staphyloc
100	294.5	23.8	239	8	ADS87890	Ads87890 Staphyloc	173	276.5	22.3	228	4	AAG63856	Aag63856 Amino aci
101	294.5	23.8	251	2	AAW12154	Aaw12154 Streptococ	174	276.5	22.3	238	2	AA13208	Aar13208 Staphyloc
102	294.5	23.8	251	2	AAW12097	Aaw12097 Streptococ	175	276.5	22.3	239	2	AAW06258	Aay06258 Staphyloc
103	294.5	23.8	251	2	AAW12097	Aaw12097 Streptococ	176	276.5	22.3	239	2	AAW06257	Aay06257 Staphyloc
104	294.5	23.8	251	2	AAW12147	Aaw12147 Streptococ	177	276.5	22.3	240	6	ABG71373	Abg71373 Staphyloc
105	294.5	23.8	251	2	AAW12147	Aaw12147 Streptococ	178	276.5	22.3	240	6	ABG71374	Abg71374 Staphyloc
106	294.5	23.8	251	2	AAW59780	Aaw59780 Amino aci	179	276.5	22.3	240	9	ABE70859	Aeb70859 Staphyloc
107	293.5	23.7	239	2	AAW59780	Aaw59780 Amino aci	180	276.5	22.3	240	9	ABE70858	Aeb70858 Staphyloc
108	293.5	23.7	239	8	ADY06254	Aay06254 Staphyloc	181	276.5	22.3	265	3	AAW70105	Aay70105 Mutant St
109	293.5	23.7	239	8	ADY06254	Aay06254 Staphyloc	182	276.5	22.3	236	9	ABE70860	Aeb70860 Staphyloc
110	293.5	23.7	240	6	ABG71370	Abg71370 Staphyloc	183	269.5	21.8	238	9	ABE70862	Aeb70862 Staphyloc
111	293.5	23.7	266	5	ABE70855	Abb70855 Staphyloc	184	267.5	21.6	239	2	AA13207	Aar13207 Staphyloc
112	293.5	23.7	266	6	ABU10083	Abu10083 Staphyloc	185	267.5	21.6	239	2	AA13207	Aar13207 Staphyloc
113	293.5	23.7	266	6	ABU10083	Abu10083 Staphyloc	186	267.5	21.6	239	5	ABE70859	Aeb70859 Staphyloc
114	293.5	23.7	266	7	AAE37678	Aae37678 Protein #	187	267.5	21.6	260	6	ADY06254	Aay06254 Staphyloc
115	293.5	23.7	266	9	AAE37678	Aae37678 Protein #	188	266.5	21.5	266	8	ADY06254	Aay06254 Staphyloc
116	292.5	23.6	221	4	AAE37678	Aae37678 Protein #	189	266.5	21.5	266	7	ADY06254	Aay06254 Staphyloc
117	292.5	23.6	221	4	AAE37678	Aae37678 Protein #	190	266.5	21.5	266	9	AAE37678	Aae37678 Staphyloc
118	292.5	23.6	239	2	AAE37678	Aae37678 Protein #	191	266.5	21.5	266	9	AAE37678	Aae37678 Staphyloc
119	292.5	23.6	239	8	ADY06254	Aay06254 Staphyloc	192	266.5	21.5	266	9	AAE37678	Aae37678 Staphyloc
120	292.5	23.6	266	3	AAE37678	Aae37678 Protein #	193	266.5	21.5	266	8	ADY06254	Aay06254 Staphyloc
121	291.5	23.5	266	7	AAE37678	Aae37678 Protein #	194	266.5	21.5	266	7	ADY06254	Aay06254 Staphyloc
122	290.5	23.5	239	5	ABE70855	Abb70855 Staphyloc	195	265.5	21.4	240	9	ABE70855	Aeb70855 Staphyloc
123	290.5	23.5	239	8	ADY06254	Aay06254 Staphyloc	196	265.5	21.4	240	9	ABE70855	Aeb70855 Staphyloc
124	290.5	23.5	251	7	ABU62460	Abu62460 Streptococ	197	258.5	20.9	266	3	AAW70108	Aay70108 Staphyloc
125	289.5	23.4	251	2	AAW59781	Aaw59781 Amino aci	198	258.5	20.9	266	6	ABU10087	Abu10087 Streptococ
126	289.5	23.4	251	2	AAW59781	Aaw59781 Amino aci	199	258.5	20.9	266	7	ABU62330	Aab62330 S. aureus
127	289.5	23.4	251	3	AAW70109	Aay70109 Streptococ	200	258.5	20.9	266	7	AAE37682	Aae37682 Staphyloc
128	289.5	23.4	251	5	ABE70858	Abb70858 Staphyloc	201	258.5	20.9	266	9	ADY93183	Ady93183 Staphyloc
129	289.5	23.4	251	6	ABU10088	Abu10088 Streptococ	202	258.5	20.9	266	9	ADY93183	Ady93183 Staphyloc
130	289.5	23.4	251	7	ABU62331	Abu62331 Streptococ	203	256.5	20.7	220	7	AAE37687	Aae37687 Streptococ
131	289.5	23.4	251	7	AAE37683	Aae37683 Streptococ	204	256.5	20.7	468	7	ABU62335	Aab62335 SFEA L42R
132	289.5	23.4	251	9	ADY93185	Ady93185 Streptococ	205	256.5	20.7	468	7	AAE37684	Aae37684 Streptococ
133	289.5	23.4	266	3	AAE37684	Aae37684 Streptococ	206	256.5	20.7	209	8	ADY93174	Aay93174 Amino aci
134	288.5	23.3	239	2	AAW54464	Aay54464 Amino aci	207	256.5	20.7	233	3	AAE37689	Aae37689 S. pyogen
135	288.5	23.3	239	5	ABE70855	Abb70855 Staphyloc	208	254.5	20.6	220	7	AAE37689	Aae37689 S. pyogen
136	288.5	23.3	239	6	ABU10085	Abu10085 Staphyloc	209	253.5	20.5	220	7	AAE37688	Aae37688 S. pyogen
137	288.5	23.3	239	6	ABU10085	Abu10085 Staphyloc	210	253.5	20.5	468	7	AAE37691	Aae37691 S. pyogen
138	288.5	23.3	239	7	AAE37680	Aae37680 Protein #	211	250	20.2	209	8	ADY93174	Aay93174 Amino aci
139	288.5	23.3	239	9	ADY93179	Ady93179 Bacterial	212	250	20.2	209	8	ADY93179	Ady93179 Bacterial
140	288.5	23.3	240	3	AAE37680	Aae37680 Protein #	213	247.5	20.0	209	8	ADY93179	Ady93179 Bacterial
141	288.5	23.3	240	6	ABG71369	Abg71369 Staphyloc	214	247.5	20.0	209	8	ADY93179	Ady93179 Bacterial
142	288.5	23.3	240	9	ABE70854	Aeb70854 Staphyloc	215	245.5	19.8	231	7	ADY93179	Ady93179 Bacterial
143	287.5	23.2	239	3	AAW062256	Aay062256 Staphyloc	216	245	19.8	231	7	ADY93179	Ady93179 Bacterial
144	287.5	23.2	239	3	AAW062256	Aay062256 Staphyloc	217	245	19.8	231	7	ADY93179	Ady93179 Bacterial
145	287.5	23.2	239	6	ABG71372	Abg71372 Staphyloc	218	245	19.8	250	7	ADY93179	Ady93179 Bacterial
146	287.5	23.2	240	9	ABE70857	Aeb70857 Staphyloc	219	245	19.8	250	7	ADY93179	Ady93179 Bacterial
147	287.5	23.2	266	7	ABU62454	Abu62454 S. aureus	220	232	18.7	258	5	ABE70855	Abb70855 Staphyloc
148	286.5	23.1	239	8	ADY06252	Aay06252 Staphyloc	221	220.5	17.8	240	8	ADY06252	Aay06252 Staphyloc
149	285.5	23.1	239	2	AAW06252	Aay06252 Staphyloc	222	217	17.5	234	3	AAE37682	Aae37682 Staphyloc
150	285.5	23.1	239	8	ADY06252	Aay06252 Staphyloc	223	217	17.5	234	3	AAE37682	Aae37682 Staphyloc
151	285.5	23.1	239	8	ADY06252	Aay06252 Staphyloc	224	216	17.4	210	8	ADY06252	Aay06252 Staphyloc
152	285.5	23.1	239	6	ABG71371	Abg71371 Staphyloc	225	215	17.4	82	6	ABU10090	Abu10090 Bacterial
153	285.5	23.1	240	9	ABE70856	Aeb70856 Staphyloc	226	215	17.4	82	6	ABU10090	Abu10090 Bacterial
154	285.5	23.1	266	8	ADY06252	Aay06252 Staphyloc	227	215	17.4	82	6	ABU10090	Abu10090 Bacterial
155	284.5	23.0	251	2	AAW12149	Aaw12149 Streptococ	228	197	15.9	236	3	AAE37682	Aae37682 Staphyloc
156	284.5	23.0	251	2	AAW12152	Aaw12152 Streptococ	229	197	15.9	236	3	AAE37682	Aae37682 Staphyloc
157	284.5	23.0	266	7	ABU62452	Abu62452 S. aureus	230	197	15.9	236	8	ADY06252	Aay06252 Staphyloc
158	284.5	23.0	266	7	ABU62451	Abu62451 S. aureus	231	197	15.9	236	8	ADY06252	Aay06252 Staphyloc
159	283.5	22.9	239	2	AAW06252	Aay06252 Staphyloc	232	193	15.6	232	5	ABE70855	Abb70855 Staphyloc
160	283.5	22.9	240	6	ABG71368	Abg71368 Staphyloc	233	191	15.4	45	2	AAW04488	Aaw04488 Staphyloc
161	283.5	22.9	240	9	ABE70853	Aeb70853 Staphyloc	234	191	15.4	45	2	AAW04488	Aaw04488 Staphyloc
162	283.5	22.9	250	2	AAW12145	Aaw12145 Streptococ	235	185	14.9	234	8	ADY06252	Aay06252 Staphyloc
163	282.5	22.8	266	5	ABE70854	Aeb70854 Staphyloc	236	183.5	14.8	235	2	AAW62788	Aaw62788 Mutant st
164	282.5	22.8	266	6	ABU10084	Abu10084 Staphyloc	237	183.5	14.8	235	2	AAW62788	Aaw62788 Mutant st
165	282.5	22.8	266	7	ABU62337	Abu62337 S. aureus	238	183.5	14.8	235	2	AAW62788	Aaw62788 Mutant st
166	282.5	22.8	266	7	AAE37679	Aae37679 Protein #	239	182.5	14.7	207	5	AAE37679	Aae37679 Protein #
167	282.5	22.8	266	9	ADY93177	Ady93177 Bacterial	240	181.5	14.7	207	5	AAE37679	Aae37679 Protein #
168	281.5	22.7	238	2	AAW45016	Aaw45016 Staphyloc	241	181.5	14.7	208	2	AAE37679	Aae37679 Protein #
169	280.5	22.7	239	8	ADY93177	Ady93177 Bacterial	242	181.5	14.7	208	2	AAE37679	Aae37679 Protein #
170	280	22.6	265	3	AAW70104	Aay70104 Staphyloc	243	181.5	14.7	208	4	AAE37679	Aae37679 Protein #

244	181.5	14.7	208	5	ABBY6241	AbbY6241	StaphyLoc
245	180.5	14.6	207	5	AAE25372	Aae25372	S. pyogen
246	180.5	14.6	207	5	AAE25374	Aae25374	S. pyogen
247	180.5	14.6	207	5	AAE25370	Aae25370	S. pyogen
248	180	14.5	235	5	ABP29257	Abp29257	Streptoco
249	180	14.5	235	8	ADR83195	Adr83195	S. pyogen
250	179.5	14.5	207	5	AAE25367	Aae25367	S. pyogen
251	179.5	14.5	207	5	AAE25371	Aae25371	S. pyogen
252	178.5	14.4	207	5	AAE25395	Aae25395	S. pyogen
253	178.5	14.4	207	5	AAE25368	Aae25368	S. pyogen
254	177.5	14.3	207	5	AAE25365	Aae25365	S. pyogen
255	176.5	14.3	207	5	AAE25369	Aae25369	S. pyogen
256	173.5	14.0	235	2	AAW62786	Aaw62786	Mutant st
257	173.5	14.0	235	2	AAW62785	Aaw62785	Mutant st
258	170	13.7	137	3	AAI93744	Aay93744	Amino aci
259	151	12.2	107	9	ADV95487	Adv95487	Ubiquitin
260	147.5	11.9	143	5	AAE25363	Aae25363	Streptoco
261	145	11.1	89	6	ADY93195	Ady93195	StaphyLoc
262	137.5	11.1	89	9	ABU10092	Abu10092	Bacterial
263	137.5	11.1	89	7	ABU62339	Abu62339	S. aureus
264	137.5	11.1	89	7	ADY93189	Ady93189	Bacterial
265	134	10.8	227	8	ADE11158	Adel1158	S. pyogen
266	129	10.4	28	2	AAW04489	Aaw04489	StaphyLoc
267	129	10.4	28	2	AAW73916	Aaw73916	StaphyLoc
268	127	10.3	24	3	AAI97857	Aay97857	StaphyLoc
269	127	10.3	24	4	AAI97815	Aay7815	Peptide f
270	126	10.2	23	2	AAW04492	Aaw04492	StaphyLoc
271	126	10.2	23	2	AAW73919	Aaw73919	StaphyLoc
272	126	10.2	233	8	ADE11156	Adel1156	S. pyogen
273	124	10.0	29	2	AAW04493	Aaw04493	StaphyLoc
274	124	10.0	29	2	AAW73915	Aaw73915	StaphyLoc
275	121	9.8	79	6	ABU10096	Abu10096	Bacterial
276	121	9.8	79	7	ABU62343	Abu62343	Streptoco
277	121	9.8	79	9	ADY93193	Ady93193	Streptoco
278	120	9.7	22	2	AAW04491	Aaw04491	StaphyLoc
279	120	9.7	22	2	AAW73914	Aaw73914	StaphyLoc
280	116.5	9.4	231	6	ABM71652	Abm71652	StaphyLoc
281	116	9.4	190	2	AAR41994	Aar41994	StaphyLoc
282	115.5	9.3	190	2	AAR41990	Aar41990	StaphyLoc
283	115	9.3	190	2	AAR42005	Aar42005	StaphyLoc
284	115	9.3	190	2	AAR42012	Aar42012	StaphyLoc
285	114	9.2	190	2	AAR41989	Aar41989	StaphyLoc
286	114	9.2	190	2	AAR42007	Aar42007	StaphyLoc
287	113	9.1	190	2	AAR41998	Aar41998	StaphyLoc
288	113	9.1	190	2	AAR41995	Aar41995	StaphyLoc
289	113	9.1	232	6	ABU42318	Abu42318	Protein e
290	112.5	9.1	89	6	ABU10094	Abu10094	Bacterial
291	112.5	9.1	89	6	ABU10095	Abu10095	Bacterial
292	112.5	9.1	89	7	ABU62342	Abu62342	S. aureus
293	112.5	9.1	89	7	ABU62341	Abu62341	S. aureus
294	112.5	9.1	89	9	ADY93192	Ady93192	StaphyLoc
295	112.5	9.1	89	9	ADY93191	Ady93191	StaphyLoc
296	112	9.0	190	2	AAR42004	Aar42004	StaphyLoc
297	112	9.0	190	2	AAR42004	Aar42004	StaphyLoc
298	112	9.0	190	2	AAR41996	Aar41996	StaphyLoc
299	112	9.0	190	2	AAR41993	Aar41993	StaphyLoc
300	112	9.0	190	2	AAR41991	Aar41991	StaphyLoc

ALIGNMENTS

RESULT 1	
ABP58456	
ID	ABP58456 standard; protein; 233 AA.
XX	
AC	ABP58456;
XX	
DT	14-APR-2003 (first entry)
XX	
DE	Staphylococcal enterotoxin E.
XX	
KW	Superantigen; staphylococcal enterotoxin E.

KW	cytostatic; vaccine.
XX	
OS	Staphylococcus sp.
PN	W02003002143-A1.
XX	
XX	09-JAN-2003.
PD	
XX	
XX	19-JUN-2002; 2002WO-SE001188.
XX	
PR	28-JUN-2001; 2001SE-00002327.
PF	
XX	
PA	(ACTI-) ACTIVE BIOTECH AB.
XX	
PI	Forsberg G, Erlandsson E, Antonsson P, Walse B;
XX	
XX	WPI; 2003-201467/19.
XX	
PT	Conjugate for therapy, has bacterial superantigen with a region in T-cell
PT	receptor and four regions to determine binding to class II major
PT	histocompatibility complex, antibody to cancer associated cell surface
PT	structure.
XX	
XX	Example 3; Fig 4; 102pp; English.
PS	
XX	
CC	The present sequence is the protein sequence of staphylococcal
CC	enterotoxin SEE. The invention provides novel conjugates (see ABP58454)
CC	for human cancer therapy. These comprise an engineered bacterial
CC	superantigen, such as novel SEA/E-120 (see ABP58455), which is based on
CC	SEE, and an antibody moiety, such as tumour reactive antibody ST4. The
CC	superantigen is engineered to reduce seroreactivity whilst maintaining
CC	biological activity and production levels. The conjugates are designed to
CC	target and destroy cancer cells, including cancer of the lung, breast,
CC	colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX	
SQ	Sequence 233 AA;
	Query Match 100.0%; Score 1238; DB 6; Length 233;
	Best Local Similarity 100.0%; Pred. NO. 8.1e-116;
	Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1 SEKSEINEKDLRKSELRNALSNLRQIYYINEKAITENKESDDQFLENTLLFKGPFPTG 60
Db	1 SEKSEINEKDLRKSELRNALSNLRQIYYINEKAITENKESDDQFLENTLLFKGPFPTG 60
Qy	61 HPWYNDLLVDLGSKDATNKYGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
Db	61 HPWYNDLLVDLGSKDATNKYGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
Qy	121 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db	121 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Qy	181 RGLIVFHSSEGSTVSVDLFDPAQGYPPTLLRIYRDNKTIENSENLHIDLILYTTT 233
Db	181 RGLIVFHSSEGSTVSVDLFDPAQGYPPTLLRIYRDNKTIENSENLHIDLILYTTT 233
RESULT 2	
AAU14103	
ID	AAU14103 standard; peptide; 257 AA.
XX	
AC	AAU14103;
XX	
DT	21-NOV-2001 (first entry)
XX	
DE	Peptide sequence from Staphylococcus aureus enterotoxin type E.
XX	
KW	Anti-retroviral; DP178-like; DP107-like; enterotoxin type E;
KW	antifusogenic; antiviral; HIV transmission.
XX	
OS	Staphylococcus aureus.
XX	

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PN WO200151673-A2.
XX
XX 19-JUL-2001.
XX
XX 05-JUL-2000; 2000WO-US035727.
XX
XX 09-JUL-1999; 99US-00350841.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX WPI; 2001-442157/47.
XX
XX Identifying a compound that inhibits the formation of or disrupts a
XX DP107/DP178 complex, especially compounds with antifusogenic, antiviral
XX or intracellular modulatory activity, by detecting the formation of a
XX DP107/DP178 complex.
XX
XX Disclosure; Fig 41; 259pp; English.
XX
XX The present invention relates to peptides which exhibit anti-retroviral
XX activity. The peptides of the invention (AAU12559-AAU14009) comprise
XX DP178-like and DP107-like peptides. The DP178 peptide corresponds to
XX amino acids 639-673 of the transmembrane protein gp41 from human
XX immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
XX corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
XX also relates to a method of identifying compounds that inhibit the
XX formation of or disrupts a DP107/DP178 complex. The method comprises
XX detecting the formation of a DP107/DP178 complex, both in the presence or
XX absence of a test compound, in a reaction mixture containing DP107 and
XX DP178 peptides. The method is useful for identifying compounds, including
XX small molecule compounds, which may themselves exhibit antifusogenic,
XX antiviral or intracellular modulatory activity. The DP178-like/DP107-like
XX peptides are useful to inhibit human and non-human retroviral,
XX particularly HIV, transmission to uninfected cells. The present sequence
XX represents a peptide sequence from Staphylococcus aureus enterotoxin type
XX E
XX
XX Sequence 257 AA;
SQ
Query Match 100.0%; Score 1238; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 9.3e-116;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db |||||
25 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
Db |||||
85 HPWYNDLLVDLGSKDATNKYKGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db |||||
145 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLIDLVLTYTT 233
Db |||||
205 RGLIVFHSSEGSTSVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLIDLVLTYTT 257
RESULT 3
ABO10268
ID ABO10268 standard; protein; 257 AA.
XX
XX ABO10268;
XX
XX 19-AUG-2003 (first entry)
XX
XX S. aureus enterotoxin E.
XX
XX HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
KW Epstein-Barr virus infection; heptad repeat motif.
XX
XX Staphylococcus aureus.
XX
XX US6518013-B1.
XX
XX 11-FEB-2003.
XX
XX 07-JUN-1995; 95US-00485546.
XX
XX 07-JUN-1993; 93US-00073028.
XX
XX 07-JUN-1994; 94US-00255208.
XX
XX 20-DEC-1994; 94US-00360107.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney SO, Lambert DM, Petteway SR;
XX WPI; 2003-465599/44.
XX
XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
XX the cell with a peptide consisting of a region of Epstein-Barr virus
XX protein.
XX
XX Example; Fig 41; 716pp; English.
XX
XX The invention relates to inhibiting (M) transmission of an Epstein-Barr
XX virus to a cell, comprising contacting the cell with an effective
XX concentration of a peptide consisting of a region of 16-39 consecutive
XX amino acids of an Epstein-Barr virus protein for an effective period of
XX time, where the region is recognised by one or more of ALLMOT15,
XX 107x178x4 or PLZIP sequence search motifs, the peptide further comprises
XX an amino terminal X, and a carboxy terminal Z in which X comprises an
XX amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
XX group or macromolecular carrier group, and Z comprises a carboxyl group,
XX amido group, hydrophobic group, or macromolecular carrier group, and
XX fusion of the virus to the cell is inhibited. The peptides were
XX identified by analysing the structure/motifs present in the HIV-1
XX glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
XX motif containing peptides were used to design the motifs cited above,
XX which in turn were used to analyse proteins from other pathogenic
XX organisms and HIV isolates, looking for DP107/178 structural analogues.
XX The method is useful for inhibiting transmission of Epstein-Barr virus to
XX a cell and Epstein-Barr virus infection. The present sequence is a
XX protein from a pathogenic organism analysed for regions analogous to
XX DP107 or DP178
XX
XX Sequence 257 AA;
SQ
Query Match 100.0%; Score 1238; DB 6; Length 257;
Best Local Similarity 100.0%; Pred. No. 9.3e-116;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db |||||
25 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
Db |||||
85 HPWYNDLLVDLGSKDATNKYKGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db |||||
145 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLIDLVLTYTT 233
Db |||||
205 RGLIVFHSSEGSTSVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLIDLVLTYTT 257
RESULT 4
ADF89830
ID ADF89830 standard; protein; 257 AA.

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```
XX AC ADF89830;
XX XX
XX DT 26-FEB-2004 (first entry)
XX XX
XX DE Staphylococcal enterotoxin E (SEE) superantigen.
XX XX
XX KW Superantigen; SAg; Staphylococcal enterotoxin; SE; SEE; cytostatic;
XX KW gene therapy; cancer.
XX XX
XX OS Staphylococcus sp.
XX XX
XX PN WO2003094846-A2.
XX XX
XX PD 20-NOV-2003.
XX XX
XX PF 08-MAY-2003; 2003WO-US014381.
XX XX
XX PR 08-MAY-2002; 2002US-0378988P.
XX PR 15-JUN-2002; 2002US-0389366P.
XX PR 28-AUG-2002; 2002US-0406697P.
XX PR 29-AUG-2002; 2002US-0406750P.
XX PR 01-OCT-2002; 2002US-0415310P.
XX PR 02-OCT-2002; 2002US-0415400P.
XX PR 09-JAN-2003; 2003US-0438686P.
XX XX
XX PA (TERM/) Terman D S.
XX XX
XX PI Terman DS;
XX XX
XX DR WPI; 2004-011997/01.
XX XX
XX PT Treating a subject with cancer or malignant diseases comprises
XX PT intratumoral, intrathecal or intracavitary administration of an amount of
XX PT a superantigen composition to the subject.
XX XX
XX PS Disclosure; SEQ ID NO 7; 91pp; English.
XX XX
XX CC The invention relates to treating a subject with cancer. The method
XX CC involves administering an amount of a superantigen (SAG) composition
XX CC comprising a molecule selected from: a native SAG protein; its
XX CC biologically active fragment or a biologically active homologue or a
XX CC biologically active fusion protein comprising the SAG or its fragment or
XX CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
XX CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
XX CC exotoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritides SAG and
XX CC Clostridium perfringens exotoxin. The method is useful in treating cancer
XX CC or malignant diseases such as malignant pleural effusion, ascites,
XX CC pericardial effusion or meningeal carcinomatosis. The present sequence
XX CC represents a Staphylococcal enterotoxin E (SEE) superantigen.
XX XX
XX SQ Sequence 257 AA;
XX XX
XX Query Match 100.0%; Score 1238; DB 8; Length 257;
XX XX Best Local Similarity 100.0%; Pred. No. 9.3e-116;
XX XX Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB |||
DB 25 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNLLVDLGSKDATNKYKGGVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB |||
DB 85 HPWYNLLVDLGSKDATNKYKGGVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB |||
DB 145 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIDLYLYTT 233
DB |||
DB 205 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIDLYLYTT 257
```

```
RESULT 5
AAB67339
ID AAB67339 standard; peptide; 230 AA.
XX
XX AC AAB67339;
XX XX
XX DT 23-APR-2001 (first entry)
XX XX
XX DE Staphylococcus aureus enterotoxin E protein.
XX XX
XX KW Tumour; cancer; immune; enterotoxin.
XX XX
XX OS Staphylococcus aureus.
XX XX
XX PN US6180097-B1.
XX XX
XX PD 30-JAN-2001.
XX XX
XX PF 30-OCT-1998; 98US-00183437.
XX XX
XX PR 03-OCT-1989; 89US-00416530.
XX PR 17-JAN-1990; 90US-00466577.
XX PR 17-JAN-1991; 91WO-US000342.
XX PR 01-JUN-1992; 92US-00891718.
XX PR 02-MAR-1993; 93US-00025144.
XX PR 31-JAN-1994; 94US-00189424.
XX PR 19-JUN-1995; 95US-00491746.
XX XX
XX PA (TERM/) Terman D S.
XX XX
XX PI Terman DS;
XX XX
XX DR WPI; 2001-158657/16.
XX XX
XX PT Tumor cell capable of stimulating antitumor immune reactivity in vitro or
XX PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
XX PT costimulatory molecule.
XX XX
XX PS Disclosure; Fig 2; 16pp; English.
XX XX
XX CC The present invention relates to a tumour cell capable of stimulating
XX CC antitumor immune reactivity in vitro or in vivo contains and expresses an
XX CC exogenous nucleic acid molecule encoding a superantigen or its active
XX CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
XX CC molecule that activates T cells in conjunction with an antigenic
XX CC stimulus. The invention may be used for cancer therapy by stimulating an
XX CC anticancer immune response in vivo or ex vivo
XX XX
XX SQ Sequence 230 AA;
XX XX
XX Query Match 98.9%; Score 1224; DB 4; Length 230;
XX XX Best Local Similarity 100.0%; Pred. No. 2e-114;
XX XX Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
QY 4 SESEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 63
DB |||
DB 1 SESEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 60
QY 64 YNDLLVDLGSKDATNKYKGGVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEK 123
DB |||
DB 61 YNDLLVDLGSKDATNKYKGGVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEK 120
QY 124 KVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKORGL 183
DB |||
DB 121 KVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKORGL 180
QY 184 IVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIDLYLYTT 233
DB |||
DB 181 IVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIDLYLYTT 230
```

```
RESULT 6
```

[illegible]

CC	This is a modified Staphylococcus enterotoxin SEE superantigen. The wild-type SEE superantigen is modified to be used in a novel conjugate. The novel conjugate comprises a target seeking moiety and a modified wild type superantigen. This modified superantigen retains its ability to activate a subset of T cells, even though 1 or more wild-type amino acid residues in at least 1 region which functions in determining binding to T cell receptor (TCR) and activation of a subset of T cells has/have been replaced. Such a modified superantigen can optionally be used as part of a conjugate with a target seeking moiety, for activating the immune system to treat a mammalian disease. A pharmaceutical composition can be prepared comprising a modified antibody (preferably a Fab fragment fused to a peptide moiety providing activation of T cells in Vbeta specific manner) in which cysteines providing for interchain cysteine linkages in the native antibody have been replaced (preferably by serine residues) to prohibit cysteine formation. The modified wild-type superantigen is used for treating cancer, viral infections, parasitic infestations and autoimmune disease. The modified wild type superantigen has a lower immunogenicity and reactivity with neutralising antibodies and has fewer side-effects when used as a drug, compared to wild type superantigen. Note: This sequence is not provided in the specification. It has been created by modifying the wild-type SEE superantigen sequence in Pages 38-39 of the specification								
XX									
SQ	Sequence 245 AA;								
Query Match 97.1%; Score 1202; DB 2; Length 245;									
Best Local Similarity 93.5%; Pred. No. 3.6e-112;									
Matches 229; Conservative 1; Mismatches 3; Indels 12; Gaps 1;									
QY	1	SEKSEINEKDLRKSELOQNALSNLROIYYNEKAITENKESDDQFLENTLLFKGFFTG	60						
DB	1	SEKSEINEKDLRKSELOQNALSNLROIYYNEKAITENKESDDQFLENTLLFKGFFTG	60						
QY	61	HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT	120						
DB	61	HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT	120						
QY	121	EKKVPINLWIDGKQTTPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ	180						
DB	121	EKKVPINLWIDGKQTTPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ	180						
QY	181	RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDKNKTINSENHLHDLYLYTT	228						
DB	181	RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDKNKTINSENHLHDLYLYTT	228						
QY	229	YLYTT 233							
DB	241	YLYTT 245							
RESULT 9									
ABU79072									
ID	ABU79072 standard; protein; 248 AA.								
XX									
AC	ABU79072;								
XX									
DT	18-JUN-2003 (first entry)								
XX									
DE	S. aureus SEE (staphylococcus enterotoxin E) protein.								
XX									
KW	Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;								
KW	gene therapy; mammalian cell receptor; tumour associated lipid; anergy;								
KW	T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;								
KW	APC; antitumour.								
XX									
OS	Staphylococcus aureus.								
XX									
PN	US2002177551-A1.								
XX									
PD	28-NOV-2002.								
XX									
XX	30-MAY-2001; 2001US-00870759.								
XX									

PR	31-MAY-2000; 2000US-0208128P.	
XX	(TERM/) Terman D S.	
PA	Terman DS;	
XX	WPI; 2003-361759/34.	
DR	N-PSDB; AC464698.	
XX	A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis in T cells and antigen presenting cells.	
PT	Disclosure; Page; 167pp; English.	
XX	The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumor associated lipids and induces anergy or apoptosis in the T cells and antigen presenting cells (APCs).	
CC	Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumor associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (M1) a tumoricidal immunocyte population in vivo in a mammal (by allowing tumor associated lipids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycolipids, sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides, sialylated glycans, lipopeptides and proteoglycolipids are inactivated or deleted), a construct useful in the treatment of cancer comprising a superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell useful in the treatment of cancer (where an adaptor protein which inhibits T cell activation by tumor associated antigens is deleted or functionally deactivated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumoricidal immunocyte population ex vivo in a mammal (by allowing tumor associated lipids to contact immunocytes, in which receptors for the lipids are inactivated or deleted to produce a tumoricidal immunocyte population, and administering the tumouricidally activated immunocytes to the host), producing (M3) a tumouricidal APC population ex vivo in a mammal (by allowing a tumour associated lipid to contact APCs, in which receptors for the tumour associated lipids are inactivated or deleted to produce a tumouricidally activated population, and administering APCs to the host), producing a tumouricidal T cell population ex vivo in a mammal (by allowing a tumour associated lipids to contact T cells, in which adaptor proteins, which inhibit T cell activation by tumor associated antigens, are deleted or functionally deactivated to produce a tumouricidal population of T cells, and administering the tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells ex vivo, and administering the tumouricidally activated T cells to the host), treating (M5) cancer in a mammal (by administering a lipid binding molecule which binds immunosuppressive tumour associated lipids in vivo), producing (M6) a tumouricidal T cell population in vivo in a mammal (by allowing a tumour associated antigen to contact immunocytes in which adaptor proteins which inhibit T cell activation by tumour associated antigens are deleted or functionally deactivated) and producing (M7) a tumouricidal T cell population ex vivo in a mammal comprising allowing a superantigen-lipid raft conjugate to contact immunocytes in vivo. The receptors, methods and compositions are useful for treating cancers and tumours. Bacterial superantigens are co-administered or administered as fusion constructs with anti-tumour proteins or motifs. The present sequence represents a bacterial superantigen protein (e.g. a staphylococcal enterotoxin). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US patent office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"	
XX	Sequence 248 AA;	
XX	Query Match	96.0%; Score 1188; DB 6; Length 248;
XX	Best Local Similarity	100.0%; Pred. No. 9.5e-111; Indels 0; Gaps 0;
XX	Matches 224; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60	
	25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84	
	61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGQCAGTGNKTACMYGGVTLHDNNRLT 120	
	85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGQCAGTGNKTACMYGGVTLHDNNRLT 144	
	121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180	
	145 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204	
	181 RGLIVFHSSEGSTVSVDLFDAGQVDPDTLLRIRYRNKNTINSEN 224	
	205 RGLIVFHSSEGSTVSVDLFDAGQVDPDTLLRIRYRNKNTINSEN 248	
	RESULT 10	
	ADP43296	
	ID ADP43296 standard; protein; 248 AA.	
	XX	
	AC ADP43296;	
	XX	
	DT 12-FEB-2004 (first entry)	
	XX	
	DE Staphylococcal enterotoxin E polypeptide seq id 16.	
	XX	
	KW receptor; lipid-based tumour associated antigen; cytostatic; antimicrobial; gene therapy; neoplastic disease; tumour; cancer; infectious disease; Staphylococcal enterotoxin E; SEE; enterotoxin E.	
	KW	
	XX	
	OS Staphylococcus.	
	XX	
	PN US2003157113-A1.	
	XX	
	PD 21-AUG-2003.	
	XX	
	PF 28-DEC-2000; 2000US-00751708.	
	XX	
	PR 28-DEC-1999; 99US-0173371P.	
	XX	
	PA (TERM/) Terman D S.	
	XX	
	PI Terman DS;	
	XX	
	DR WPI; 2003-787326/74.	
	XX	
	PT New receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumor associated antigens, useful for treating a neoplastic disease or tumor, and infectious diseases.	
	XX	
	PS Example 3; SEQ ID NO 16; 151pp; English.	
	XX	
	CC The invention describes a receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumour associated antigen. The receptor has cytostatic and antimicrobial properties and is suitable for use in gene therapy. The receptor, methods and compositions are useful for treating a neoplastic disease or tumour (cancer), and infectious diseases. This is the amino acid sequence of an enterotoxin superantigen polypeptide the DNA encoding which can be transfected in to a cell alone or with DNA encoding a cell surface moiety to generate antitumour immunity.	
	XX	
	SQ Sequence 248 AA;	
	Query Match	96.0%; Score 1188; DB 7; Length 248;
	Best Local Similarity	100.0%; Pred. No. 9.5e-111; Indels 0; Gaps 0;
	Matches 224; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60	
DB	25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84	
QY	61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGQCAGTGNKTACMYGGVTLHDNNRLT 120	

85	HPWYNDLLLVDLGSKDNTKVKKGVLDLGYANGYQCAGGTENKTKACMYGGVTLHDNNRLT	144
Db		
121	EEKVVPINLWIDGKQTTPVIDKVTKSKEVTVQELDLQARHYLHGKFGFLYNSDSFGSKVQ	180
Qy		
145	EEKVVPINLWIDGKQTTPVIDKVTKSKEVTVQELDLQARHYLHGKFGFLYNSDSFGSKVQ	204
Db		
181	RGILVPHSSSEGSTVSVDLFDAGQCPDPTLLRIYRDNKTINSNL	224
Qy		
205	RGHIVPHSSSEGSTVSVDLFDAGQCPDPTLLRIYRDNKTINSNL	248
Db		

RESULT 11
AEA02990
ID AEA02990 standard; protein; 248 AA.
XX
AC AEA02990;
XX
DT 28-JUL-2005 (first entry)
XX
DE Staphylococcal enterotoxin E (SEE) amino acid sequence SEQ ID NO:16.

xx New composition for treating a tumor or neoplastic disease in a subject
pt PT comprises conjugates comprising superantigen polypeptides or nucleic
pt PT acids with other molecules that produce a tumoricidal response.

Example 3: SEO ID NO 16: 125pp: English.

The invention relates to a composition for treating a tumor or neoplastic disease in a subject. Also described: (1) a mammalian cell comprising an exogenous nucleic acid encoding a superantigen expressed in the cell, which cell also produces or expresses all alpha-anomers of monoglycosylceramide or diglycosylceramide, where expression of the superantigen and the mono- or diglycosylceramide is capable of eliciting an antitumor immune response in a mammal into which the cell is introduced; (2) treating a tumor or neoplastic disease in a subject; (3) preparing a population of immunotherapeutic T or natural killer T (NKT) cells useful to treat a tumor or neoplastic disease in a subject; (4) an apoptotic cell preparation or lysate useful for treating a tumor or neoplastic disease in a subject, comprising a cell population that has been transfected with naked DNA encoding a superantigen, and treated to undergo apoptosis or lysis; and (5) a cell that has ingested or been transfected with the above apoptotic preparation or lysate, thus, rendering the cell effective in presenting material expressed from transfecting nucleic acid or material ingested to the immune system of a mammal to elicit an anti-tumor immune response. The composition and methods are useful for treating tumors or neoplastic diseases. The present sequence represents a Staphylococcal enterotoxin E (SEE) protein sequence, which is used in an example from the present invention. Note - The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from the USPTO web site.

Sequence 248 AA;

The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)

Query Match	96.0%;	Score 1188;	DB 9;	Length 248;
Best Local Similarity	100.0%;	Pred. No. 9.5e-11;		
Matches 224;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	SEKSEEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG	60	
Db	25	SEKSEEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG	84	
Qy	61	HPWYNDDLVLGSKDANTKYKGKVDLYGAYGYQCAGGTPNTACMYGGVTLHDNNRLT	120	
Db	85	HPWYNDDLVLGSKDANTKYKGKVDLYGAYGYQCAGGTPNTACMYGGVTLHDNNRLT	144	
Qy	121	BEKKVPINLMIDGQTTPVDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ	180	
Db	145	BEKKVPINLMIDGQTTPVDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ	204	
Qy	181	RGLIVFHSSGGSTVSYDLFDAQGYPTLLRIYRDNKTIINSEN	224	
Db	205	RGLIVFHSSGGSTVSYDLFDAQGYPTLLRIYRDNKTIINSEN	248	

RESULT 12
AAR45012
ID AAR45012 standard; protein; 230 AA.

XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference	120	
PT		/note= "Given in the specification as J, no further details given"	
PT			
FT	Misc-difference	121	
FT		/note= "Given in the specification as J, no further details given"	
PT			
FT	Misc-difference	123	
FT		/note= "Given in the specification as O, no further details given"	
PT			
FT	Misc-difference	124	
FT		/note= "Given in the specification as U, no further details given"	
PT			

WO9324136-A1.

09-DEC-1993.

01-JUN-1993; 93WO-US005213.

01-JUN-1992: 92US-00891718.

(TERM/) Terman D S
(STON/) Stone J L.

Terman DS, Stone JL;

WPI; 1993-405418/50.

PT Use of staphylococcal enterotoxin(s) and homologues - for treating cancer

Disclosure: Fig 1: 90pp; English: English.

The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)

CC which may be used in the methods of the invention for treating cancer in
CC a patient. These SEs, and homologues of them, can be used as tumouricidal
CC agents for treating cancers and autoimmune disease. They exhibit
CC tumouricidal activity and toxicity identical to that observed for the
CC Protein A perfusion system. They may be administered by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ

Query Match 95.2%; Score 1179; DB 2; Length 230;
Best Local Similarity 96.1%; Pred. No. 6.9e-110;
Matches 221; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 4 SEEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 63
DB 1 SEEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 60
QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYYGQCAGTTPNKTCMYGGVTLHDNNRLTEEK 123
DB 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYYGQCAGTTPNKTCMYGGVTLHDNNRLTEEK 120
QY 124 KVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 183
DB 121 XVXXBKWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 180
QY 184 IVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHIDLYLYTT 233
DB 181 IVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHIDLYLYTT 230

RESULT 13
ABB76235
ID ABB76235 standard; protein; 230 AA.
XX
AC ABB76235;
DT 09-AUG-2002 (first entry)
XX
DE Staphylococcus aureus enterotoxin E.
KW Enterotoxin E; SEE; superantigen; antigen; tumour; cancer; antitumour;
KW therapy.
XX
OS Staphylococcus aureus.
XX
PH Key Location/Qualifiers
FT Misc-difference 120
FT Misc-difference 121 /note= "given as 'J' in the specification"
FT Misc-difference 123 /note= "given as 'J' in the specification"
FT Misc-difference 123 /note= "given as 'O' in the specification"
FT Misc-difference 124 /note= "given as 'U' in the specification"
FT Misc-difference 125 /note= "given as 'V' in the specification"
FT

XX
XX US2002051765-A1.
XX
XX 02-MAY-2002.
XX
XX 19-DEC-2000; 2000US-00741503.
XX
XX 03-OCT-1989; 89US-00416530.
XX 17-JAN-1990; 90US-00466577.
XX 17-JAN-1991; 91WO-US000342.
XX 01-JUN-1992; 92US-00891718.
XX 02-MAR-1993; 93US-00025144.
XX 31-JAN-1994; 94US-00189424.
XX 19-JUN-1995; 95US-00491746.
XX
XX (TERM/) Terman D S.
XX

PI Terman DS;
XX
DR WPI; 2002-415198/44.
XX
PT Reagent for treating cancer without the need for e.g. radiotherapy,
PT comprises a specific V beta subset of T cells sensitized to a growing
PT tumor and stimulated with superantigens.
XX
PS Disclosure; Fig 2; 17pp; English.
XX
CC The present sequence is the protein sequence of enterotoxin E (SEE) of
CC Staphylococcus aureus. Similarity is shown, in several stretches of
CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
CC present invention, synthetic polypeptides useful in tumour therapy and in
CC blocking or destroying autoreactive T and B lymphocyte populations are
CC characterised by substantial structural homology to staphylococcal
CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
CC exotoxins, with statistically significant sequence homology and
CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
CC analysis exceeding 6) to include alignment of cysteine residues and
CC similar hydrophathy profiles. These superantigens are used to treat solid
CC tumours, including their metastases, without radiation, surgery or
CC standard chemotherapeutic agents. A claimed method of human cancer
CC treatment involves contacting haematopoietic cells from a patient with
CC one or more superantigens ex vivo to generate stimulated cells, selecting
CC a specific V beta subset of cells, and reintroducing these cells into the
CC patient to induce an in vivo therapeutic, tumouricidal reaction
XX
SQ Sequence 230 AA;

Query Match 94.9%; Score 1175; DB 5; Length 230;
Best Local Similarity 96.1%; Pred. No. 1.7e-109;
Matches 221; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
QY 4 SEEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 63
DB 1 SEEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 60
QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYYGQCAGTTPNKTCMYGGVTLHDNNRLTEEK 123
DB 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYYGQCAGTTPNKTCMYGGVTLHDNNRLTEEK 120
QY 124 KVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 183
DB 121 XVXXBKWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 180
QY 184 IVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHIDLYLYTT 233
DB 181 IVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHIDLYLYTT 230

RESULT 14
AAR13204
ID AAR13204 standard; protein; 230 AA.
XX
AC AAR13204;
XX
DT 15-OCT-1991 (first entry)
XX
DE Staphylococcal enterotoxin E.
XX
KW SEE; cancer treatment; pyrogen; tumouricide.
XX
OS Staphylococcus aureus.
XX
PN WO9110680-A.
XX
PD 25-JUL-1991.
XX
PF 17-JAN-1990; 90US-00466577.
XX
XX 17-JAN-1990; 90US-00466577.
PR

XX (TERM/) Terman D S.
 XX Terman DS;
 XX WPI; 1991-237984/32.
 XX Treating cancer with enterotoxin from *Staphylococcus aureus* -
 PT administered by IV injection, having same tumoricidal activity as
 PT Staphylococcal protein A without potential toxic reactions.
 XX
 XX Disclosure; Fig 1; 74pp; English.
 XX SEE was isolated and purified from *S. aureus*. It can be used for treating
 CC cancer, activating cytokine mediators and procoagulant systems,
 CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
 CC administered intravenously, optionally with ibuprofen to attenuate toxic
 CC reaction to SEE. Synthetic polypeptides having structural homology to
 CC Staphylococcal exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydropathy profiles. See AAR13203-R13211
 XX
 XX Sequence 230 AA;
 SQ
 Query Match 93.4%; Score 1156; DB 2; Length 230;
 Best Local Similarity 93.9%; Pred. No. 1.4e-107;
 Matches 216; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 4 SEINEKDLRKSELOLNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 63
 DB 1 SEINEKDLRKSELOLNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 60
 QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 123
 DB 61 YNDLLVDKSGSDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEX 120
 QY 124 KVPINLWIDGKQTTPIDKVTSSKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQGL 183
 DB 121 XVQXBKWIDGKQTTPIDKVTSSKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQGL 180
 QY 184 IVFHSSEGSTVSYDLFDAQGYQPDTLRLIYRDNKTINSENHLDLYLYTT 233
 DB 181 IVFHSSEGSTVSYDLFDAQGYQPDTLRLIYRDNKTINSENHLDLYLYTT 230
 RESULT 15
 ABP58455
 ID ABP58455 standard; protein; 233 AA.
 XX
 AC ABP58455;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Engineered superantigen SEA/E-120 for human cancer therapy.
 XX
 KW Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
 KW cytostatic; vaccine; SEA/E-120; mutant; mutein.
 XX
 OS *Staphylococcus* sp.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 20
 FT /note= "wild-type Arg substituted by Gly"
 FT
 FT Misc-difference 21
 FT /note= "wild-type Asn substituted by Thr"
 FT
 FT Misc-difference 24
 FT /note= "wild-type Ser substituted by Gly"
 FT
 FT Misc-difference 27
 FT /note= "wild-type Arg substituted by Lys"
 FT
 FT Misc-difference 79
 FT /note= "wild-type Lys substituted by Glu"
 FT
 FT Misc-difference 81

FT Misc-difference 83 /note= "wild-type Lys substituted by Glu"
 FT
 FT Misc-difference 84 /note= "wild-type Lys substituted by Ser"
 FT
 FT Misc-difference 227 /note= "wild-type Lys substituted by Ser"
 FT
 FT /note= "wild-type Asp substituted by Ser"
 XX
 PN WO2003002143-A1.
 XX
 PD 09-JAN-2003.
 XX
 PF 19-JUN-2002; 2002WO-SE001188.
 XX
 PR 28-JUN-2001; 2001SE-00002327.
 XX
 PA (ACTI-) ACTIVE BIOTECH AB.
 XX
 XX Forsberg G, Erlandsson E, Antonsson P, Walse B;
 XX WPI; 2003-201467/19.
 XX
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX
 PS Claim 8; Fig 2; 102pp; English.
 XX
 CC The present sequence is the protein sequence of engineered staphylococcal
 CC superantigen SEA/E-120. The superantigen is derived from staphylococcal
 CC enterotoxin E (SEE) by the incorporation of the following amino acid
 CC substitutions to reduce seroreactivity whilst maintaining production
 CC levels and biological activity: R20G, N21T, S24G, R27K, K79E, K81E, K83S
 CC and D227S. SEA/E-120 has been genetically fused to the Fab moiety of the
 CC tumour reactive antibody 5T4 to form a claimed conjugate (see ABP58454)
 CC designed to target and destroy cancer cells, including cancer of the
 CC lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and
 CC prostate (claimed)
 XX
 SQ Sequence 233 AA;
 Query Match 89.4%; Score 1107; DB 6; Length 233;
 Best Local Similarity 89.7%; Pred. No. 1.2e-102;
 Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOLNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 1 SEKSEINEKDLRKSELOLNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 QY 121 EEKKVPINLWIDGKQTTPIDKVTSSKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 121 EEKKVPINLWIDGKQTTPIDKVTSSKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 180
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGYQPDTLRLIYRDNKTINSENHLDLYLYTT 233
 DB 181 RGLIVFHSSEGSTVSYDLFDAQGYQPDTLRLIYRDNKTINSENHLDLYLYTT 233
 RESULT 16
 ABP58454
 ID ABP58454 standard; protein; 672 AA.
 XX
 AC ABP58454;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Engineered superantigen for human cancer therapy.
 XX

XX The present invention relates to peptides which exhibit anti-retroviral
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
 CC amino acids 639-673 of the transmembrane protein gp41 from human
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
 CC also relates to a method of identifying compounds that inhibit the
 CC formation of or disrupts a DP107/DP178 complex. The method comprises
 CC detecting the formation of a DP107/DP178 complex, both in the presence or
 CC absence of a test compound, in a reaction mixture containing DP107 and
 CC DP178 peptides. The method is useful for identifying compounds, including
 CC small molecule compounds which may themselves exhibit antiretroviral,
 CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
 CC peptides are useful to inhibit human and non-human retroviral,
 CC particularly HIV, transmission to uninfected cells. The present sequence
 CC represents a peptide sequence from Staphylococcus aureus enterotoxin A
 XX Sequence 257 AA;
 SQ
 Query Match 82.6%; Score 1023; DB 4; Length 257;
 Best Local Similarity 82.0%; Pred. No. 4e-94;
 Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDKRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 25 SEKSEINEKDKRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTD 84
 QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
 DB 85 HSWYNLLVDLGSKDIVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKGLYNSDSFGKVKQ 180
 DB 145 EEKVPINLWIDGKQNTVPLETKNKXNTVQELDLQARRYLQEKYLYNSDSVDFGKVKQ 204
 QY 181 RGLIVPHSSEGSTVSVDLFDAGQGYPTDTLRIYRDNKTINSENHLDLYLTT 233
 DB 205 RGLIVPHSTEPSVNYDLFGAQGYNTLLRIYRDNKTINSENHLDLYLTS 257
 RESULT 20
 ABO10269
 ID ABO10269 standard; protein; 257 AA.
 XX
 AC ABO10269;
 XX
 DT 19-AUG-2003 (first entry)
 XX
 DE S. aureus enterotoxin A.
 XX
 KW HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
 KW Epstein-Barr virus infection; heptad repeat motif.
 XX
 OS Staphylococcus aureus.
 XX
 XX US6518013-B1.
 PN 11-FEB-2003.
 XX
 XX 07-JUN-1995; 95US-00485546.
 XX
 PR 07-JUN-1993; 93US-00073028.
 PR 07-JUN-1994; 94US-00255208.
 PR 20-DEC-1994; 94US-00360107.
 XX
 XX (TRIM-) TRIMERIS INC.
 XX
 XX Barney SO, Lambert DM, Petteway SR;
 PI WPI; 2003-465599/44.
 DR
 XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting

PT the cell with a peptide consisting of a region of Epstein-Barr virus
 PT protein.
 XX
 PS Example; Fig 42; 716pp; English.
 XX
 CC The invention relates to inhibiting (M) transmission of an Epstein-Barr
 CC virus to a cell, comprising contacting the cell with an effective
 CC concentration of a peptide consisting of a region of 16-39 consecutive
 CC amino acids of an Epstein-Barr virus protein for an effective period of
 CC time, where the region is recognised by one or more of ALLM0115,
 CC 107x178x4 or PLZIP sequence search motifs, the peptide further comprises
 CC an amino terminal X, and a carboxy terminal Z in which X comprises an
 CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
 CC group or macromolecular carrier group, and Z comprises a carboxyl group,
 CC amido group, hydrophobic group, or macromolecular carrier group, and
 CC fusion of the virus to the cell is inhibited. The peptides were
 CC identified by analysing the structure/motifs present in the HIV-1
 CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
 CC motif containing peptides were used to design the motifs cited above,
 CC which in turn were used to analyse proteins from other pathogenic
 CC organisms and HIV isolates, looking for DP107/178 structural analogues.
 CC The method is useful for inhibiting transmission of Epstein-Barr virus to
 CC a cell and Epstein-Barr virus infection. The present sequence is a
 CC protein from a pathogenic organism analysed for regions analogous to
 CC DP107 or DP178
 XX Sequence 257 AA;
 SQ
 Query Match 82.6%; Score 1023; DB 6; Length 257;
 Best Local Similarity 82.0%; Pred. No. 4e-94;
 Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDKRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 25 SEKSEINEKDKRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTD 84
 QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
 DB 85 HSWYNLLVDLGSKDIVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKGLYNSDSFGKVKQ 180
 DB 145 EEKVPINLWIDGKQNTVPLETKNKXNTVQELDLQARRYLQEKYLYNSDSVDFGKVKQ 204
 QY 181 RGLIVPHSSEGSTVSVDLFDAGQGYPTDTLRIYRDNKTINSENHLDLYLTT 233
 DB 205 RGLIVPHSTEPSVNYDLFGAQGYNTLLRIYRDNKTINSENHLDLYLTS 257
 RESULT 21
 ADD44368
 ID ADD44368 standard; protein; 257 AA.
 XX
 AC ADD44368;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Staphylococcus aureus enterotoxin A protein.
 XX
 KW enterotoxin A; ent A; food poisoning; bacterium; food; milk; fruit juice;
 KW ice cream.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO2003080865-A1.
 XX
 XX 02-OCT-2003.
 PD
 XX 26-MAR-2002; 2002WO-IB001150.
 PF
 XX 26-MAR-2002; 2002WO-IB001150.
 PR
 XX (COUL) COUNCIL SCI & IND RES.
 PA

XX Padmapriya BP, Ramesh A, Chandrashekar A, Varadaraj MC;
XX WPI: 2003-779273/73.
DR N-PSDB; ADD44369.
XX Novel oligonucleotide primers directed against enterotoxin A gene of
PT Staphylococcus aureus and heat stable enterotoxin gene of Yersinia
PT enterocolitica, useful for detecting food poisoning causing bacteria.
XX Example 2; Page 14-15; 34pp; English.
XX The invention relates to novel oligonucleotide primers directed against
CC enterotoxin A gene (ent A) of Staphylococcus aureus and heat stable
CC enterotoxin gene (yst) of bacteria Yersinia enterocolitica. The novel
CC oligonucleotide primers are useful for simultaneously detecting food
CC poisoning bacterial species Staphylococcus aureus and/or Yersinia
CC enterocolitica in food systems e.g., milk, fruit juices and ice creams,
CC without prior enrichment for preventing food poisoning outbreak. The PCR
CC detection method is useful for detecting the bacteria strains in quantity
CC as low as one cell. The method can be directly used for detecting
CC bacterial strains. The oligonucleotide primers allow quick and highly
CC sensitive detection of the food poisoning bacterial species. This
CC sequence represents the protein derived from the enterotoxin A gene from
CC Staphylococcus aureus of the invention.
XX Sequence 257 AA;
SQ

Query Match 82.6%; Score 1023; DB 7; Length 257;
Best Local Similarity 82.0%; Pred. No. 4e-94;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTACWYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTACWYGGVTLHDNNRLT 144
QY 121 EEKVPINLWDGKQTPVDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EEKVPINLWDGKQTPVDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFDAQOQYNTLLRIYRDNKTINSENHLDLYLYTS 257

RESULT 22
ADH10956
ID ADH10956 standard; protein; 257 AA.
XX ADH10956;
XX
XX 11-MAR-2004 (first entry)
DE Enterotoxin A protein.
XX Enterotoxin A; Computational design; protein binding peptide;
KW hydrophobic potential; solvent contact surface;
KW protein three-dimensional structure; two-dimensional characteristic map;
KW Fourier transformation.
XX Staphylococcus aureus.
OS Staphylococcus aureus.
XX JF2003263465-A.
PN
XX 19-SEP-2003.
XX
XX 07-MAR-2002; 2002JP-00062348.
PF
XX 07-MAR-2002; 2002JP-00062348.
PR

XX (ENKA-) ENKAKU IRYO KENKYUSHO KK.
XX WPI: 2004-075279/08.
XX Designing and selecting protein binding peptide by identifying peptide
PT binding region of protein, and designing peptides that bind to the region
PT using structure-biological activity relationship program of computer.
XX Example; SEQ ID NO 1; 11pp; Japanese.
XX The invention relates to a method for computational design and selection
CC of protein binding peptides, comprising computing the hydrophobic
CC potential of all surface points arranged on the solvent contact surface
CC of a protein three-dimensional structure, developing a two-dimensional
CC characteristic map by a self-assembly method, identifying a region of
CC hydrophobic amino acids by Fourier transformation and designing a protein
CC binding peptide corresponding to the hydrophobic region. The method is
CC useful for designing and selecting protein binding peptides. This
CC sequence represents an Enterotoxin A protein used in the scope of the
CC invention.
XX Sequence 257 AA;
SQ

Query Match 82.6%; Score 1023; DB 8; Length 257;
Best Local Similarity 82.0%; Pred. No. 4e-94;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTACWYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTACWYGGVTLHDNNRLT 144
QY 121 EEKVPINLWDGKQTPVDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EEKVPINLWDGKQTPVDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFDAQOQYNTLLRIYRDNKTINSENHLDLYLYTS 257

RESULT 23
ADV11662
ID ADV11662 standard; protein; 257 AA.
XX ADV11662;
XX
XX 24-FEB-2005 (first entry)
DE Staphylococcus aureus enterotoxin A.
XX DNA amplification; DNA detection; food poisoning; food; toxin;
KW enterotoxin; enterotoxin A; entA.
XX Staphylococcus aureus.
OS Staphylococcus aureus.
XX US2004248089-A.
PN
XX 09-DEC-2004.
XX
XX 27-MAR-2002; 2002US-00107879.
PF
XX 27-MAR-2002; 2002US-00107879.
PR
XX (BANA/) BANADA P P.
PA (RAME/) RAMESH A.
PA (CHAN/) CHANDRASHEKAR A.
PA (VARA/) VARADARAJ M C.
XX

PI Banada PP, Ramesh A, Chandrashekar A, Varadaraj MC;
 XX WPI; 2005-046727/05.
 DR N-PSDB; ADV11663.
 XX
 PT New oligonucleotide primers useful for detecting poisoning in food
 PT systems and particles, in particular food poisoning from Staphylococcus
 PT aureus and/or Yersinia enterocolitica.
 XX
 PS Disclosure; Page 6; 13pp; English.
 XX
 CC The invention relates to PCR primers specific for the Staphylococcus
 CC aureus enterotoxin A (entA) gene (ADV1658-ADV11659) and the Yersinia
 CC enterocolitica heat stable enterotoxin (yest) gene (ADV11660-ADV11661),
 CC and to their use in a highly sensitive and quick PCR-based method for the
 CC detection of these food poisoning-associated bacteria in food systems
 CC such as milk, fruit juice or ice cream. The invention also relates to a
 CC method of preparing the primers of the invention by identifying conserved
 CC sequences of the entA and yest genes and using software programs to
 CC generate the primers. The primers and detection method are used to detect
 CC enterotoxigenic/pathogenic strains of Staphylococcus aureus and Yersinia
 CC enterocolitica in food samples, and therefore help to prevent food
 CC poisoning outbreaks. The detection method is highly sensitive, being able
 CC to detect the presence of a single target organism in a food sample. The
 CC present sequence represents Staphylococcus aureus enterotoxin A.
 XX
 SQ Sequence 257 AA;
 Query Match 82.6%; Score 1023; DB 9; Length 257;
 Best Local Similarity 82.0%; Pred. No. 4e-94;
 Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
 QY 61 HPWYNDLLVDFSGKQATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 120
 DB 85 HSWYNDLLVDFSGKQATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 144
 QY 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 180
 DB 145 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 204
 QY 181 RGLIVPHSSEGTSVSYDLFDAGQYPTDILLRIYRDNKTINSENHLDLYLTT 233
 DB 205 RGLIVPHSTSTEPSVNYDLFAGQYPTDILLRIYRDNKTINSENHLDLYLTT 257
 RESULT 24
 AEB13483
 ID AEB13483 standard; protein; 301 AA.
 XX
 AC AEB13483;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE EGF-SEA fusion construct protein SEQ ID NO 2.
 XX
 KW fusion protein; cell proliferation; antigen; cancer;
 KW endothelial growth factor; EGF; vascular endothelial growth factor; VEGF;
 KW SEA; enterotoxin family; enterotoxin A; cytostatic; immunomodulator.
 XX
 OS Synthetic.
 XX
 PN WO2005061531-A1.
 XX
 PD 07-JUL-2005.
 XX
 PF 31-MAY-2004; 2004WO-CN000569.
 XX
 PR 21-DEC-2003; 2003CN-01109829.
 XX

PA (SUNJ/) SUN J.
 XX
 PI Sun J;
 XX
 DR WPI; 2005-488638/49.
 DR N-PSDB; AEB13482.
 XX
 PT Preparation of superantigen fusion proteins containing specific proteins
 PT and superantigens based on recombinant expression vectors and host cells,
 PT for producing medicines in e.g. antitumor therapy.
 XX
 PS Example 6; SEQ ID NO 2; 33pp; Chinese.
 XX
 CC This invention describes a novel fusion protein comprising a ligand which
 CC can promote the growth of cancer cells and also corresponds to the
 CC receptor of cancer-cell overexpression, as well as a specific polypeptide
 CC which has avidity to and antagonism against the cancer cell receptor or
 CC may interact directly with the cancer-cell surface, and a superantigen
 CC which can induce an antitumor immunological reaction. The invention also
 CC describes 1) a recombinant vector containing the nucleotide sequence for
 CC the fusion protein; 2) host cells containing the recombinant vector and
 CC 3) a method of producing the fusion protein by culturing the host cells
 CC before collecting the expressed fusion protein. The ligand is selected
 CC from endothelial growth factor (EGF) family, vascular endothelial growth
 CC factor (VEGF) family, basic fibroblast growth factor (bFGF) and GGF
 CC families, transforming growth factor (TGF-alpha), interleukin-4,
 CC interleukin-2, heregulin, interleukin-6, interleukin-13, interleukin-8,
 CC heparin-binding EGF-like growth factor, insulin-like growth factor, nerve
 CC growth factor, placenta growth factor, stem-cell growth factor,
 CC thrombospondin, ephrin family, erbB ligand, desialic-acid glycoprotein,
 CC angiotensin, clotting factor VII, urokinase-type plasminogen activator,
 CC growth- hormone receptor hormone, growth inhibitor, chemotactic factor,
 CC low- density lipoprotein, transferrin and other ligands associated with
 CC cancer immunological diseases. The superantigen is chosen from SEA, SEB,
 CC SEC, SED and SEE of Staphylococcus aureus enterotoxin family, SPE-A, SPE-
 CC B and SPE-C of streptococci, especially SEA of Staphylococcus aureus
 CC enterotoxin family. The fusion protein preferably contains staphylococcal
 CC -enterotoxin A (SEA) as the superantigen and a ligand selected from EGF
 CC and VEG. The prepared proteins are useful in producing medicines for
 CC antitumor therapy or immunological reaction. Such drugs are more specific
 CC with enhanced activity and less toxic. This sequence represents a fusion
 CC construct composed of EGF and SEA.
 XX
 SQ Sequence 301 AA;
 Query Match 82.6%; Score 1023; DB 9; Length 301;
 Best Local Similarity 82.0%; Pred. No. 5.1e-94;
 Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 69 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 128
 QY 61 HPWYNDLLVDFSGKQATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 120
 DB 129 HSWYNDLLVDFSGKQATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 188
 QY 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 180
 DB 189 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 248
 QY 181 RGLIVPHSSEGTSVSYDLFDAGQYPTDILLRIYRDNKTINSENHLDLYLTT 233
 DB 249 RGLIVPHSTSTEPSVNYDLFAGQYPTDILLRIYRDNKTINSENHLDLYLTT 301
 RESULT 25
 AEB13485
 ID AEB13485 standard; protein; 369 AA.
 XX
 AC AEB13485;
 XX

08-SEP-2005 (first entry)
VEGF-SEA fusion construct protein SEQ ID NO 4.
fusion protein; cell proliferation; antigen; cancer;
endothelial growth factor; EGF; vascular endothelial growth factor; VEGF;
SEA; enterotoxin family; enterotoxin A; cytostatic; immunomodulator.
Synthetic.
WO2005061531-A1.
07-JUL-2005.
31-MAY-2004; 2004WO-CN000569.
21-DEC-2003; 2003CN-01109829.
(SUNJ/) SUN J.
Sun J;
WPI; 2005-488638/49.
N-PSDB; AEB13484.
Preparation of superantigen fusion proteins containing specific proteins
and superantigens based on recombinant expression vectors and host cells,
for producing medicines in e.g. antitumor therapy.
Example 6; SEQ ID NO 4; 33pp; Chinese.
This invention describes a novel fusion protein comprising a ligand which
can promote the growth of cancer cells and also corresponds to the
receptor of cancer-cell overexpression, as well as a specific polypeptide
which has avidity to and antagonism against the cancer cell receptor or
may interact directly with the cancer-cell surface, and a superantigen
which can induce an antitumor immunological reaction. The invention also
describes 1) a recombinant vector containing the nucleotide sequence for
the fusion protein; 2) host cells containing the recombinant vector and
3) a method of producing the fusion protein by culturing the host cells
before collecting the expressed fusion protein. The ligand is selected
from endothelial growth factor (EGF) family, vascular endothelial growth
factor (VEGF) family, basic fibroblast growth factor (bFGF) and GGF
families, transforming growth factor (TGF-alpha), interleukin-4,
interleukin-2, heregulin, interleukin-6, interleukin-13, interleukin-8,
heparin-binding EGF-like growth factor, insulin-like growth factor,
hepatocyte growth factor, platelet-derivatizing growth factor, nerve
growth factor, placenta growth factor, stem-cell growth factor,
thrombopoietin, ephrin family, erbB ligand, desialic-acid glycoprotein,
angiopoietin, clotting factor VII, urokinase-type plasminogen activator,
growth- hormone receptor hormone, growth inhibitor, chemotactic factor,
low- density lipoprotein, transferrin and other ligands associated with
cancer immunological diseases. The superantigen is chosen from SEA, SEB,
SEC, SED and SEE of *Staphylococcus aureus* enterotoxin family, SPE-A, SPE-
B and SPE-C of streptococci, especially SEA of *Staphylococcus aureus*
enterotoxin family. The fusion protein preferably contains staphylococcal
-enterotoxin A (SEA) as the superantigen and a ligand selected from EGF
and VEGF. The prepared proteins are useful in producing medicines for
anticancer therapy or immunological reaction. Such drugs are more specific
with enhanced activity and less toxic. This sequence represents a fusion
construct composed of VEGF and SEA.
Sequence 369 AA;
Query Match 82.6%; Score 1023; DB 9; Length 369;
Best Local Similarity 82.0%; Pred. No. 6.8e-94;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
1 SEKSEINEKDLRKSELOALNLRQIYYNEKAITENKESDDQPLENTLLPKGFPTG 60
137 SEKSEINEKDLRKSELOALNLRQIYYNEKAITENKESDDQPLENTLLPKGFPTD 196
61 HPWYNDLLVGLSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

DT 08-SEP-2005 (first entry)
DE VEGF-SEA fusion construct protein SEQ ID NO 4.
DE fusion protein; cell proliferation; antigen; cancer;
DE endothelial growth factor; EGF; vascular endothelial growth factor; VEGF;
DE SEA; enterotoxin family; enterotoxin A; cytostatic; immunomodulator.
DE Synthetic.
DE WO2005061531-A1.
DE 07-JUL-2005.
DE 31-MAY-2004; 2004WO-CN000569.
DE 21-DEC-2003; 2003CN-01109829.
DE (SUNJ/) SUN J.
DE Sun J;
DE WPI; 2005-488638/49.
DE N-PSDB; AEB13484.
DE Preparation of superantigen fusion proteins containing specific proteins
DE and superantigens based on recombinant expression vectors and host cells,
DE for producing medicines in e.g. antitumor therapy.
DE Example 6; SEQ ID NO 4; 33pp; Chinese.
DE This invention describes a novel fusion protein comprising a ligand which
DE can promote the growth of cancer cells and also corresponds to the
DE receptor of cancer-cell overexpression, as well as a specific polypeptide
DE which has avidity to and antagonism against the cancer cell receptor or
DE may interact directly with the cancer-cell surface, and a superantigen
DE which can induce an antitumor immunological reaction. The invention also
DE describes 1) a recombinant vector containing the nucleotide sequence for
DE the fusion protein; 2) host cells containing the recombinant vector and
DE 3) a method of producing the fusion protein by culturing the host cells
DE before collecting the expressed fusion protein. The ligand is selected
DE from endothelial growth factor (EGF) family, vascular endothelial growth
DE factor (VEGF) family, basic fibroblast growth factor (bFGF) and GGF
DE families, transforming growth factor (TGF-alpha), interleukin-4,
DE interleukin-2, heregulin, interleukin-6, interleukin-13, interleukin-8,
DE heparin-binding EGF-like growth factor, insulin-like growth factor,
DE hepatocyte growth factor, platelet-derivatizing growth factor, nerve
DE growth factor, placenta growth factor, stem-cell growth factor,
DE thrombopoietin, ephrin family, erbB ligand, desialic-acid glycoprotein,
DE angiopoietin, clotting factor VII, urokinase-type plasminogen activator,
DE growth- hormone receptor hormone, growth inhibitor, chemotactic factor,
DE low- density lipoprotein, transferrin and other ligands associated with
DE cancer immunological diseases. The superantigen is chosen from SEA, SEB,
DE SEC, SED and SEE of *Staphylococcus aureus* enterotoxin family, SPE-A, SPE-
DE B and SPE-C of streptococci, especially SEA of *Staphylococcus aureus*
DE enterotoxin family. The fusion protein preferably contains staphylococcal
DE -enterotoxin A (SEA) as the superantigen and a ligand selected from EGF
DE and VEGF. The prepared proteins are useful in producing medicines for
DE anticancer therapy or immunological reaction. Such drugs are more specific
DE with enhanced activity and less toxic. This sequence represents a fusion
DE construct composed of VEGF and SEA.
DE Sequence 369 AA;
DE Query Match 82.6%; Score 1023; DB 9; Length 369;
DE Best Local Similarity 82.0%; Pred. No. 6.8e-94;
DE Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
DE 1 SEKSEINEKDLRKSELOALNLRQIYYNEKAITENKESDDQPLENTLLPKGFPTG 60
DE 137 SEKSEINEKDLRKSELOALNLRQIYYNEKAITENKESDDQPLENTLLPKGFPTD 196
DE 61 HPWYNDLLVGLSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

Db 197 HSWYNDLLVDFDSKDIYKYGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 256
Qy 121 EEKKVPINLWIDGKQTTVPIDKVKTSKVEYVQELDLQARHYLHGKFGLYNSDSFGGKQV 180
Db 257 EEKKVPINLWIDGKQTTVPIDKVKTSKVEYVQELDLQARHYLHGKFGLYNSDSFGGKQV 316
Qy 181 RGLIVFHSSEGSTSVSYDLFDAQQYPTDLLRIYRDNKTINSENHLIDLILYTT 233
Db 317 RGLIVFHTSTEPSVNYDLFGAQQYNTLLRIYRDNKTINSENHNHIDILYTS 369

RESULT 26
AAW06738
ID AAW06738 standard; protein; 233 AA.
XX AAW06738;
XX 08-MAR-1997 (first entry)
XX Staphylococcus enterotoxin A.
DE Enterotoxin A; superantigen; antigen; cytokine; chemokine; T cell;
KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;
KW adjuvant.
XX Staphylococcus sp.
XX WO9636366-A1.
XX 21-NOV-1996.
XX 20-MAY-1996; 96WO-US007432.
XX 18-MAY-1995; 95US-00446918.
XX 23-DEC-1995; 95US-00580806.
XX (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX Dow SW, Elmslie RB, Potter TA;
XX WPI; 1997-011857/01.
XX N-PSDB; AAT45699.
XX Recombinant molecule encoding superantigen and opt. cytokine or
PT chemokine - controls activity of effector cells (T cells, monocytes,
PT natural killer cells), used for gene therapy of cancer.
XX Example 1; Page 98-99; 131pp; English.
XX A cDNA clone (AAT45699) codes for staphylococcal enterotoxin A (AAW06738)
XX superantigen. Nucleic acids encoding superantigens (see also AAW06737,
XX AAW06739), esp. truncated forms of the superantigen lacking the leader
XX peptide, can be used in the gene therapy of cancer, infectious diseases
XX and immunological disorders. The nucleic acid, optionally in combination
XX with cytokine or chemokine nucleic acids, is delivered to an animal using
XX e.g. liposomes. It acts by controlling the activity of effector cells,
XX such as T-cells, macrophages, monocytes and/or natural killer cells.
XX Localised prodn. of an effective but non-toxic amount of encoded proteins
XX allows safe treatment of the animal
XX Sequence 233 AA;
Query Match 82.3%; Score 1019; DB 2; Length 233;
Best Local Similarity 81.9%; Pred. No. 8.9e-94;
Matches 190; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
Qy 2 EKSEINEKDLRKSELOALNLRQIYYNEKAITENKESDDQPLENTLLPKGFPTG 61
Db 2 EKSEINEKDLRKSELOALNLRQIYYNEKAITENKESDDQPLENTLLPKGFPTD 61
Qy 62 PWTNDLLVGLSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121

Db 62 SNWYNDLLVDFDSKDIDYKYGKGVLDLYGAYGYQCAGGTPNKTAQCMYGGVTLHDNNRLTE 121

QY 122 EKKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 181

Db 122 EKKVPINLWIDGKQNTVPLETVKTNKQNTVQELDLQARRYLQEKYNLYNSDVDFGKVQ 181

QY 182 GLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNKTINSENHIDLYLYTT 233

Db 182 GLIVFHTSTEPSVNYDLFQAQGYNTLLRIYRDNKTINSENHIDLYLYTS 233

RESULT 28

AAW35373

ID ADI95318 standard; protein; 233 AA.

XX ADI95318;

XX ADI95318;

DT 04-NOV-2004 (first entry)

XX OSPP-related Staphylococcus aureus enterotoxin A protein.

DE immune response; overlapping synthetic peptide formulation; OSPP;

XX immunostimulant; viricide; antibacterial; antiparasitic; cytostatic;

KW vaccine; viral; bacterial; parasitic infection; prion disease;

KW neoplastic; toxin; enterotoxin A.

XX Staphylococcus aureus.

OS WO2004002415-A2.

PN 08-JAN-2004.

XX 27-JUN-2003; 2003WO-US020322.

PF 27-JUN-2002; 2002US-0392718P.

PR (DAND) DANA FARBER CANCER INST INC.

XX Ruprecht RM, Jiang S;

PI WPI; 2004-082868/08.

DR Modulating an immune response, useful for treating immune disorders, e.g.

XX viral, bacterial and parasitic infections, prion diseases, or neoplastic

PT diseases, administering to a subject an overlapping synthetic peptide

PT formulation.

XX Claim 13; SEQ ID NO 226; 175pp; English.

PS The invention relates to a novel method for modulating an immune response

XX comprising administering to a subject an overlapping synthetic peptide

CC formulation (OSPP) which comprises a combination of single chain peptides

CC corresponding to the amino acid sequence of a protein of interest. The

CC method of the invention has immunostimulant, viricide, antibacterial,

CC antiparasitic and cytostatic applications and may be useful during

CC vaccine production and for treating immune disorders including viral,

CC bacterial and parasitic infections, prion diseases, neoplastic diseases,

CC as well as providing protection against toxins. The current sequence is

CC that of the OSPP-related Staphylococcus aureus enterotoxin A protein of

CC the invention.

XX Sequence 233 AA;

SQ

Query Match 82.3%; Score 1019; DB 8; Length 233;

Best Local Similarity 81.5%; Pred. No. 8.9e-94;

Matches 190; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60

Db 1 SEKSEINEKDLRKKSSELQALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60

QY 61 HPWYNDLLVDLGSKDATNKGKGVLDLYGAYGYQCAGGTPNKTAQCMYGGVTLHDNNRLT 120

Db 61 HSWYNDLLVDFDSKDIDYKYGKGVLDLYGAYGYQCAGGTPNKTAQCMYGGVTLHDNNRLT 120

QY 121 EKKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180

Db 121 EKKVPINLWIDGKQNTVPLETVKTNKQNTVQELDLQARRYLQEKYNLYNSDVDFGKVQ 180

QY 181 RGLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNKTINSENHIDLYLYTT 233

Db 181 RGLIVFHTSTEPSVNYDLFQAQGYNTLLRIYRDNKTINSENHIDLYLYTS 233

RESULT 28

AAW35373

ID AAW35373 standard; peptide; 233 AA.

XX AAW35373;

XX AAW35373;

DT 20-APR-1998 (first entry)

XX Staphylococcus enterotoxin SEA wild-type superantigen.

DE SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;

XX cancer; infection; autoimmune disease; antibody.

KW Staphylococcus sp.

OS WO9736932-A1.

PN 09-OCT-1997.

XX 26-MAR-1997; 97WO-SF000537.

XX 29-MAR-1996; 96SE-00001245.

PR 12-AUG-1996; 96US-00695692.

XX (PHAA) PHARMACIA & UPJOHN AB.

PA Antonsson P, Hansson J, Bjoerk P, Dohlaten M, Kalland T;

PI Abrahamson L, Forsberg G;

XX WPI; 1997-503052/46.

DR Conjugate of target seeking moiety and modified superantigen - useful for

XX activating the immune system to treat cancer, viral infections, parasitic

PT infestations and autoimmune diseases.

PT Claim 8; Page 36-37; 58pp; English.

PS This is the wild-type Staphylococcus enterotoxin SEA superantigen. This

XX SEA superantigen can be modified to be used in a novel conjugate. The

CC novel conjugate comprises a target seeking moiety and a modified wild

CC type superantigen. The modified superantigen retains its ability to

CC activate a subset of T cells, even though 1 or more wild-type amino acid

CC residues in at least 1 region which functions in determining binding to T

CC cell receptor (TCR) and activation of a subset of T cells has/have been

CC replaced. Such a modified superantigen can optionally be used as part of

CC a conjugate with a target seeking moiety, for activating the immune

CC system to treat a mammalian disease. A pharmaceutical composition can be

CC prepared comprising a modified antibody (preferably a Fab fragment fused

CC to a peptide moiety providing activation of T cells in Vbeta specific

CC manner) in which cysteines providing for interchain cysteine linkages in

CC the native antibody have been replaced (preferably by serine residues) to

CC prohibit cysteine formation. The modified wild-type superantigen is used

CC for treating cancer, viral infections, parasitic infestations and

CC autoimmune disease. The modified wild type superantigen has a lower

CC immunogenicity and reactivity with neutralising antibodies and has fewer

CC side-effects when used as a drug, compared to wild type superantigen

XX Sequence 233 AA;

SQ

Query Match 82.1%; Score 1016; DB 2; Length 233;

Best Local Similarity 81.5%; Pred. No. 1.8e-93;

Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

```
QY 1 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGGTPNKTACMYGGVTLHDNNRLT 120
Db 61 HSWYNDLLVDLGSKDIDVYKYGKGVLDLYGAYGYQACAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 121 RGLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHLDLYLTT 233
Db 181 RGLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHLDLYLTS 233

RESULT 29
AAB67338
ID AAB67338 standard; peptide; 233 AA.
XX
AC AAB67338;
XX
DT 23-APR-2001 (first entry)
XX
DE Staphylococcus aureus enterotoxin A protein.
XX
KW Tumour; cancer; immune; enterotoxin.
XX
OS Staphylococcus aureus.
XX
PN US6180097-B1.
XX
PD 30-JAN-2001.
XX
PF 30-OCT-1998; 98US-00183437.
XX
PR 03-OCT-1989; 89US-00416530.
PR 17-JAN-1990; 90US-00466577.
PR 17-JAN-1991; 91WO-US000342.
PR 01-JUN-1992; 92US-00891718.
PR 02-MAR-1993; 93US-00025144.
PR 31-JAN-1994; 94US-00189424.
PR 19-JUN-1995; 95US-00491746.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
DR WPI; 2001-158657/16.
XX
PT Tumor cell capable of stimulating antitumor immune reactivity in vitro or
PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
PT costimulatory molecule.
XX
PS Disclosure; Fig 2; 16pp; English.
XX
CC The present invention relates to a tumour cell capable of stimulating
CC antitumor immune reactivity in vitro or in vivo contains and expresses an
CC exogenous nucleic acid molecule encoding a superantigen or its active
CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
CC molecule that activates T cells in conjunction with an antigenic
CC stimulus. The invention may be used for cancer therapy by stimulating an
CC anticancer immune response in vivo or ex vivo
XX
SQ Sequence 233 AA;
Query Match 82.1%; Score 1016; DB 4; Length 233;
Best Local Similarity 81.5%; Pred. No. 1.8e-93;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
```

```
Db 1 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGGTPNKTACMYGGVTLHDNNRLT 120
Db 61 HSWYNDLLVDLGSKDIDVYKYGKGVLDLYGAYGYQACAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHLDLYLTT 233
Db 181 RGLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHLDLYLTS 233

RESULT 30
AAR45011
ID AAR45011 standard; protein; 233 AA.
XX
AC AAR45011;
XX
DT 25-MAR-2003 (revised)
DT 08-JUN-1994 (first entry)
XX
DE Staphylococcus enterotoxin SEA.
XX
KW Staphylococcus enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; perfusion system.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Misc-difference 49
FT /notes= "Given in the specification as O, no further
FT details given"
XX
PN WO9324136-A1.
XX
PD 09-DEC-1993.
XX
PF 01-JUN-1993; 93WO-US005213.
XX
PR 01-JUN-1992; 92US-00891718.
XX
PA (TERM/) TERMAN D S.
PA (STON/) STONE J L.
XX
PI Terman DS, Stone JL;
XX
DR WPI; 1993-405418/50.
XX
PT Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
PT in a patient or for the treatment of auto-immune diseases.
XX
PS Disclosure; Fig 1; 90pp; English.
XX
CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer in
CC a patient. These SEs, and homologues of them, can be used as tumouricidal
CC agents for treating cancers and autoimmune disease. They exhibit
CC tumouricidal activity and toxicity identical to that observed for the
CC Protein A perfusion system. They may be administered by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 233 AA;
Query Match 81.8%; Score 1013; DB 2; Length 233;
Best Local Similarity 81.5%; Pred. No. 3.6e-93;
Matches 190; Conservative 16; Mismatches 27; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
```

1 SEKSEINEKDLRKSELOCTALGNLKQIYYVNEKAKTENKESHQDLXHTILFKGFFTD 60
61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT 120
61 HSWYNDLLVDFDSKDVIYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT 120
121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFGLYNSDSFGGKVQ 180
121 BEKKVPINLWIDGKQNTVPLEIVTKNKNVTQVELDQARRYLQEKYNLYNSDVFEGKVQ 180
181 RGLIVFHSSEGSTVSYDLFDAQGYQPTDLLRIYRDNKTINSENHLIDLYLTT 233
181 RGLIVFHTSTEPSVNYDLFGAQGYQNTLLRIYRDNKTINSENHMHIDVLYTS 233

RESULT 31
ABU79068
ID ABU79068 standard; protein; 257 AA.
XX ABU79068;
AC ABU79068;
XX
DT 18-JUN-2003 (first entry)
DE S. aureus SEA (staphylococcus enterotoxin A) protein.
XX
KW Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;
KW Gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
KW APC; antitumour.
XX
OS Staphylococcus aureus.
XX
XX US2002177551-A1.
PN
XX
XX 28-NOV-2002.
PD
XX
XX 30-MAY-2001; 2001US-00870759.
PF
XX
XX
PR 31-MAY-2000; 2000US-0208128P.
XX
XX (TERM/) TERMAN D S.
PA
XX
XX Terman DS;
PI
XX
XX WPI; 2003-361759/34.
DR
XX
XX N-PSDB; ACA64694.
DR
XX
XX A mammalian cell receptor, useful in the treatment of cancer by binding
PT to tumor associated lipids where the binding induces anergy or apoptosis
PT in T cells and antigen presenting cells.
XX
XX
XX Disclosure; Page; 167pp; English.

The invention relates to a mammalian cell receptor, useful in the
XX treatment of cancer, which binds to tumour associated lipids and induces
XX anergy or apoptosis in the T cells and antigen presenting cells (APCs).
XX Also included are a mammalian cell useful in the treatment of cancer
XX where the receptor which binds tumour associated lipids and induces
XX cellular inactivation or death is deleted or functionally deactivated,
XX producing (M1) a tumouricidal immunocyte population in vivo in a mammal
XX (by allowing tumour associated lipids to contact immunocytes in which
XX receptors for immunosuppressive fatty acids, ceramides, glycolipids,
XX sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
XX sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
XX deleted), a construct useful in the treatment of cancer comprising a
XX superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
XX useful in the treatment of cancer (where an adaptor protein which
XX inhibits T cell activation by tumour associated antigens is deleted or
XX functionally deactivated), a composition useful in the treatment of
XX cancer (comprising a lipid raft conjugated to a superantigen), producing
XX (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
XX allowing tumour associated lipids to contact immunocytes, in which
XX receptors for the lipids are inactivated or deleted to produce a

tumouricidal immunocyte population, and administering the tumouricidally
CC activated immunocytes to the host), producing (M3) a tumouricidal APC
CC population ex vivo in a mammal (by allowing a tumour associated lipid to
CC contact APCs, in which receptors for the tumour associated lipids are
CC inactivated or deleted to produce a tumouricidally activated population,
CC and administering APCs to the host), producing a tumouricidal T cell
CC population ex vivo in a mammal) by allowing a tumour associated lipids to
CC contact T cells, in which adaptor proteins, which inhibit T cell
CC activation by tumour associated antigens, are deleted or functionally
CC deactivated to produce a tumouricidal population of T cells, and
CC administering the tumouricidally activated T cells to the host, or
CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
CC administering the tumouricidally activated T cells to the host), treating
CC (M5) cancer in a mammal (by administering a lipid binding molecule which
CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
CC a tumouricidal T cell population in vivo in a mammal (by allowing a
CC tumour associated antigen to contact immunocytes in which adaptor
CC proteins which inhibit T cell activation by tumour associated antigens
CC are deleted or functionally deactivated) and producing (M7) a
CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
CC receptors, methods and compositions are useful for treating cancers and
CC tumours. Bacterial superantigens are co-administered or administered as
CC fusion constructs with anti-tumour proteins or motifs. The present
CC sequence represents a bacterial superantigen protein (e.g. a
CC staphylococcal enterotoxin). Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format from the US patent office website at
CC "seqdata.uspto.gov/sequence.html?docid=20020177551"
XX
XX Sequence 257 AA;
SQ

Query Match 81.8%; Score 1013; DB 6; Length 257;
Best Local Similarity 81.5%; Pred. No. 4.1e-93;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQNALSNLRQIYYVNEKAKTENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQNALGNLKQIYYVNEKAKTENKESHQDLQHTILFKGFFTN 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDVIYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 BEKKVPINLWIDGKQNTVPLEIVTKNKNVTQVELDQARRYLQEKYNLYNSDVFEGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYQPTDLLRIYRDNKTINSENHLIDLYLTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGYQNTLLRIYRDNKTINSENHMHIDVLYTS 257

RESULT 32
ADP43288
ID ADP43288 standard; protein; 257 AA.
XX ADP43288;
AC ADP43288;
XX
XX 12-FEB-2004 (first entry)
DT
XX Staphylococcal enterotoxin A polypeptide seq id 8.
DE
XX receptor; lipid-based tumour associated antigen; cytostatic;
KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
KW infectious disease; Staphylococcal enterotoxin A; SEA; enterotoxin A.
XX
OS Staphylococcus.
XX
XX US2003157113-A1.
PN
XX
XX 21-AUG-2003.
PD

```
PF 28-DEC-2000; 2000US-00751708.
XX
XX 28-DEC-1999; 99US-0173371P.
XX
XX (TERM/) Terman D S.
XX
XX Terman DS;
XX
XX WPI; 2003-787326/74.
XX
XX New receptor in a mammalian cell that inhibits regular activation by
XX receptors specific for lipid-based tumor associated antigens, useful for
XX treating a neoplastic disease or tumor, and infectious diseases.
XX
XX Example 3; SEQ ID NO 8; 151pp; English.
XX
XX The invention describes a receptor in a mammalian cell that inhibits
XX regular activation by receptors specific for lipid-based tumor
XX associated antigen. The receptor has cytostatic and antimicrobial
XX properties and is suitable for use in gene therapy. The receptors,
XX methods and compositions are useful for treating a neoplastic disease or
XX tumor (cancer), and infectious diseases. This is the amino acid sequence
XX of an enterotoxin superantigen polypeptide the DNA encoding which can be
XX transfected in to a cell alone or with DNA encoding a cell surface moiety
XX to generate antitumor immunity.
XX
XX Sequence 257 AA;
XX
Query Match 81.8%; Score 1013; DB 7; Length 257;
Best Local Similarity 81.5%; Pred. No. 4.1e-93;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSLEQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFPTG 60
DB 25 SEKSEINEKDLRKKSLEQNALGNLQIYYNEKAKTENKESHDPLOHTILFKGFPTN 84
QY 61 HPWYNLLVLDGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDFDSKDIVDKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTPVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKKVPINLWIDGKQNTVPLETVTNKKNTVQELDLQARRYLOEKYNLNSDVFDGKVQ 204
QY 181 RGLIVFHSSSGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGQNSNTLLRIYRDNKTINSENHLDIYLYTS 257
RESULT 33
AEA02982
ID AEA02982 standard; protein; 257 AA.
XX
XX AEA02982;
XX
XX 28-JUL-2005 (first entry)
XX
XX Staphylococcal enterotoxin A (SEA) amino acid sequence SEQ ID NO:8.
XX
XX tumor; neoplasm; gene therapy; immunotherapy; cytostatic;
XX Staphylococcal enterotoxin A.
XX
XX Staphylococcus sp.
XX
XX US2005112141-A1.
XX
XX 26-MAY-2005.
XX
XX 08-SEP-2004; 2004US-00937758.
XX
XX 30-AUG-2000; 2000US-00650884.
XX
XX (TERM/) Terman D S.
XX
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XX
XX Terman DS;
XX
XX WPI; 2005-394926/40.
XX
XX N-PSDB; AEA02981.
XX
XX New composition for treating a tumor or neoplastic disease in a subject
XX comprises conjugates comprising superantigen polypeptides or nucleic
XX acids with other molecules that produce a tumoricidal response.
XX
XX Example 3; SEQ ID NO 8; 125pp; English.
XX
XX The invention relates to a composition for treating a tumor or neoplastic
XX disease in a subject. Also described: (1) a mammalian cell comprising an
XX exogenous nucleic acid encoding a superantigen expressed in the cell,
XX which cell also produces or expresses all alpha-anomers of the
XX monoglycosylceramide or diglycosylceramide, where expression of the
XX superantigen and the mono- or diglycosylceramide is capable of eliciting
XX an antitumor immune response in a mammal into which the cell is
XX introduced; (2) treating a tumor or neoplastic disease in a subject; (3)
XX preparing a population of immunotherapeutic T or natural killer T (NKT)
XX cells useful to treat a tumor or neoplastic disease in a subject; (4) an
XX apoptotic cell preparation or lysate useful for treating a tumor or
XX neoplastic disease in a subject, comprising a cell population that has
XX been transfected with naked DNA encoding a superantigen, and treated to
XX undergo apoptosis or lysis; and (5) a cell that has ingested or been
XX transfected with the above apoptotic preparation or lysate, thus,
XX rendering the cell effective in presenting material expressed from
XX transfecting nucleic acid or material ingested to the immune system of a
XX mammal to elicit an anti-tumor immune response. The composition and
XX methods are useful for treating tumors or neoplastic diseases. The
XX present sequence represents a Staphylococcal enterotoxin A (SEA) protein
XX sequence, which is used in an example from the present invention. Note -
XX The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from the
XX USPTO web site.
XX
XX Sequence 257 AA;
XX
Query Match 81.8%; Score 1013; DB 9; Length 257;
Best Local Similarity 81.5%; Pred. No. 4.1e-93;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSLEQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFPTG 60
DB 25 SEKSEINEKDLRKKSLEQNALGNLQIYYNEKAKTENKESHDPLOHTILFKGFPTN 84
QY 61 HPWYNLLVLDGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDFDSKDIVDKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTPVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKKVPINLWIDGKQNTVPLETVTNKKNTVQELDLQARRYLOEKYNLNSDVFDGKVQ 204
QY 181 RGLIVFHSSSGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGQNSNTLLRIYRDNKTINSENHLDIYLYTS 257
RESULT 34
ABB76234
ID ABB76234 standard; protein; 233 AA.
XX
XX ABB76234;
XX
XX 09-AUG-2002 (first entry)
XX
XX Staphylococcus aureus enterotoxin A.
XX
XX Enterotoxin A; SEA; superantigen; antigen; tumour; cancer; antitumour;
XX therapy.
XX
```


OS Staphylococcus aureus.

XX Key Location/Qualifiers

FT Misc-difference 49 /note= "amino acid residue given as 'O' in the

FT specification"

XX

PN US2002051765-A1.

XX

PD 02-MAY-2002.

XX

XX 19-DEC-2000; 2000US-00741503.

XX

XX 03-OCT-1989; 89US-00418530.

PR 17-JAN-1990; 90US-00466577.

PR 17-JAN-1991; 91WO-US000342.

PR 01-JUN-1992; 92US-00891718.

PR 02-MAR-1993; 93US-00025144.

PR 19-JAN-1994; 94US-00189424.

PR 11-JUN-1995; 95US-00491746.

XX

PA (TERM/) TERNAN D S.

XX

XX Terman DS;

XX

XX WPI; 2002-415198/44.

DR

XX Reagent for treating cancer without the need for e.g. radiotherapy,

FT comprises a specific V beta subset of T cells sensitized to a growing

PT tumor and stimulated with superantigens.

PT

XX Disclosure; Fig 2; 17pp; English.

XX

XX The present sequence is the protein sequence of enterotoxin A (SEA) of

CC Staphylococcus aureus. Similarity is shown, in several stretches of

CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic

CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the

CC present invention, synthetic polypeptides useful in tumour therapy and in

CC blocking or destroying autoreactive T and B lymphocyte populations are

CC characterised by substantial structural homology to staphylococcal

CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic

CC exotoxins, with statistically significant sequence homology and

CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo

CC analysis exceeding 6) to include alignment of cysteine residues and

CC similar hydropathy profiles. These superantigens are used to treat solid

CC tumours, including their metastases, without radiation, surgery or

CC standard chemotherapeutic agents. A claimed method of human cancer

CC treatment involves contacting haematopoietic cells from a patient with

CC one or more superantigens ex vivo to generate stimulated cells, selecting

CC a specific V beta subset of cells, and reintroducing these cells into the

CC patient to induce an in vivo therapeutic, tumouricidal reaction

XX

SQ Sequence 233 AA;

Query Match 81.1%; Score 1004; DB 5; Length 233;

Best Local Similarity 81.1%; Pred. No. 2.9e-92; Indels 0; Gaps 0;

Matches 169; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLFGKFFTG 60

DB 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLFGKFFTD 60

QY 61 HPYNDLLVDLGSKDATNKKYKGVLDLYGAYGYQCAGGTPNKTCMGYGVTLHDNNRLT 120

DB 61 HSWYNDLLVDLGSKDIDVDRYKGVLDLYGAYGYQCAGGTPNKTCMGYGVTLHDNNRLT 120

QY 121 EEKKVPINLWIDGQKQTVPIIDKVKTSKEVTVQELDLQARHYLHGKGLYNSDFGKVKQ 180

DB 121 EEKKVPINLWIDGQKQTVPIETVTKNKNVTUQELDPQARRYLOEKYLNVSDFGKVKQ 180

QY 181 RGLIVFHSSEGSTSVSYDLFDAQGOYQPTLLRIYRDKNKTINSENLHIDLXYTT 233

DB 181 RGLIVFHTSTPEPSVNYDLFGAQGOYSNTLLRIYRDKNKTINSENHIDIVLYTS 233

RESULT 35

ABB79501

ID ABB79501 standard; protein; 257 AA.

XX

AC ABB79501;

XX

DT 23-SEP-2002 (first entry)

XX

DE Staphylococcal enterotoxin A vaccine, periplasmic (A489270P).

XX

KW Enterotoxin A; superantigen; antigen; toxin; vaccine; A489270P;

KW attenuation; mutant; mucin.

XX

OS Staphylococcus sp.

XX Synthetic.

XX

XX Key Location/Qualifiers

FT Peptide 1..25

FT Protein /label= Signal_peptide

FT /label= Mature_protein

FT Misc-difference 72 /note= "wild-type Leu substituted by Arg"

FT Misc-difference 94 /note= "wild-type Asp substituted by Arg"

FT Misc-difference 116 /note= "wild-type Tyr substituted by Ala"

XX

PN US6399332-B1.

XX

PD 04-JUN-2002.

XX

PF 01-SEP-1998; 98US-00144776.

XX

PR 25-JUN-1997; 97US-00882431.

XX

PA (USSA) US SEC OF ARMY.

XX

PI Ulrich RG, Olson MA, Bavari S;

DR WPI; 2002-546281/58.

DR N-PSDB; ABB84222.

XX

XX Novel isolated and purified superantigen toxin DNA fragment which has

PT been genetically altered, useful for producing vaccine for treatment of

PT superantigen toxin-associated bacterial diseases.

XX

PS Claim 4; Col 33-35; 46pp; English.

XX

CC The present sequence is the protein sequence of staphylococcal

CC enterotoxin A (SEA) vaccine, periplasmic (A489270P). The vaccine

CC comprises 3 amino acid substitutions introduced into the SEA sequence:

CC L48R, Y89A and D70R. These mutations reduce the binding of the toxin to

CC major histocompatibility complex (MHC) Class II and/or T cell receptors.

CC The full-length expressed product is secreted into the periplasmic space

CC of Escherichia coli host cells, and the leader peptide is recognised and

CC cleaved by a native mechanism. The vaccine is used to protect against

CC superantigen toxin infections. Superantigen attributes are absent, but

CC the superantigen is effectively recognised by the immune system and an

CC appropriate antibody response is produced. In examples from the

CC invention, attenuated superantigen toxins were shown to protect animals

CC against challenge with wild-type toxin. Methods of producing and using

CC the altered superantigen toxins as vaccines, and in diagnosis and

CC therapy, are provided. A multivalent vaccine consisting of altered

CC superantigen toxins from SEA, SEB, SEC-1, TSST-1 and streptococcal SPEA

CC is predicted to provide protective immunity against the majority of

CC bacterial superantigen toxins

XX

SQ Sequence 257 AA;

Query Match 80.8%; Score 1000; DB 5; Length 257;

Best Local Similarity 80.7%; Pred. No. 8.3e-92;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVRFDSKDIIVDKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLSNDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLSNDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYSNTLLRIYRDNKTINSENHLDLYLYTS 257

RESULT 36
ABU10081
ID ABU10081 standard; protein; 257 AA.
XX AC ABU10081;
XX DT 11-AUG-2003 (first entry)
XX DE Staphylococcal enterotoxin A #1.
XX KW Enterotoxin A; superantigen-associated bacterial infection; vaccine;
XX KW superantigen toxin.
XX OS Staphylococcus sp.
XX PN US2003009015-A1.
XX PD 09-JAN-2003.
XX PF 25-JUN-1997; 97US-00882431.
XX PR 25-JUN-1997; 97US-00882431.
XX PA (ULRI/) ULRICH R G.
XX PA (OLSO/) OLSON M A.
XX PA (BAVA/) BAVARI S.
XX PI Ulrich RG, Olson MA, Bavari S;
XX WPI; 2003-401542/38.
XX N-PSDB; ACA61177.
XX PT New superantigen toxin and/or DNA fragment with an altered binding of the
XX PT encoded altered toxin to either MHC class II or T cell antigen receptor,
XX PT useful for treating or ameliorating superantigen-associated bacterial
XX PT infection.
XX PS Claim 10; Page 18-19; 50pp; English.
XX CC The invention relates to an isolated and purified superantigen toxin
XX CC and/or DNA fragment, which has been altered so that the binding of the
XX CC encoded toxin to either major histocompatibility complex (MHC) class II
XX CC or T cell antigen receptor is altered. The superantigen toxins, DNA
XX CC fragments, and vaccines are useful for treating or ameliorating
XX CC superantigen-associated bacterial infection. The DNA fragments are
XX CC particularly useful for producing vaccine against superantigen toxin
XX CC infections. The transformed host cells are useful for analysing the
XX CC effectiveness of drugs and agents that affect the binding of
XX CC superantigens to MHC class II or T-cell antigen receptors. The present
XX CC sequence represents the amino acid sequence of staphylococcal enterotoxin
XX CC A #1
XX SQ Sequence 257 AA;

Query Match 80.8%; Score 1000; DB 6; Length 257;
Best Local Similarity 80.7%; Pred. No. 8.3e-92;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVRFDSKDIIVDKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLSNDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLSNDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYSNTLLRIYRDNKTINSENHLDLYLYTS 257

RESULT 37
ABU62324
ID ABU62324 standard; protein; 257 AA.
XX AC ABU62324;
XX DT 27-AUG-2003 (first entry)
XX DE S. aureus periplasmic enterotoxin A mutant #1.
XX KW SEA; staphylococcal enterotoxin A; mutein; mutant; vaccine;
XX KW superantigen toxin; MHC; superantigen-associated bacterial infection;
XX KW bacterial infection; antibacterial.
XX OS Staphylococcus aureus.
XX OS Synthetic.
XX PH Location/Qualifiers
FT Peptide 1..24
FT /label= Signal_peptide
FT Protein 25..257
FT /label= Mature_SEA_mutant #1
FT Misc-difference 66
FT /note= "Wild-type Leu substituted by Glu"
FT Misc-difference 72
FT /note= "Wild-type Leu substituted by Arg"
FT Misc-difference 94
FT /note= "Wild-type Asp substituted by Arg"
FT Misc-difference 113
FT /note= "Wild-type Tyr substituted by Gly"
FT Misc-difference 116
FT /note= "Wild-type Tyr substituted by Ala"
XX PN US2003036644-A1.
XX PD 20-FEB-2003.
XX PF 26-NOV-2001; 2001US-00002784.
XX PR 25-JUN-1997; 97US-00882431.
XX PR 01-SEP-1998; 98US-00144776.
XX PA (ULRI/) ULRICH R G.
XX PI Ulrich RG;
XX WPI; 2003-492125/46.
XX N-PSDB; ACD28894.
XX PT New superantigen toxin DNA fragment, useful for preparing a composition
XX PT for treating or preventing bacterial infection.

XX PS Disclosure; Page 22-23; 68pp; English.

XX CC The invention relates to an isolated and purified superantigen toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) superantigen toxin peptide, diagnosing superantigen-associated bacterial infection, a vaccine (comprising an altered superantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection), CC treating/ameliorating a superantigen-associated bacterial infection, an antisera isolated from individuals immunised with one or more altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA, SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and SPEb). The superantigen toxin DNA fragment is useful for preparing a composition for treating or preventing bacterial infection. The present CC sequence represents the L42E/L48R/D70R/Y89G/Y92A (with reference to the mature protein sequence) mutant of periplasmic SEA

XX CC Sequence 257 AA;

Query Match 80.8%; Score 1000; DB 7; Length 257;
Best Local Similarity 80.7%; Pred. No. 8.3e-92;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDQFROHTILFKGFPTD 84

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVRFDSKDIDVYKGGKVDLYGAYAGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVKQ 180
DB 145 EEKKVPINLWLDGKQNTVPLETKNKQNTVQELDLQARRYLQEKYKLYNSDVDFGKVKQ 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLIDLXYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYSNTLLRIYRDNKTINSENHIDIVLYTS 257

RESULT 38
AAE37676
ID AAE37676 standard; protein; 257 AA.

XX AC AAE37676;

XX DT 06-OCT-2003 (first entry)

XX DE Protein #1 related to the invention.

XX KW Superantigen toxin; vaccine; infection; gene therapy.

XX OS Unidentified.

XX PN WO2003056015-A1.

XX PD 10-JUL-2003.

XX PF 26-NOV-2001; 2001WO-US046540.

XX PR 26-NOV-2001; 2001US-00002784.

XX PA (USMB-) US MEDICAL RES INST INFECTIOUS DISEASES.

XX PI Ulrich RG;

DR WPI; 2003-492125/46.
DR N-PSDB; AAD56764.

XX PT New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.

XX PS Disclosure; Page 108-109; 141pp; English.

XX CC The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of CC vaccines against bacterial superantigen toxin infections. They are also CC useful in gene therapy. The present sequence is a protein related to the CC invention

XX CC Sequence 257 AA;

Query Match 80.8%; Score 1000; DB 7; Length 257;
Best Local Similarity 80.7%; Pred. No. 8.3e-92;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDQFROHTILFKGFPTD 84

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVRFDSKDIDVYKGGKVDLYGAYAGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVKQ 180
DB 145 EEKKVPINLWLDGKQNTVPLETKNKQNTVQELDLQARRYLQEKYKLYNSDVDFGKVKQ 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLIDLXYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYSNTLLRIYRDNKTINSENHIDIVLYTS 257

RESULT 39
ADY93171
ID ADY93171 standard; protein; 257 AA.

XX AC ADY93171;

XX DT 02-JUN-2005 (first entry)

XX DE Bacterial superantigen toxin related protein, SEQ ID NO: 2.

XX KW Vaccine; toxin; diagnosis; bacterial infection; antibacterial; infection; antigen.

XX OS Unidentified.

XX PN US2005064526-A1.

XX PD 24-MAR-2005.

XX PF 29-JAN-2004; 2004US-00767687.

XX PR 25-JUN-1997; 97US-00882431.

XX PA (ULRI/) ULRICH R G.
PA (OLSO/) OLSON M A.
PA (BAVA/) BAVARI S.

XX PI Ulrich RG, Olson MA, Bavari S;

XX WPI; 2005-252679/26.
DR N-PSDB; ADY93170.

XX PT Novel altered superantigen toxin that alters binding of encoded altered toxin to major histocompatibility complex class II or T cell antigen

```
PT receptor, useful for preparing vaccine for treating superantigen-
PT associated bacterial infection.
PS Disclosure; SEQ ID NO 2; 51pp; English.
XX
XX
CC The present invention relates to a altered superantigen toxin that alters
CC binding of encoded altered toxin to major histocompatibility complex
CC class II or T cell antigen receptor. The invention is useful for
CC preparing vaccine for treating superantigen-associated bacterial
CC infection. The present sequence is the bacterial superantigen toxin
CC related protein.
XX
XX SQ Sequence 257 AA;
Query Match 80.8%; Score 1000; DB 9; Length 257;
Best Local Similarity 80.7%; Pred. No. 8.1e-92;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOLNALSNLQIYYINEKAITENKESDDQPLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOLNALSNLQIYYINEKAITENKESDDQPLENTLLFKGFFTD 84
QY 61 HPWYNDLLVGLSKDATNKYKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVRFDSKDIVDKYKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EEKVPINLWIDGKQNTVPLETKNKNVTQVQLDLQARYLQEKYNLYNSDVFQKQV 204
QY 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTDILLRIYRDNKTINSENHLIDLYLTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGYSNLTLRIYRDNKTINSENHMDIYLYTS 257
RESULT 40
AAV54463
ID AAV54463 standard; protein; 233 AA.
XX
AC AAV54463;
XX
XX 25-APR-2000 (first entry)
XX
DE Amino acid sequence of a mutant Staphylococcal enterotoxin A.
XX
KW Mutant; SEA gene; enterotoxin A; SEB gene; nucleic acid vaccine;
KW Venezuelan equine encephalitis virus; vaccine vector; vaccine;
KW Staphylococcal intoxication; Staphylococcus exotoxin.
XX
OS Staphylococcus aureus.
XX
XX Key Location/Qualifiers
FT Misc-difference 2 /note= "Glu encoded by AGAA"
FT FT Misc-difference 4
FT FT Misc-difference 4 /note= "Ser encoded by C"
XX
XX W0200002523-A2.
XX
XX 20-JAN-2000.
XX
XX 09-JUL-1999; 99WO-US015569.
XX
XX 10-JUL-1998; 98US-0092416P.
XX
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
XX Lee JS, Pushko P, Smith JF, Ulrich RG;
XX
XX WPI; 2000-160826/14.
XX
XX N-PSDB; AAZ45833.
XX
XX New DNA construct useful as vaccines against enterotoxins of
PT
```

```
PT Staphylococcus aureus which causes gastrointestinal distress, or toxic
PT shock syndrome.
PS Disclosure; Page 28; 30pp; English.
XX
XX
CC The present sequence is represents a mutant Staphylococcal enterotoxin A.
CC It is encoded by a mutant SEA gene. The mutant gene product is unable to
CC bind to the MHC on T-cells, and so is non-toxic. Mutant SEA and SEB genes
CC were inserted into a Venezuelan equine encephalitis (VEE) replicon
CC vector, to produce vaccine vectors. The mutant gene product is unable to
CC bind to the MHC on T-cells, and so is non-toxic. Self-replicating RNA
CC derived from the recombinant VEE vectors can be used as a nucleic acid
CC vaccine, or to transfect cells along with RNA from helper plasmids. The
CC recombinant proteins produced are used as vaccines for providing immunity
CC against Staphylococcal intoxication or as a diagnostic tool for detection
CC of Staphylococcus exotoxin. The transformed host cells are used to
CC analyse the effectiveness of drugs and agents which inhibit S. aureus
CC exotoxins or release of exotoxins. Infectious alpha-virus particles
CC comprising the mutant SEA or SEB genes are used for providing immunity
CC against Staphylococcal exotoxins by generating a protective immune
CC reaction in humans or animals. The vaccines are used to reduce disease
CC symptoms or reduce severity of disease caused by enterotoxins of S.
CC aureus
XX
XX SQ Sequence 233 AA;
Query Match 80.5%; Score 996; DB 3; Length 233;
Best Local Similarity 80.6%; Pred. No. 1.8e-91;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;
QY 2 EKSEINEKDLRKSELOLNALSNLQIYYINEKAITENKESDDQPLENTLLFKGFFTG 61
DB 2 EKSEINEKDLRKSELOLNALSNLQIYYINEKAITENKESDDQFRQHTILFKGFFTDH 61
QY 62 PWYNDLLVGLSKDATNKYKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVRFDSKDIVDKYKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 181
DB 122 EKKVPINLWIDGKQNTVPLETKNKNVTQVQLDLQARYLQEKYNLYNSDVFQKQV 181
QY 182 GLIVFHSSEGSTVSVDLFDQAQGYPTDILLRIYRDNKTINSENHLIDLYLTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAQGYSNLTLRIYRDNKTINSENHMDIYLYTS 233
RESULT 41
ABB79502
ID ABB79502 standard; protein; 233 AA.
XX
AC ABB79502;
XX
XX 23-SEP-2002 (first entry)
XX
DE Staphylococcal enterotoxin A vaccine, cytoplasmic (A489270C).
XX
KW Enterotoxin A; superantigen; antigen; toxin; vaccine; A489270C;
KW attenuation; mutant; mutein.
XX
XX Staphylococcus sp.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 1 /note= "encoded by AT, apparent frameshift"
FT FT Misc-difference 48
FT FT Misc-difference 48 /note= "wild-type Leu substituted by Arg"
FT FT Misc-difference 70 /note= "wild-type Asp substituted by Arg"
FT FT Misc-difference 92 /note= "wild-type Tyr substituted by Ala"
FT FT
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```
QY 62 PNYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKDIYDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR 181
Db 122 EKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLOEKYLNLYNSDVFDGKVQR 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLDLYLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFQAQGYSNLTLLRIYRDNKTINSENHLDIYLYTS 233

RESULT 45
ADY93173
ID ADY93173 standard; protein; 233 AA.
XX
AC ADY93173;
XX
DT 02-JUN-2005 (first entry)
XX
DE Bacterial superantigen toxin related protein, SEQ ID NO: 4.
XX
KW Vaccine; toxin; diagnosis; bacterial infection; antibacterial; infection;
KW antigen.
XX
OS Unidentified.
XX
Key Location/Qualifiers
FH Misc-difference 1..2 /note= "Encoded by AT"
FT
FT
XX
XX US2005064526-A1.
XX
XX 24-MAR-2005.
XX
XX 29-JAN-2004; 2004US-00767687.
XX
XX 25-JUN-1997; 97US-00882431.
XX
XX {ULRI//} ULRICH R G.
PA {OLSO//} OLSON M A.
PA {BAVA//} BAVARI S.
XX
XX Ulrich RG, Olson MA, Bavari S;
PI
XX
XX WPI; 2005-252679/26.
DR N-PSDB; ADY93172.
XX
XX Novel altered superantigen toxin that alters binding of encoded altered
PT toxin to major histocompatibility complex class II or I cell antigen
PT receptor, useful for preparing vaccine for treating superantigen-
PT associated bacterial infection.
XX
XX Disclosure; SEQ ID NO 4; 51pp; English.
XX
XX The present invention relates to a altered superantigen toxin that alters
CC binding of encoded altered toxin to major histocompatibility complex
CC class II or T cell antigen receptor. The invention is useful for
CC preparing vaccine for treating superantigen-associated bacterial
CC infection. The present sequence is the bacterial superantigen toxin
CC related protein.
XX
XX Sequence 233 AA;
SQ
Query Match 80.5%; Score 996; DB 9; Length 233;
Best Local Similarity 80.6%; Pred. No. 1.8e-91;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;
QY 2 EKSEINEKDLRKKSELQRNALNRQIYYNNEKAITENKESDDQFLENTLLPKGFPTH 61
Db 2 EKSEINEKDLRKKSELQGTALNQLKIYYNNEKAKTENKESHDQPRQHTILPKGFPTH 61
```

RESULT 46

```
ABU10099
ID ABU10099 standard; protein; 233 AA.
XX
AC ABU10099;
XX
DT 11-AUG-2003 (first entry)
XX
DE Staphylococcus enterotoxin A K14E substitution mutant.
XX
KW Enterotoxin A; superantigen-associated bacterial infection; mutant;
KW superantigen toxin; vaccine; mutein.
XX
XX Staphylococcus sp.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 14 /note= "Wild-type Lys substituted by Glu"
FT
FT
XX
XX US2003009015-A1.
XX
XX 09-JAN-2003.
XX
XX 25-JUN-1997; 97US-00882431.
XX
XX 25-JUN-1997; 97US-00882431.
XX
XX {ULRI//} ULRICH R G.
PA {OLSO//} OLSON M A.
PA {BAVA//} BAVARI S.
XX
XX Ulrich RG, Olson MA, Bavari S;
PI
XX
XX WPI; 2003-401542/38.
DR
XX
XX New superantigen toxin and/or DNA fragment with an altered binding of the
PT encoded altered toxin to either MHC class II or T cell antigen receptor,
PT useful for treating or ameliorating superantigen-associated bacterial
PT infection.
XX
XX Example 7; Page; 50pp; English.
XX
XX The invention relates to an isolated and purified superantigen toxin
CC and/or DNA fragment, which has been altered so that the binding of the
CC encoded toxin to either major histocompatibility complex (MHC) class II
CC or T cell antigen receptor is altered. The superantigen toxins, DNA
CC fragments, and vaccines are useful for treating or ameliorating
CC superantigen-associated bacterial infection. The DNA fragments are
CC particularly useful for producing vaccine against superantigen toxin
CC infections. The transformed host cells are useful for analysing the
CC effectiveness of drugs and agents that affect the binding of
CC superantigens to MHC class II or T-cell antigen receptors. The present
CC sequence represents the amino acid sequence of the staphylococcus
CC enterotoxin A K14E mutant. Note: The present sequence is not present in
CC the specification but was created by the indexer from the wild-type
CC staphylococcus enterotoxin A sequence (see ACA61178)
XX
XX Sequence 233 AA;
```

Query Match 80.1%; Score 992; DB 6; Length 233;
 Best Local Similarity 80.2%; Pred. No. 4.6e-91;
 Matches 186; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
 DB 2 EKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFTGH 61

QY 62 PWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTE 121
 DB 62 SWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTE 121

QY 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQVOR 181
 DB 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQVOR 181

QY 182 GLIVFHSSEGSTVSYDLFDAQGYPTDILLRIYRDNKTINSENHIDLYLTT 233
 DB 182 GLIVFHTSTEPSVNYDLFGAQGYSTNTLLRIYRDNKTINSENHIDLYLTS 233

RESULT 47
 ADF89824
 ID ADF89824 standard; protein; 231 AA.
 XX
 AC ADF89824;
 AC
 DT 26-FEB-2004 (first entry)
 XX
 DE Staphylococcal enterotoxin A (SEA) superantigen.
 DE
 KW Superantigen; SAg; Staphylococcal enterotoxin; SE; SEA; cytostatic;
 KW gene therapy; cancer.
 KW
 KW Staphylococcus sp.
 OS
 XX WO2003094846-A2.
 PN
 XX
 PD 20-NOV-2003.
 XX
 XX
 PF 08-MAY-2003; 2003WO-US014381.
 XX
 PR 08-MAY-2002; 2002US-0378988P.
 PR 15-JUN-2002; 2002US-0389366P.
 PR 28-AUG-2002; 2002US-0406697P.
 PR 29-AUG-2002; 2002US-0406750P.
 PR 01-OCT-2002; 2002US-0415310P.
 PR 02-OCT-2002; 2002US-0415400P.
 PR 09-JAN-2003; 2003US-0438686P.
 XX
 PA (TERM/) Terman D S.
 XX
 PI Terman DS;
 XX
 DR WPI; 2004-011997/01.
 XX
 PT Treating a subject with cancer or malignant diseases comprises
 PT intratumoral, intrathecal or intracavitary administration of an amount of
 PT a superantigen composition to the subject.
 XX
 XX Disclosure; SEQ ID NO 1; 91pp; English.
 PS
 XX
 CC The invention relates to treating a subject with cancer. The method
 CC involves administering an amount of a superantigen (SAG) composition
 CC comprising a molecule selected from: a native SAG protein; its
 CC biologically active fragment or a biologically active homologue or a
 CC biologically active fusion protein comprising the SAG or its fragment or
 CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
 CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
 CC exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritis SAg and
 CC Clostridium perfringens exotoxin. The method is useful in treating cancer
 CC or malignant diseases such as malignant pleural effusion, ascites,
 CC pericardial effusion or meningeal carcinomatosis. The present sequence

CC represents a Staphylococcal enterotoxin A (SEA) superantigen.
 XX
 SQ Sequence 231 AA;
 Query Match 80.0%; Score 991; DB 8; Length 231;
 Best Local Similarity 80.3%; Pred. No. 5.8e-91;
 Matches 187; Conservative 18; Mismatches 26; Indels 2; Gaps 1;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
 DB 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 58

QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
 DB 59 HSWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 118

QY 121 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 180
 DB 119 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 178

QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDILLRIYRDNKTINSENHIDLYLTT 233
 DB 179 RGLIVFHTSTEPSVNYDLFGAQGYSTNTLLRIYRDNKTINSENHIDLYLTS 231

RESULT 48
 ABU10098
 ID ABU10098 standard; protein; 233 AA.
 XX
 AC ABU10098;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Staphylococcus enterotoxin A Y64A substitution mutant.
 DE
 XX Enterotoxin A; superantigen-associated bacterial infection; mutant;
 KW superantigen toxin; vaccine; mutein.
 OS
 OS Staphylococcus sp.
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 64 /note= "Wild-type Tyr substituted by Ala"
 FT
 XX US2003009015-A1.
 XX
 PD 09-JAN-2003.
 XX
 XX 25-JUN-1997; 97US-00882431.
 XX
 XX 25-JUN-1997; 97US-00882431.
 XX
 PA (ULRI/) ULRICH R G.
 PA (OLSO/) OLSON M A.
 PA (BAVA/) BAVARI S.
 XX
 PI Ulrich RG, Olson MA, Bavari S;
 XX
 DR WPI; 2003-401542/38.
 XX
 XX New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.
 XX
 XX Example 7; Page; 50pp; English.
 PS
 CC The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating


```
FT /note= "Wild type Tyr substituted with Ala"
FT Misc-difference 157
FT /note= "Encoded by CTT"
FT Misc-difference 180
FT /note= "Encoded by CAG"
XX WO200009154-A1.
XX
XX 24-FEB-2000.
XX
XX 13-AUG-1998; 98WO-US016766.
XX
XX 13-AUG-1998; 98WO-US016766.
XX (REED-) REED ARMY INST RES WALTER.
XX
XX Ulrich RG, Olson MA, Bavari S;
XX
XX WPI; 2000-224177/19.
XX N-PSDB; AA251106.
XX
XX Nucleic acid encoding superantigen toxin useful as a vaccine and for
XX diagnosis of superantigen-associated bacterial infections.
XX
XX Claim 8; Page 74-76; 118pp; English.
XX
XX The present amino acid sequence is the mutant Staphylococcal enterotoxin
XX A (SEA), a bacterial superantigen toxin (SAG), used for the formulation
XX of SEA vaccine A489270P. The coding region of this SAG toxin is altered
XX by site directed mutagenesis, that results in disruption of binding of
XX the toxin to both the MHC class II or T-cell antigen receptor. This
XX altered SAG toxin has the leader peptide cleaved by native bacterial
XX enzymatic mechanism and the first residue of the mature protein is
XX encoded by the transcriptional start site (ATG). SEA has antibacterial
XX and cytostatic activity. This sequence is useful for the production of
XX SEA vaccines and specific antibodies. This vaccine overcomes the
XX disadvantages of the chemically inactivated toxins and is designed to
XX protect individuals against one or several related staphylococcal and
XX streptococcal toxins. It is used for the diagnosis and treatment or
XX amelioration of superantigen-associated bacterial infections
XX
XX Sequence 233 AA;
XX
XX Query Match 79.0%; Score 978; DB 3; Length 233;
XX Best Local Similarity 79.3%; Pred. No. 1.2e-89;
XX Matches 184; Conservative 17; Mismatches 31; Indels 0; Gaps 0;
XX
QY 2 EKSEINEKDLRKSELRNALNLRQIYYVNEKAITENKESDDQFLENTLLPKGFTGH 61
DB 2 EKSEINEKDLRKSEKQGTALGNLQIYYVNEKAKTENKESHQDQFQHTILPKGFTDH 61
QY 62 PWNDDLVLGSKDATNKYKGVVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTE 121
DB 62 SWNDLLVRPDSKDIVDKYKGVVDLYGAYGAGVQCAGGTENKTACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLGYNDSFGGKVQR 181
DB 122 EKKVPINLWDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLGYNDSFGGKVQR 181
QY 182 GLIVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNKTINSENHLIDLYLTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAQGVYSNTLLRIYRDNKTINSENHMDIYLYTS 233
XX
XX RESULT 51
XX ADF89835
XX ID ADF89835 standard; protein; 268 AA.
XX AC ADF89835;
XX
XX 26-FEB-2004 (first entry)
XX
XX Staphylococcal enterotoxin J (SEJ) superantigen.
```

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XX Superantigen; SAG; Staphylococcal enterotoxin; SE; SEJ; cytostatic;
XX gene therapy; cancer.
XX Staphylococcus sp.
XX WO2003094846-A2.
XX
XX 20-NOV-2003.
XX
XX 08-MAY-2003; 2003WO-US014381.
XX
XX 08-MAY-2002; 2002US-0378988P.
XX 15-JUN-2002; 2002US-0389366P.
XX 28-AUG-2002; 2002US-0406697P.
XX 29-AUG-2002; 2002US-0406750P.
XX 01-OCT-2002; 2002US-0415310P.
XX 02-OCT-2002; 2002US-0415400P.
XX 09-JAN-2003; 2003US-0438686P.
XX
XX (TERM/) TERMAN D S.
XX
XX Terman DS;
XX
XX WPI; 2004-011997/01.
XX
XX Treating a subject with cancer or malignant diseases comprises
XX intratumoral, intrathecal or intracavitary administration of an amount of
XX a superantigen composition to the subject.
XX
XX Disclosure; SEQ ID NO 12; 91pp; English.
XX
XX The invention relates to treating a subject with cancer. The method
XX involves administering an amount of a superantigen (SAG) composition
XX comprising a molecule selected from: a native SAG protein; its
XX biologically active fragment or a biologically active homologue or a
XX biologically active fusion protein comprising the SAG or its fragment or a
XX homologue fused to a fusion partner polypeptide or peptide. The SAG is
XX selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
XX exotoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritides SAG and
XX Clostridium perfringens exotoxin. The method is useful in treating cancer
XX or malignant diseases such as malignant pleural effusion, ascites,
XX pericardial effusion or meningeal carcinomatosis. The present sequence
XX represents a Staphylococcal enterotoxin J (SEJ) superantigen.
XX
XX Sequence 268 AA;
XX
XX Query Match 67.0%; Score 830; DB 8; Length 268;
XX Best Local Similarity 64.9%; Pred. No. 1.1e-74;
XX Matches 150; Conservative 38; Mismatches 43; Indels 0; Gaps 0;
XX
QY 3 KSEINEKDLRKSELRNALNLRQIYYVNEKAITENKESDDQFLENTLLPKGFTGHP 62
DB 27 KNETIKEKLNKSELSITLNLRIHYFNEKGISEKIMTEQFDLYTLFLKSFISHS 86
QY 63 WYNDLLVLGSKDATNKYKGVVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEE 122
DB 87 QYNDLLVQPSKETVKNKGVVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTYD 146
QY 123 KKVPINLWDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLGYNDSFGGKVQR 182
DB 147 KKVPINLWDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLGYNDSFGGKVQR 206
QY 183 LIVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNKTINSENHLIDLYLTT 233
DB 207 LIVFHTSKSEPLYSVDLFWVIGQYDPDKLLKIQDNKLIENHMDIYLYTS 257
XX
XX RESULT 52
XX ABU79071
XX ID ABU79071 standard; protein; 258 AA.
XX AC ABU79071;
```


PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
PT costimulatory molecule.

PS Disclosure; Fig 2; 16pp; English.

XX The present invention relates to a tumour cell capable of stimulating
CC antitumor immune reactivity in vitro or in vivo contains and expresses an
CC exogenous nucleic acid molecule encoding a superantigen or its active
CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
CC molecule that activates T cells in conjunction with an antigenic
CC stimulus. The invention may be used for cancer therapy by stimulating an
CC anticancer immune response in vivo or ex vivo

XX SQ Sequence 228 AA;

Query Match 53.1%; Score 657; DB 4; Length 228;
Best Local Similarity 55.6%; Pred. No. 2.3e-57;
Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0;

QY 7 INEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTHGHPWYND 66

Db 2 VKEKELHKSELSSTALNNMKHSYADKNPIIGENKSTGDFLENTLLYKKFFTDLINFED 61

QY 67 LLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTAQMGVTLHDNNRLTEKKVP 126

Db 62 LLINFNSKEMAHQHFKNVDVPIRYSINCYGGEIDRTACTYGGVTPHGNKLERKKIP 121

QY 127 INLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVGRLIVF 186

Db 122 INLWINGVQKEVSLDKVQTDKNVTVOELDAQARYLQKDLKLYNNDTLGGKIQRGKIEF 181

QY 187 HSSEGSTSVSYDLFDAQGYPTDLLRIYRDNKTINSENHLHIDLVIY 231

Db 182 DSSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTLSLHHLHIDLVIY 226

RESULT 58

ABBB76236

ID ABB76236 standard; protein; 228 AA.

AC ABB76236;

DT 09-AUG-2002 (first entry)

XX Staphylococcus aureus enterotoxin D.

DE Enterotoxin D; SED; superantigen; antigen; tumour; cancer; antitumour;
KW therapy.

OS Staphylococcus aureus.

XX US2002051765-A1.

XX 02-MAY-2002.

XX 19-DEC-2000; 2000US-00741503.

XX 03-OCT-1989; 89US-00416530.

XX 17-JAN-1990; 90US-00466577.

XX 01-JAN-1991; 91WO-US000342.

XX 02-MAR-1993; 92US-00891718.

XX 31-JAN-1994; 94US-00189424.

XX 19-JUN-1995; 95US-00491746.

XX (TERM/) Terman D S.

XX Terman DS;

XX WPI; 2002-415198/44.

XX Reagent for treating cancer without the need for e.g. radiotherapy,
PT comprises a specific V beta subset of T cells sensitized to a growing

PT tumor and stimulated with superantigens.

PS Disclosure; Fig 2; 17pp; English.

XX The present sequence is the protein sequence of enterotoxin D (SED) of
CC Staphylococcus aureus. Similarity is shown, in several stretches of
CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
CC present invention, synthetic polypeptides useful in tumour therapy and in
CC blocking or destroying autoreactive T and B lymphocyte populations are
CC characterised by substantial structural homology to staphylococcal
CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
CC exotoxins, with statistically significant sequence homology and
CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
CC analysis exceeding 6) to include alignment of cysteine residues and
CC similar hydropathy profiles. These superantigens are used to treat solid
CC tumours, including their metastases, without radiation, surgery or
CC standard chemotherapeutic agents. A claimed method of human cancer
CC treatment involves contacting haematopoietic cells from a patient with
CC one or more superantigens ex vivo to generate stimulated cells, selecting
CC a specific V beta subset of cells, and reintroducing these cells into the
CC patient to induce an in vivo therapeutic, tumouricidal reaction

XX SQ Sequence 228 AA;

Query Match 53.1%; Score 657; DB 5; Length 228;
Best Local Similarity 55.6%; Pred. No. 2.3e-57;
Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0;

QY 7 INEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTHGHPWYND 66

Db 2 VKEKELHKSELSSTALNNMKHSYADKNPIIGENKSTGDFLENTLLYKKFFTDLINFED 61

QY 67 LLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTAQMGVTLHDNNRLTEKKVP 126

Db 62 LLINFNSKEMAHQHFKNVDVPIRYSINCYGGEIDRTACTYGGVTPHGNKLERKKIP 121

QY 127 INLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVGRLIVF 186

Db 122 INLWINGVQKEVSLDKVQTDKNVTVOELDAQARYLQKDLKLYNNDTLGGKIQRGKIEF 181

QY 187 HSSEGSTSVSYDLFDAQGYPTDLLRIYRDNKTINSENHLHIDLVIY 231

Db 182 DSSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTLSLHHLHIDLVIY 226

RESULT 59

AAR13205

ID AAR13205 standard; protein; 228 AA.

XX AAR13205;

DT 15-OCT-1991 (first entry)

XX Staphylococcal enterotoxin D.

DE SED; cancer treatment; pyrogen; tumouricide.

OS Staphylococcus aureus.

XX WO9110680-A.

XX 25-JUL-1991.

XX 17-JAN-1990; 90US-00466577.

XX 17-JAN-1990; 90US-00466577.

XX (TERM/) Terman D S.

XX Terman DS;

XX WPI; 1991-237984/32.

XX
PT Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity as
PT Staphylococcal protein A without potential toxic reactions.
XX
PS Disclosure; Fig 1; 74pp; English.
XX
CC SED was isolated and purified from S.aureus. It can be used for treating
CC cancer, activating cytokine mediators and procoagulant systems,
CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
CC administered intravenously, optionally with ibuprofen to attenuate toxic
CC reaction to SED. Synthetic polypeptides having structural homology to
CC Staphylococcal exotoxins are claimed, provided the homology includes
CC statistically significant sequence homology, alignment of Cysteine
CC residues and similar hydropathy profiles. See AAR13203-R13211
XX
SQ Sequence 228 AA;
Query Match 52.4%; Score 649; DB 2; Length 228;
Best Local Similarity 55.1%; Pred. No. 1.5e-56;
Matches 124; Conservative 33; Mismatches 68; Indels 0; Gaps 0;
QY 7 INEKDLRKSEQLRNALSLNRQIYYNYNEKAITENKESDDQFLENTLLFKGFTGHPWYND 66
DB 2 VKEKELHKKSELSTALNNMKHSYADKNPIIGENKSTGDFLENTLLYKKFTDLINPED 61
QY 67 LLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTEKKVP 126
DB 62 LLINFSKEMACHFKSKNDVPIRYSINCYGGEIDRTACTYGGVTPHEGNLKERKKIP 121
QY 127 INLWIDGKOTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQGLIVF 186
DB 122 IMLWINGQKVELSKVDKQTKGNVTVOELDAQARRYLQKDLKLYNNDTLGGKIQRKIEF 181
QY 187 HSSEGSTVYDLFDAQGYPDTLRLIYRDNKTINSENHLIDLYLY 231
DB 182 DSSDGSKVSVDLFDVKGDFPEKQLRIYSDNKTLSLSTLHLDIYLY 226
RESULT 60
ABP58459
ID ABP58459 standard; protein; 203 AA.
XX
AC ABP58459;
XX
DT 14-APR-2003 (first entry)
XX
DE Staphylococcal enterotoxin D.
XX
KW Superantigen; staphylococcal enterotoxin D; antibody; cancer; tumour;
KW cytostatic; vaccine.
XX
OS Staphylococcus sp.
XX
PN WO2003002143-A1.
XX
PD 09-JAN-2003.
XX
PF 19-JUN-2002; 2002WO-SE001188.
XX
PR 28-JUN-2001; 2001SE-00002327.
XX
PA (ACTI-) ACTIVE BIOTECH AB.
XX
PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
XX
DR WPI; 2003-201467/19.
XX
PT Conjugate for therapy, has bacterial superantigen with a region in T-cell
PT receptor and four regions to determine binding to class II major
PT histocompatibility complex, antibody to cancer associated cell surface
PT structure.
XX

PS
XX
CC The present sequence is the protein sequence of staphylococcal
CC enterotoxin D (SED). The invention provides novel conjugates (see
CC ABP58454) for human cancer therapy. These comprise an engineered
CC bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an
CC antibody moiety, such as tumour reactive antibody ST4. Bacterial
CC enterotoxins such as SEA, SEE, SED and SEH were used in the molecular
CC modelling of the engineered superantigens. The superantigens were
CC engineered to reduce seroreactivity whilst maintaining biological
CC activity and production levels. The novel conjugates were designed to
CC target and destroy cancer cells, including cancer of the lung, breast,
CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX
SQ Sequence 203 AA;
Query Match 42.2%; Score 523; DB 6; Length 203;
Best Local Similarity 49.5%; Pred. No. 6e-44;
Matches 109; Conservative 25; Mismatches 66; Indels 20; Gaps 3;
QY 12 LRKKSLEQARNALSLNRQIYYNYNEKAITENKESDDQFLENTLLFKGFTGHPWYNDLLVDL 71
DB 2 LHKSELSTALNNMKHSYADANPIIGANKSTGDFLENTLLYKAFP-----LLINF 53
QY 72 GSKDATNKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTEKKVPINLWI 131
DB 54 NSAEWAQHFPSKNDVYAIRYAAAC-----RTACTYGGVTPHAGNALKARKKIPINLWI 107
QY 132 DGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQGLIVFHSSEG 191
DB 108 IGQKSEVSLDKVQTDKGNVTVOELDAQARRYLQKDLKLYNA-----IQRGKLEFDSAAA 161
QY 192 STVSVDLFDPAQGYPDTLRLIYRDNKTINSENHLIDLYLY 231
DB 162 SKVSVDLFDVAGDFPEKQLRIYSDNKTLSLSTLHLDIYLY 201
RESULT 61
ABM70958
ID ABM70958 standard; protein; 250 AA.
XX
AC ABM70958;
XX
DT 20-NOV-2003 (first entry)
XX
DE Staphylococcus aureus protein #198.
XX
KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KW enzymatic assay; antibiotic target.
XX
OS Staphylococcus aureus.
XX
PN WO200294868-A2.
XX
PD 28-NOV-2002.
XX
PF 27-MAR-2002; 2002WO-IB002637.
XX
PR 27-MAR-2001; 2001GB-00007661.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Masignani V, Mora M, Scarselli M;
XX
DR WPI; 2003-120786/11.
DR N-PSDB; ACF72518.
XX
PT New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
XX S. aureus, e.g. sepsis.
XX
PT Claim 1; SEQ ID NO 396; 49pp; English.
XX

CC The invention relates to novel genes and encoded proteins from
 CC *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to *Staphylococcus aureus*, specifically an
 CC infection caused by *S. aureus*. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel *S. aureus* proteins of the invention
 XX
 XX
 SQ Sequence 250 AA;

Query Match 39.8%; Score 492.5; DB 6; Length 250;
 Best Local Similarity 39.8%; Pred. No. 9.5e-41;
 Matches 92; Conservative 48; Mismatches 86; Indels 5; Gaps 3;
 QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 23 TNSASAIYSYDLHKSFKDSKRLSNK-MSFINPTQL-ENKNTNDRLLKHDLLFHDNFVN 80
 QY 61 HPWYNDLLVGLSKDATNKYKGVLDLYGAYGYQCAGGTFNKTACMYGGVTLHDNNRLT 120
 DB 81 DWKKDFKEFENEALSKRFINKDIDIFAGNYGYGCHGATNKTQSYGGVTLSDNNKYD 140
 QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGGRVQ 180
 DB 141 DYKNIPCNLWIDGQTEIELTAVTKKKIVTIQELVQLRNLNLYKVLVEQ---GGDIV 197
 QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDKNKTINSENHLIDLYL 231
 DB 198 KGYVKNYNDQNVYDFYNLNGEYGREVLKMYADNKTINSKGLHLDLYL 248

RESULT 62
 ABU10091
 ID ABU10091 standard; protein; 82 AA.
 AC ABU10091;
 DT 11-AUG-2003 (first entry)
 XX Bacterial superantigen toxin SEE.
 DE Superantigen-associated bacterial infection; superantigen toxin; vaccine;
 KW SEE.
 XX
 OS Unidentified.
 XX
 PN US2003009015-A1.
 XX
 PD 09-JAN-2003.
 XX
 PF 25-JUN-1997; 97US-00882431.
 XX
 PR 25-JUN-1997; 97US-00882431.
 XX
 PA (ULRI/) ULRICH R G.
 PA (OLSO/) OLSON M A.
 PA (BAVA/) BAVARI S.
 XX
 PI Ulrich RG, Olson MA, Bavari S;
 XX
 DR WPI; 2003-401542/38.
 XX
 CC New superantigen toxin and/or DNA fragment with an altered binding of the
 CC encoded altered toxin to either MHC class II or T cell antigen receptor,
 CC useful for treating or ameliorating superantigen-associated bacterial
 CC infection.
 XX
 PS Example 1; Page 36; 50pp; English.
 XX
 CC The invention relates to an isolated and purified superantigen toxin

CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of the bacterial superantigen
 CC toxin SEE
 XX
 SQ Sequence 82 AA;
 Query Match 36.9%; Score 457; DB 6; Length 82;
 Best Local Similarity 100.0%; Pred. No. 7.2e-38;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 43 SDQFLENTLLFKGPTGHPWYNDLLVGLSKDATNKYKGVLDLYGAYGYQCAGGTPN 102
 DB 1 SDQFLENTLLFKGPTGHPWYNDLLVGLSKDATNKYKGVLDLYGAYGYQCAGGTPN 60
 QY 103 KTACMYGGVTLHDNNRLTEKK 124
 DB 61 KTACMYGGVTLHDNNRLTEKK 82
 RESULT 63
 ABU62338
 ID ABU62338 standard; protein; 82 AA.
 AC ABU62338;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE *S. aureus* enterotoxin E, SEE, MHC binding region.
 XX
 KW SEE; *Staphylococcus enterotoxin E*; vaccine; superantigen toxin; MHC;
 KW superantigen-associated bacterial infection; bacterial infection;
 KW antibacterial.
 XX
 OS *Staphylococcus aureus*.
 XX
 PN US2003036644-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 26-NOV-2001; 2001US-00002784.
 XX
 PR 25-JUN-1997; 97US-00882431.
 PR 01-SEP-1998; 98US-00144776.
 XX
 PA (ULRI/) ULRICH R G.
 XX
 PI Ulrich RG;
 XX
 DR WPI; 2003-492125/46.
 XX
 PT New superantigen toxin DNA fragment, useful for preparing a composition
 PT for treating or preventing bacterial infection.
 XX
 PS Disclosure; Fig 3; 68pp; English.
 XX
 CC The invention relates to an isolated and purified superantigen toxin DNA
 CC fragment is altered so that binding of the encoded altered toxin to
 CC either the MHC class II or T cell antigen receptor is altered. Also
 CC included are a recombinant DNA construct (comprising a vector and an
 CC isolated and purified altered superantigen toxin DNA fragment), a host
 CC cell transformed with the recombinant DNA construct, producing altered
 CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
 CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
 CC infection, a vaccine (comprising an altered superantigen toxin for
 CC producing antigenic and immunogenic response resulting in the protection

CC of a mammal against superantigen-associated bacterial infection),
 CC treating/ameliorating a superantigen-associated bacterial infection, an
 CC antiserum isolated from individuals immunised with one or more altered
 CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
 CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
 CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
 CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
 CC composition for treating or preventing bacterial infection. The present
 CC sequence represents the *S. aureus* enterotoxin E, SEE, MHC binding region
 XX
 XX Sequence 82 AA;

Query Match 36.9%; Score 457; DB 7; Length 82;
 Best Local Similarity 100.0%; Pred. No. 7.2e-38;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 43 SDDQFLENTLLPKGFTHPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPN 102
 DB 1 SDDQFLENTLLPKGFTHPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPN 60
 QY 103 KTACMYGGVTLHDNNRLTEKK 124
 DB 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 64
 ADY93188
 ID ADY93188 standard; protein; 82 AA.
 XX
 AC ADY93188;
 DT 02-JUN-2005 (first entry)
 XX
 XX Staphylococcal enterotoxin E (SEE) protein, SEQ ID NO: 19.
 XX Vaccine; toxin; diagnosis; bacterial infection; antibacterial; infection;
 KW enterotoxin.
 XX Staphylococcus aureus.
 OS
 XX US2005064526-A1.
 PN 24-MAR-2005.
 XX
 XX 29-JAN-2004; 2004US-00767687.
 PF
 XX 25-JUN-1997; 97US-00882431.
 PR
 XX (ULRI/) ULRICH R G.
 PA (OLSO/) OLSON M A.
 PA (BAVA/) BAVARI S.
 XX
 PI Ulrich RG, Olson MA, Bavari S;
 XX WPI; 2005-252679/26.
 DR
 XX Novel altered superantigen toxin that alters binding of encoded altered
 PT toxin to major histocompatibility complex class II or T cell antigen
 PT receptor, useful for preparing vaccine for treating superantigen-
 PT associated bacterial infection.
 XX
 XX Disclosure; SEQ ID NO 19; 51pp; English.
 PS
 XX The present invention relates to a altered superantigen toxin that alters
 CC binding of encoded altered toxin to major histocompatibility complex
 CC class II or T cell antigen receptor. The invention is useful for
 CC preparing vaccine for treating superantigen-associated bacterial
 CC infection. The present sequence is the Staphylococcal enterotoxin E (SEE)
 CC protein.
 XX
 XX Sequence 82 AA;
 QY
 DB 36.9%; Score 457; DB 9; Length 82;
 Query Match

Best Local Similarity 100.0%; Pred. No. 7.2e-38;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 43 SDDQFLENTLLPKGFTHPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPN 102
 DB 1 SDDQFLENTLLPKGFTHPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPN 60
 QY 103 KTACMYGGVTLHDNNRLTEKK 124
 DB 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 65
 ABU10089
 ID ABU10089 standard; protein; 82 AA.
 XX
 AC ABU10089;
 DT 11-AUG-2003 (first entry)
 XX
 DE Bacterial superantigen toxin SEA.
 XX
 KW Superantigen-associated bacterial infection; superantigen toxin; vaccine;
 KW SEA.
 XX Unidentified.
 OS
 XX US2003009015-A1.
 PN
 XX 09-JAN-2003.
 PD
 XX 25-JUN-1997; 97US-00882431.
 PF
 XX 25-JUN-1997; 97US-00882431.
 PR
 XX (ULRI/) ULRICH R G.
 PA (OLSO/) OLSON M A.
 PA (BAVA/) BAVARI S.
 XX
 PI Ulrich RG, Olson MA, Bavari S;
 XX WPI; 2003-401542/38.
 DR
 XX New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.

Example 1; Page 35; 50pp; English.
 XX
 PS The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of the bacterial superantigen
 CC toxin SEA
 XX
 XX Sequence 82 AA;

Query Match 32.2%; Score 399; DB 6; Length 82;
 Best Local Similarity 86.6%; Pred. No. 5e-32;
 Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 43 SDDQFLENTLLPKGFTHPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPN 102
 DB 1 SHDQFLQHTILPKGFTHSWYNDLLVDFDSKDIDVKYKGVLDLYGAYGYQCAGGTPN 60


```

QY 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 66
ABU62336
ID ABU62336 standard; protein; 82 AA.
XX
AC ABU62336;
XX
DT 27-AUG-2003 (first entry)
XX
DE S. aureus enterotoxin A, SEA, MHC binding region.
XX
KW SEA; staphylococcal enterotoxin A; vaccine; superantigen toxin; MHC;
KW superantigen-associated bacterial infection; bacterial infection;
KW antibacterial.
XX
OS Staphylococcus aureus.
XX
PN US2003036644-A1.
XX
PD 20-FEB-2003.
XX
PF 26-NOV-2001; 2001US-00002784.
XX
PR 25-JUN-1997; 97US-00882431.
PR 01-SEP-1998; 98US-0014776.
XX
PA (ULRI/) ULRICH R G.
XX
PI Ulrich RG;
XX
DR WPI; 2003-492125/46.
XX
PT New superantigen toxin DNA fragment, useful for preparing a composition
PT for treating or preventing bacterial infection.
XX
PS Disclosure; Fig 3; 68pp; English.
XX
CC The invention relates to an isolated and purified superantigen toxin DNA
CC fragment is altered so that binding of the encoded altered toxin to
CC either the MHC class II or T cell antigen receptor is altered. Also
CC included are a recombinant DNA construct comprising a vector and an
CC isolated and purified altered superantigen toxin DNA fragment), a host
CC cell transformed with the recombinant DNA construct, producing altered
CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
CC infection, a vaccine (comprising an altered superantigen toxin for
CC producing antigenic and immunogenic response resulting in the protection
CC of a mammal against superantigen-associated bacterial infection),
CC treating/ameliorating a superantigen-associated bacterial infection, an
CC antiserum isolated from individuals immunised with one or more altered
CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
CC composition for treating or preventing bacterial infection. The present
CC sequence represents the S. aureus enterotoxin A, SEA, MHC binding region
XX
SQ Sequence 82 AA;

Query Match 32.2%; Score 399; DB 7; Length 82;
Best Local Similarity 86.6%; Pred. No. 5e-32;
Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 43 SDQFLENTLLFKGFFTHPWYNDLLVLSKSDATNKYKGGKVDLYGAYGYQCAGTGN 102
Db 1 SHDQFLQHTILFKGFFTHSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGTGN 60

QY 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 67
ADY93186
ID ADY93186 standard; protein; 82 AA.
XX
AC ADY93186;
XX
DT 02-JUN-2005 (first entry)
XX
DE Staphylococcal enterotoxin A (SEA) protein, SEQ ID NO: 17.
XX
KW Vaccine; toxin; diagnosis; bacterial infection; antibacterial; infection;
KW enterotoxin.
XX
OS Staphylococcus aureus.
XX
PN US2005064526-A1.
XX
PD 24-MAR-2005.
XX
PF 29-JAN-2004; 2004US-00767687.
XX
PR 25-JUN-1997; 97US-00882431.
XX
PA (ULRI/) ULRICH R G.
PA (OLSO/) OLSON M A.
PA (BAVA/) BAVARI S.
XX
PI Ulrich RG, Olson MA, Bavari S;
XX
DR WPI; 2005-252679/26.
XX
PT Novel altered superantigen toxin that alters binding of encoded altered
PT toxin to major histocompatibility complex class II or T cell antigen
PT receptor, useful for preparing vaccine for treating superantigen-
PT associated bacterial infection.
XX
PS Disclosure; SEQ ID NO 17; 51pp; English.
XX
CC The present invention relates to a altered superantigen toxin that alters
CC binding of encoded altered toxin to major histocompatibility complex
CC class II or T cell antigen receptor. The invention is useful for
CC preparing vaccine for treating superantigen-associated bacterial
CC infection. The present sequence is the Staphylococcal enterotoxin A (SEA)
CC protein.
XX
SQ Sequence 82 AA;

Query Match 32.2%; Score 399; DB 9; Length 82;
Best Local Similarity 86.6%; Pred. No. 5e-32;
Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 43 SDQFLENTLLFKGFFTHPWYNDLLVLSKSDATNKYKGGKVDLYGAYGYQCAGTGN 102
Db 1 SHDQFLQHTILFKGFFTHSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGTGN 60

QY 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 68
AAW24299
ID AAW24299 standard; protein; 91 AA.
XX
AC AAW24299;
XX
DT 14-APR-1998 (first entry)
XX
DE Staphylococcus aureus Gene #5 polypeptide sequence 2.
XX

```


Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.

Streptococcus pyogenes.

WO200234771-A2.

02-MAY-2002.

29-OCT-2001; 2001WO-GB004789.

27-OCT-2000; 2000GB-00026333.

24-NOV-2000; 2000GB-00028727.

07-MAR-2001; 2001GB-00005640.

(CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.

Telford J, Maignani V, Margarit Y Rosi, Grandi G, Fraser C; Tettelin H;

WPI; 2002-352536/38.
N-PSDB; ABN69988.

New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.

Claim 1; Page 3920; 4525pp; English.

The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins

Sequence 259 AA;

Query Match 27.2%; Score 336.5; DB 5; Length 259;
Best Local Similarity 33.6%; Pred. No. 5e-25;
Matches 77; Conservative 44; Mismatches 85; Indels 23; Gaps 6;

QY 17 ELQRALSNLRIRIYYNEKAITENKESDDQFLENTLLFKGFTGHPWN---DLLVDLGS 73
DB 34 EMSSGVNLRNLSTYDPTVEVKGKINEGPPFSGSLFYKNI---PYGNSSIELKVELNS 89
QY 74 KDATNKYGGKVDLYGAYGYQCAGGTNPKTACMYGGVTLHDNNRLTEKKVPINLWIDG 133
DB 90 VEKANFFSGKRVDFITLVEYSPPCNSNIKNNS---YGGITLSDGNRI-DKKNIPNIFIDG 145
QY 134 ---KQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLY-----NSDSFGGKQVOR 181
DB 146 VQOKYSYTDISTGSDTKKEVTIQELDKVRSRYLLQKHFNIGYGDVKDFGRSSRFQSGFEE 205
QY 182 GLIVFHSSEGSTVSYDLPDAQOYPTLLRIYRDNKNTINSENHLIDL 230
DB 206 GNIIFHLSGERISYNLFDTGHDRESMLKKYSNDKNTAYSQQLHIDIYL 254

RESULT 74

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:13:35 ; Search time 13.3878 Seconds
(without alignments)
1674.542 Million cell updates/sec

Title: US-09-900-766-7

Perfect score: 1238

Sequence: 1 SEKSEBNEKDLKKSELQR.....RDNKTINSENHIDLYLTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	257	2 A28179	enterotoxin E prec
2	1023	82.6	257	2 A28664	enterotoxin A prec
3	994	80.3	260	2 C89884	enterotoxin P imp
4	663	53.6	258	2 A33953	enterotoxin D prec
5	461.5	37.3	258	2 H89968	enterotoxin SeN [i
6	387.5	31.3	260	2 H89969	enterotoxin SeO [i
7	339.5	27.4	242	2 C89969	extracellular ente
8	337	27.2	240	2 G89951	extracellular ente
9	320	25.8	239	2 D89969	enterotoxin SEM [i
10	300.5	24.3	266	1 ENSAB6	enterotoxin B prec
11	295.5	23.9	251	1 S29659	enterotoxin type A pr
12	285.5	23.1	266	2 S11885	enterotoxin C3 - S
13	281.5	22.7	266	2 A60114	enterotoxin C-2 pr
14	279.5	22.6	236	2 S18789	exotoxin A precurs
15	277.5	22.4	236	2 S18783	exotoxin type A pr
16	272.5	22.0	236	2 S18786	exotoxin type A pr
17	266.5	21.5	266	1 ENSAC1	enterotoxin C-1 pr
18	255.5	20.6	258	2 G89968	extracellular ente
19	245	19.8	250	1 A26152	streptococcal pyro
20	201	16.2	157	2 A89942	hypothetical prote
21	197	15.9	136	2 A89969	enterotoxin YENT2
22	183.5	14.8	235	2 A30509	exotoxin C precurs
23	144	11.6	62	2 H89941	hypothetical prote
24	123	9.9	133	2 H89969	enterotoxin Yent1
25	113	9.1	232	2 F89807	exotoxin 13 [impor
26	107.5	8.7	234	1 XCSA51	toxic shock syndro
27	105.5	8.5	234	2 H89992	toxic shock syndro
28	101	8.2	232	2 H89807	exotoxin 12 [impor
29	99.5	8.0	231	2 D89807	exotoxin 11 [impor

exotoxin 14 [impor
cell shape determi
transferrin-binding
hypothetical prote
exotoxin 6 [impor
multidrug resistan
trse-like protein
B. subtilis YjK p
flagellar hook pro
flagellar hook pro
hypothetical prote
phospholipase A2-1
DNA-directed DNA p
hypothetical prote
hypothetical prote
MG032 homolog B01
beta-fructofuranos
arginyl tRNA synth
protein with DnaJ
conserved hypothe
cell wall-associat
probable periplasm
major blood-stage
DNA endonuclease a
glycosidase homolo
hypothetical prote
arginyl tRNA synth
hypothetical prote
diphosphate-fructo
lactocepin [EC 3.4
MG288 homolog P02
ABC transporter, A
erythrocyte membra
exotoxin 15 [impor
transposase of IS1
glycerol kinase -
chitinase chi-A or
penicillin-binding
penicillin-binding
penicillin-binding
major surface glyc
hypothetical prote
ABC protein - human
outer membrane ush
ABC transporter, A
transposase of IS1
hypothetical prote
hypothetical prote
probable transcrip
hypothetical prote
transferrin-binding
hypothetical prote
hypothetical prote
uncharacterized pr
exotoxin 9 [impor
rare lipoprotein A
p-aminobenzoate sy
hypothetical secre
membrane conserved
putative autotransp
probable ferric si
hypothetical prote
hypothetical prote
upiquitin-like pro
hypothetical prote
DNA-directed RNA p
tetracycline synthet
exotoxin 8 [impor
replication protei
hypothetical prote
protein F53H1.4 [i
hypothetical prote
hypothetical prote

103	81.5	6.6	1893	2	G82875	hypothetical prote	176	77.5	6.3	361	2	E86692	N-acetylmutamoyl-L
104	81.5	6.6	2870	2	H96974	cyclic beta 1-2 gl	177	77.5	6.3	372	2	C53312	HD-GYP hydrolase d
105	81	6.5	299	2	AF1193	hypothetical prote	178	77.5	6.3	419	1	G93312	thymidine phosphor
106	81	6.5	333	2	A99582	hypothetical prote	179	77.5	6.3	429	2	A25145	keratin, 47k type
107	81	6.5	402	2	F72340	probable carboxyl-	180	77.5	6.3	467	2	G98849	endo-1,4-beta-xyla
108	81	6.5	528	2	S23207	DNA-directed RNA p	181	77.5	6.3	522	2	D69913	GTPase, sulfate ad
109	81	6.5	562	2	S01312	alpha-amylase (EC	182	77.5	6.3	547	2	S49815	transferrin-bindin
110	81	6.5	580	2	S49308	beta-fructofuranos	183	77.5	6.3	554	2	S41526	hemolysin accessor
111	81	6.5	616	2	A36094	diphosphate-fructo	184	77.5	6.3	581	2	T51580	ovule development
112	81	6.5	626	2	B98115	hypothetical prote	185	77.5	6.3	590	2	H70130	oligodendropeptidase
113	81	6.5	1021	2	I40805	collagenase - Clos	186	77.5	6.3	609	2	T32302	hypothetical prote
114	81	6.5	1217	2	T21403	hypothetical prote	187	77.5	6.3	707	2	S78538	site-specific reco
115	81	6.5	1561	1	S06839	surface antigen ap	188	77.5	6.3	709	2	A41976	structure-specific
116	81	6.5	1997	2	F71607	DNA helicase II BR	189	77.5	6.3	817	2	F86742	ribonuclease limpo
117	81	6.5	2144	2	A97942	metalloproteinase	190	77.5	6.3	1269	2	A90267	proteinase related
118	81	6.5	2485	1	H71621	serine/threonine-s	191	77.5	6.3	1325	1	S73723	probable lipoprote
119	80.5	6.5	261	2	A84077	transposase (06) B	192	77.5	6.3	3206	1	GNVSPV	genome polyprotein
120	80.5	6.5	344	2	C81920	hypothetical prote	193	77	6.2	421	2	A11112	hypothetical prote
121	80.5	6.5	413	2	S59650	hypothetical prote	194	77	6.2	425	2	T43772	hypothetical prote
122	80.5	6.5	933	2	A97334	type II restrictio	195	77	6.2	500	2	B43577	perfringolysin O p
123	80.5	6.5	1151	2	A45226	integrin alpha-1 c	196	77	6.2	620	2	E90575	lipoprotein [impor
124	80.5	6.5	1427	2	S22695	restin - human	197	77	6.2	646	2	H95155	prolyl oligopeptid
125	80.5	6.5	1520	2	T23620	hypothetical prote	198	77	6.2	797	2	D71621	hypothetical prote
126	80.5	6.5	1959	2	AG1085	porin - common ice	199	77	6.2	876	2	A89944	alanyl-tRNA synthe
127	80	6.5	276	2	T12558	hypothetical prote	200	77	6.2	893	2	S64926	probable membrane
128	80	6.5	1008	2	T18508	hypothetical prote	201	77	6.2	1118	2	H97298	subtilisin like pr
129	80	6.5	1231	2	S70553	chromosome-associa	202	77	6.2	1422	2	T18404	chromatin remodell
130	80	6.5	1388	2	T38720	chromodomain helic	203	77	6.2	1449	2	T30857	glucosyltransferas
131	80	6.5	1902	2	S06997	lactocepin (EC 3.4	204	77	6.2	1484	2	T42632	breast cancer tumo
132	79.5	6.4	156	2	AG0817	bacterioferritin c	205	77	6.2	1707	2	T18951	hypothetical prote
133	79.5	6.4	243	2	H71082	hypothetical prote	206	76.5	6.2	246	2	I40763	hypothetical prote
134	79.5	6.4	344	2	E81183	copper ABC transpo	207	76.5	6.2	272	2	C86642	transposase of IS1
135	79.5	6.4	358	2	G84550	hypothetical prote	208	76.5	6.2	331	2	D84413	cysteine proteinas
136	79.5	6.4	532	2	C97228	probable peptide A	209	76.5	6.2	350	2	T76651	hypothetical prote
137	79.5	6.4	556	2	C72204	alpha-amylase - Th	210	76.5	6.2	423	2	T15309	hypothetical prote
138	79.5	6.4	637	2	S36523	E1 protein - human	211	76.5	6.2	443	2	S23771	outer membrane por
139	79.5	6.4	677	2	B82870	DNA topoisomerase	212	76.5	6.2	455	2	S39663	aminopeptidase hom
140	79.5	6.4	1211	2	D64702	DNA polymerase III	213	76.5	6.2	480	2	T34294	hypothetical prote
141	79.5	6.4	1392	2	A43336	microtubule-vesicl	214	76.5	6.2	601	2	S74239	secretogranin II p
142	79.5	6.4	2269	2	T18472	hypothetical prote	215	76.5	6.2	669	2	S78050	high mobility grou
143	79.5	6.4	2894	2	G64474	hypothetical prote	216	76.5	6.2	729	2	QJ1898	probable RNA-direc
144	79	6.4	348	2	F96997	uncharacterized co	217	76.5	6.2	776	2	AH1506	preprotein translo
145	79	6.4	368	2	A82148	probable porin VCI	218	76.5	6.2	801	2	H90574	lipoprotein [impor
146	79	6.4	378	2	F64446	chromatase synthas	219	76.5	6.2	873	2	F71092	ATP-dependent RNA
147	79	6.4	419	2	H81667	transcription term	220	76.5	6.2	963	2	B83502	ribonucleoside red
148	79	6.4	426	2	B97126	cystathionine beta	221	76.5	6.2	1002	2	T09438	toxR-activated lip
149	79	6.4	628	2	AF2393	hypothetical prote	222	76.5	6.2	1013	2	B82276	toxR-activated gen
150	79	6.4	660	2	S70904	transferrin-bindin	223	76.5	6.2	1018	2	A32192	fibronectin-bindin
151	79	6.4	745	2	D82568	conserved hypotet	224	76.5	6.2	1047	2	S19508	endo-1,4-beta-xyla
152	79	6.4	788	2	A71076	hypothetical prote	225	76.5	6.2	1086	2	T17628	hypothetical prote
153	79	6.4	1104	2	A60999	alpha-amylase (EC	226	76.5	6.2	1113	2	T19835	DNA-directed DNA p
154	79	6.4	1131	2	T19442	hypothetical prote	227	76.5	6.2	1312	2	S68593	hypothetical prote
155	79	6.4	1902	2	B45764	lactocepin (EC 3.4	228	76.5	6.2	1379	2	C89921	hypothetical prote
156	79	6.4	2183	2	T42764	coagulation factor	229	76.5	6.2	3890	2	C89921	26.4k hypotethical
157	79	6.4	4981	2	T18489	hypothetical prote	230	76	6.1	225	2	D86370	formyltetrahydrofo
158	78.5	6.3	359	2	B82348	probable lipopolys	231	76	6.1	274	2	F81350	conserved hypotet
159	78.5	6.3	318	2	T38519	conserved hypotet	232	76	6.1	370	2	A83782	glucuronyl hydrola
160	78.5	6.3	627	2	G97975	hypothetical prote	233	76	6.1	396	2	A95038	unsaturated glucur
161	78.5	6.3	722	2	E71403	hypothetical prote	234	76	6.1	409	2	D97908	processing protein
162	78.5	6.3	781	2	T36143	probable secreted	235	76	6.1	432	2	A64602	processing protein
163	78.5	6.3	836	2	AB0540	outer-membrane fim	236	76	6.1	511	2	T11940	ribosomal protein
164	78.5	6.3	998	2	I41078	hemolysin - Escher	237	76	6.1	527	2	C70130	glycerol-3-phospha
165	78	6.3	416	2	A11760	B. subtilis xylB p	238	76	6.1	530	2	G64480	hypothetical prote
166	78	6.3	476	2	G90512	p60-like (mycoplas	239	76	6.1	630	1	W1WL35	E1 protein - human
167	78	6.3	626	2	E95250	glycosyl hydrolase	240	76	6.1	636	2	F90094	hypothetical prote
168	78	6.3	669	2	T05212	hypothetical prote	241	76	6.1	650	2	T40830	nitrogen permease
169	78	6.3	681	2	F69295	acetyl-CoA synthet	242	76	6.1	680	2	D90575	lipoprotein [impor
170	78	6.3	692	2	B64381	hypothetical prote	243	76	6.1	747	1	A27366	AMP deaminase (EC
171	78	6.3	933	2	AE1905	outer membrane sec	244	76	6.1	762	2	A34355	cell surface prote
172	78	6.3	1091	2	AF1380	glycosidase homolo	245	76	6.1	827	2	A90544	hypothetical prote
173	78	6.3	2013	2	C71610	probable membrane	246	76	6.1	834	2	B82940	conserved hypotet
174	77.5	6.3	241	2	B89888	hypothetical prote	247	76	6.1	847	2	T19544	hypothetical prote
175	77.5	6.3	252	2	E95884	hypothetical prote	248	76	6.1				

249	76	6.1	882	2	H70199	translation initia
250	76	6.1	960	2	AF1940	isoleucyl-tRNA syn
251	76	6.1	1069	1	KUHU	ferroxidase (EC 1.
252	76	6.1	1132	2	H82887	hypothetical prote
253	76	6.1	1377	2	D90538	hypothetical prote
254	76	6.1	1449	2	T30552	glucosyltransferas
255	76	6.1	1856	2	C95008	immunoglobulin A1
256	76	6.1	1876	2	E97944	zinc metalloprotei
257	76	6.1	1948	2	S00485	gene 11-1 protein
258	76	6.1	2233	2	B95075	beta-galactosidase
259	75.5	6.1	156	2	B85891	bacterioferritin c
260	75.5	6.1	156	2	F91046	bacterioferritin c
261	75.5	6.1	156	2	B49749	thioedoxin-depend
262	75.5	6.1	244	2	H89942	conserved hypothet
263	75.5	6.1	246	2	E81373	hypothetical prote
264	75.5	6.1	266	2	C90520	lipoprotein [impor
265	75.5	6.1	359	2	G82197	RstA1/RstA2 protei
266	75.5	6.1	419	2	S06784	hypothetical prote
267	75.5	6.1	420	2	A28882	alpha-1-antitrypsi
268	75.5	6.1	555	2	S71365	ovule development
269	75.5	6.1	592	2	S56681	beta-fructofuranos
270	75.5	6.1	627	2	E95107	choline binding pr
271	75.5	6.1	655	2	S57119	hypothetical prote
272	75.5	6.1	808	2	A82877	hypothetical prote
273	75.5	6.1	816	2	C88196	protein ZK1127.7 l
274	75.5	6.1	1121	2	S30862	DNA dependent ATPa
275	75.5	6.1	1123	2	T28139	PK4 protein kinase
276	75.5	6.1	1157	2	F97255	fusion of alpha-gl
277	75.5	6.1	2712	2	T05113	hypothetical prote
278	75.5	6.1	3066	2	T28625	variant-specific s
279	75.5	6.1	3649	1	S18268	delta-(u-alpha)-am
280	75	6.1	194	2	AE1195	B. subtilis YjbK p
281	75	6.1	253	2	C97026	thioesterase II of
282	75	6.1	254	2	B64011	hypothetical prote
283	75	6.1	299	2	AB0440	hypothetical prote
284	75	6.1	313	2	C71428	hypothetical prote
285	75	6.1	345	2	E82469	hypothetical prote
286	75	6.1	351	2	D96958	HD-GYP domain [imp
287	75	6.1	364	2	AB1918	hypothetical prote
288	75	6.1	375	2	S73530	MG438 homolog E30
289	75	6.1	438	2	S42581	neutral metallopro
290	75	6.1	462	1	WTHUB	semenogelin I prec
291	75	6.1	502	2	T13620	hypothetical prote
292	75	6.1	512	1	WMCVFM	inclusion body mat
293	75	6.1	717	2	S50852	cleavage stimulati
294	75	6.1	730	2	A96988	FUSION ribonucleas
295	75	6.1	849	2	G64342	hypothetical prote
296	75	6.1	1009	2	C89310	hypothetical prote
297	75	6.1	1025	2	T44802	type I site-specif
298	75	6.1	1250	2	A96586	hypothetical prote
299	75	6.1	1434	2	C82923	DNA-directed RNA p
300	75	6.1	1549	2	T21809	hypothetical prote

ALIGNMENTS

RESULT 1	
A28179	enterotoxin E precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus	
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004	
C:Accession: A28179	
J:Couch, J.L.; Soltis, M.T.; Betley, M.J.	
J: Bacteriol. 170, 2954-2960, 1988	
A:Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.	
A:Reference number: A28179; MUID:88257005; PMID:3384800	
A:Accession: A28179	
A:Molecule type: DNA	
A:Residues: 1-257 <COU>	
A:Cross-references: UNIPROT:P12993; UNIPARC:UPI000012A275; GB:M21319; NID:g153001; PIDN:	
C:Superfamily: enterotoxin B	

Query Match	100.0%;	Score 1238;	DB 2;	Length 257;
Best Local Similarity	100.0%;	Pred. No. 2.3e-93;		
Matches 233;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTC	60	
Db	25	SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTC	84	
Qy	61	HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT	120	
Db	85	HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT	144	
Qy	121	EKKKVPINLWIDGKQTTVPIDVKVTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ	180	
Db	145	EKKKVPINLWIDGKQTTVPIDVKVTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ	204	
Qy	181	RGLIVPHSSEGSTVSYDLFDAOGQYPTLLRIYRDKNKTINSENHLHDLYTT	233	
Db	205	RGLIVPHSSEGSTVSYDLFDAOGQYPTLLRIYRDKNKTINSENHLHDLYTT	257	
RESULT 2				
A28664	enterotoxin A precursor - Staphylococcus aureus			
C:Species: Staphylococcus aureus				
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004				
C:Accession: A28664; A29566				
J:Betley, M.J.; Mekalanos, J.J.				
J: Bacteriol. 170, 34-41, 1988				
A:Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.				
A:Reference number: A28664; MUID:88086892; PMID:3335483				
A:Accession: A28664				
A:Molecule type: DNA				
A:Residues: 1-257 <BET>				
A:Cross-references: UNIPROT:P13163; UNIPARC:UPI000012A273; GB:M18970; NID:g153120; PIDN:				
A:Experimental source: strain FR1337				
R:Huang, I.Y.; Hughes, J.B.; Bergdoll, M.S.; Schantz, E.J.				
J. Biol. Chem. 262, 7006-7013, 1987				
A:Title: Complete amino acid sequence of staphylococcal enterotoxin A.				
A:Reference number: A29566; MUID:87222293; PMID:3584106				
A:Accession: A29566				
A:Molecule type: protein				
A:Residues: 25-241, S',243-257 <HUA>				
A:Cross-references: UNIPARC:UPI00001766F5				
C:Genetics:				
A:Gene: entA				
A:Map position: 6				
C:Superfamily: enterotoxin B				
Query Match	82.6%;	Score 1023;	DB 2;	Length 257;
Best Local Similarity	82.0%;	Pred. No. 7.1e-76;		
Matches 191;	Conservative 17;	Mismatches 25;	Indels 0;	Gaps 0;
Qy	1	SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTC	60	
Db	25	SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTC	84	
Qy	61	HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT	120	
Db	85	HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT	144	
Qy	121	EKKKVPINLWIDGKQTTVPIDVKVTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ	180	
Db	145	EKKKVPINLWIDGKQTTVPIDVKVTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ	204	
Qy	181	RGLIVPHSSEGSTVSYDLFDAOGQYPTLLRIYRDKNKTINSENHLHDLYTT	233	
Db	205	RGLIVPHSSEGSTVSYDLFDAOGQYPTLLRIYRDKNKTINSENHLHDLYTT	257	
RESULT 3				
C89984	enterotoxin P [imported] - Staphylococcus aureus (strain N315)			

C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: C89984
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: C89984
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <KUR>
A:Cross-references: UNIPROT:Q99SU3; UNIPARC:UPI00000C7F8A; GB:BA000018; PID:gl3701743; E
A:Experimental source: strain N315
C:Genetics:
A:Gene: sep
C:Superfamily: enterotoxin B

Query Match 80.3%; Score 994; DB 2; Length 260;
Best Local Similarity 79.0%; Pred. NO. 1.7e-73;
Matches 184; Conservative 17; Mismatches 32; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOARNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 28 SEKSEINGKDLQKSELOGTALSNLRQIYYHNGSAIENKESNDQFLKNTILFNDFFTG 87

QY 61 HPWYNLLVDLGSKDATNKKYKGVLDYGYAYGYQCAGTTPNKTCMYGGVTLHDNNRLT 120
DB 88 HQWYNLLVDLGSKDANIYKGVLDYGYAYGYQCTGGTPPKTACMYGGVTLHDNNQLE 147

QY 121 EEKVPINLWDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVKQ 180
DB 148 EEKVPINLWDGKQNTVPLGTVTKNKVETVVOELDLQSRHYLHETNYLNNTDAFNGKIQ 207

QY 181 RGLIVPHSSEGSTSVSYDLFDAQGOYPTDLLRIYRDNKNTINSENHLHDLYLT 233
DB 208 RGLIEPHSPSGDSVGVLDLFGAQGOYPTQLRIYRDNKNTIKSNKHDIYLYTT 260

RESULT 4
A33953
enterotoxin D precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C:Accession: A33953
R:Bayles, K.W.; Iandolo, J.J.
J. Bacteriol. 171, 4799-4806, 1989
A:Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin
A:Reference number: A33953; MUID:89359112; PMID:2549000
A:Accession: A33953
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <BAY>
A:Cross-references: UNIPROT:P20723; UNIPARC:UPI000012A274; GB:M28521; NID:g1492109; PIDN
C:Superfamily: enterotoxin B

Query Match 53.6%; Score 663; DB 2; Length 258;
Best Local Similarity 54.5%; Pred. NO. 1.4e-46;
Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOARNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 26 NENIDSVKEKELKKSELSALNNMKHSYADKNPIGENKSGDQFLENTLLYKKFFTD 85

QY 61 HPWYNLLVDLGSKDATNKKYKGVLDYGYAYGYQCAGTTPNKTCMYGGVTLHDNNRLT 120
DB 86 LINFEDLLINFNSKEMAHFKSKNVDPYRYSINCVGGEIDRTACTYGGVTPHEGNKLG 145

QY 121 EEKVPINLWDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVKQ 180
DB 146 ERKKIPINLWINGVQKESLDKVTQDKKNVTVOELDAQARRYLQKDLKLYNNDTLGGKIQ 205

QY 181 RGLIVPHSSEGSTSVSYDLFDAQGOYPTDLLRIYRDNKNTINSENHLHDLYLY 231
DB 206 RKIEFDSDSGSKSVYDLFDVKDPKQLRIYSDNKTLSTEHLHDIVLY 256

RESULT 5
H89968
enterotoxin SeO [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H89968
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89968
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: UNIPROT:Q99ZM4; UNIPARC:UPI00000CABF7; GB:BA000018; PID:gl3701618; P
A:Experimental source: strain N315
C:Genetics:
A:Gene: sen
C:Superfamily: enterotoxin B

Query Match 37.3%; Score 461.5; DB 2; Length 258;
Best Local Similarity 41.2%; Pred. NO. 3.4e-30;
Matches 96; Conservative 45; Mismatches 77; Indels 15; Gaps 6;

QY 6 EINEKDLRKSELOARNALSNLRQIYYNEKAIT-----ENKESDDQFLENTLLFKGFFTG 60
DB 32 EVDKDLKKKSDLSKSLFNLT--YYTD--ITWQLDENKISTDQLLNTILKNIDIS 87

QY 61 HPWYNLLVDLGSKDATNKKYKGVLDYGYAYGYQCAGTTPNKTCMYGGVTLHDNNRLT 120
DB 88 VLKTSLSLKVEFNSSDLLANQFKGNIDYGLYFGNKCVGLTEKTSCLYGGVTHDGNQLD 147

QY 121 EEKVPINLWDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVKQ 180
DB 148 EEKVGIVNVFVKGVOQGEFV--IKTKKAKVTVOELDKVRFKLENYKIYNKDT--GNIQ 203

QY 181 RGLIVPHS--SEGSTSVSYDLFDAQGOYPTDLLRIYRDNKNTINSENHLHDLYLY 231
DB 204 KGCIFPHSHNHQDSFYDLYNVKSGVGAFFQFYSDNRTVSSSNVHIDVFLY 256

RESULT 6
E89969
enterotoxin SeO [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E89969
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: E89969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <KUR>
A:Cross-references: UNIPROT:Q99T46; UNIPARC:UPI00000CAC87; GB:BA000018; PID:gl3701623; P
A:Experimental source: strain N315
C:Genetics:
A:Gene: seo
C:Superfamily: enterotoxin B

Query Match 31.3%; Score 387.5; DB 2; Length 260;
Best Local Similarity 39.9%; Pred. NO. 3.6e-24;
Matches 97; Conservative 31; Mismatches 86; Indels 29; Gaps 8;

QY	191	GSTVSVDLFDQAQQYPTLLRIYRDNKTINSENHLIDL 228
Db	194	GSFSYDLFDGTGQAEFLKIYNDKNKTETEKFLHDV 231
RESULT 10		
ENSAB6		
enterotoxin B precursor - Staphylococcus aureus		
C:Species: Staphylococcus aureus		
C:Date: 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004		
C:Accession: S27360; A92065; S27240; A01815		
R:Jones, C.L.; Khan, S.A.		
J. Bacteriol. 166, 29-33, 1986		
A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.		
A:Reference number: S27360; MUID:86168029; PMID:3957869		
A:Accession: S27360		
A:Molecule type: DNA		
A:Residues: 1-266 <JON>		
A:Cross-references: UNIPROT:P01552; UNIPARC:UPI0000010DB; EMBL:M11118; NID:g152999; PID		
R:Huang, I.Y.; Bergdoll, M.S.		
J. Biol. Chem. 245, 3518-3525, 1970		
A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide		
A:Reference number: A92065; MUID:71007902; PMID:5470821		
A:Accession: A92065		
A:Molecule type: protein		
A:Residues: 28-55, 'NND', 59-68, 'NE', 71, 'FDLIYL', 78-117, 119-127, 'N', 129, 'D', 131-132, 'ENT',		
A:Cross-references: UNIPARC:UPI000014FD39		
A:Experimental source: strain S-6		
R:Huang, I.Y.; Bergdoll, M.S.		
J. Biol. Chem. 245, 3511-3517, 1970		
A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, compositi		
A:Reference number: A92064; MUID:71007901; PMID:5470820		
A:Contents: annotation; chymotryptic peptides		
R:Huang, I.Y.; Bergdoll, M.S.		
J. Biol. Chem. 245, 3493-3510, 1970		
A:Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, compositi		
A:Reference number: A92063; MUID:71007900; PMID:5470819		
A:Contents: annotation; tryptic peptides		
R:Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunmery, D.A.; Bergdoll, M.S.		
Biochemistry 4, 1011-1016, 1965		
A:Title: Purification of staphylococcal enterotoxin B.		
A:Reference number: A90548; MUID:66035792; PMID:4953912		
A:Contents: annotation; biological source of protein		
R:Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshni		
Eur. J. Biochem. 209, 823-828, 1992		
A:Title: Identification of functionally active fragments of staphylococcal enterotoxin B		
A:Reference number: S27240; MUID:93049338; PMID:1425690		
A:Accession: S27240		
A:Molecule type: protein		
A:Residues: 28-42; 128-148 <ALA>		
A:Cross-references: UNIPARC:UPI0000173634; UNIPARC:UPI0000173635		
C:Superfamily: enterotoxin B		
C:Keywords: enterotoxin; extracellular protein; toxin		
F:1-27/Domain: signal sequence #status predicted <SIG>		
F:28-266/Product: enterotoxin B #status experimental <MAT>		
F:120-140/Disulfide bonds: #status experimental		
Query Match 24.3%; Score 300.5; DB 1; Length 266;		
Best Local Similarity 33.6%; Pred. No. 4.4e-17;		
Matches 82; Conservative 47; Mismatches 96; Indels 19; Gaps 8;		
QY	1	SEKSEBEINKEKDLKKSELORNALSNLRQIYYNEKAITENKESDDDFLENTLLFGKFFPG 60
Db	27	AESQDPKPELDHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLFDLIYSIKOTK 84
QY	61	HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYGYQC-----AGGTPNKTACMYGG 110
Db	85	LGNYNDRVEFFNKDLADKKYDVDFGANYIYQCYFSKKTNDINSHQTDKRTCMYGG 144
QY	111	VTLHDNNRLTEKKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDQARHYLHGKFGLY 170
Db	145	VTEHNGNQLDKYRSITVRVFEDGK-NLLGFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202

QY	171	NSDSFGKQVORGLIVFHSSEGSTVSVDLFDQAQQYPD--TLRIYRDNKTINSENHLIDL 228
Db	203	EFNN--SPYETGYIKFIENENG-FWYDMMPAPGDPDQSKYLMYNDNKNKVDKVKIEV 259
QY	229	YLYT 232
Db	260	YLYT 263
RESULT 11		
S29659		
exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12		
N:Alternate names: erythrogenic toxin; scarlet fever toxin		
C:Species: Streptococcus pyogenes phage T12		
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999		
C:Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18800		
R:Weeks, C.R.; Ferretti, J.J.		
Infect. Immun. 52, 144-150, 1986		
A:Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) ge		
A:Reference number: S29659; MUID:86166804; PMID:3514452		
A:Accession: S29659		
A:Molecule type: DNA		
A:Residues: 1-251 <WEE>		
A:Cross-references: UNIPARC:UPI0000135DD7; GB:U40453; EMBL:M19350; NID:g1877426; PIDN:AA		
R:Nelson, K.; Schlievert, P.M.; Sclander, R.K.; Museer, J.M.		
J. Exp. Med. 174, 1271-1274, 1991		
A:Title: Characterization and clonal distribution of four alleles of the speA gene encodi		
A:Reference number: S18782; MUID:92044323; PMID:1940804		
A:Accession: S18782		
A:Status: nucleic acid sequence not shown; translation not shown		
A:Molecule type: DNA		
A:Residues: 9-244 <NEU>		
A:Cross-references: UNIPARC:UPI00000B1BCE; EMBL:X61560; NID:g47287; PIDN:CAA43758.1; PID:		
A:Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigned		
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991		
A:Accession: S18784		
A:Status: nucleic acid sequence not shown; translation not shown		
A:Molecule type: DNA		
A:Residues: 9-244 <NEA>		
A:Cross-references: UNIPARC:UPI00000B1BCE; EMBL:X61556; NID:g47291; PIDN:CAA43754.1; PID:		
A:Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassigned		
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991		
A:Accession: S18785		
A:Status: nucleic acid sequence not shown; translation not shown		
A:Molecule type: DNA		
A:Residues: 9-244 <NEZ>		
A:Cross-references: UNIPARC:UPI00000B1BCE; EMBL:X61559; NID:g47293; PIDN:CAA43757.1; PID:		
A:Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned ph		
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991		
A:Accession: S18791		
A:Status: nucleic acid sequence not shown; translation not shown		
A:Molecule type: DNA		
A:Residues: 9-244 <NEY>		
A:Cross-references: UNIPARC:UPI00000B1BCE; EMBL:X61555; NID:g47309; PIDN:CAA43753.1; PID:		
A:Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned I		
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991		
A:Accession: S18796		
A:Status: nucleic acid sequence not shown; translation not shown		
A:Molecule type: DNA		
A:Residues: 9-244 <NEO>		
A:Cross-references: UNIPARC:UPI00000B1BCE; EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:		
A:Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned ph		
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991		
A:Accession: S18797		
A:Status: nucleic acid sequence not shown; translation not shown		
A:Molecule type: DNA		
A:Residues: 9-244 <NEH>		
A:Cross-references: UNIPARC:UPI00000B1BCE; EMBL:X61558; NID:g47321; PIDN:CAA43756.1; PID:		
A:Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned ph		
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991		
A:Accession: S18800		
A:Status: nucleic acid sequence not shown; translation not shown		

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18792
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEO>
A;Cross-references: UNIPARC:UPI00000BEA6A; EMBL:X61565; NID:g47311; PIDN:CAA43763.1; PID
A;Experimental source: strain MGAS480 isolate Yugoslavia unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18795
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEH>
A;Cross-references: UNIPARC:UPI00000BEA6A; EMBL:X61566; NID:g47317; PIDN:CAA43764.1; PID
A;Experimental source: strain MGAS492 isolate United Kingdom unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18799
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NES>
A;Cross-references: UNIPARC:UPI00000BEA6A; EMBL:X61567; NID:g47325; PIDN:CAA43765.1; PID
A;Experimental source: strain MGAS496 isolate Germany unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C;Genetics:
A;Gene: speA2
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 22.0%; Score 272.5; DB 2; Length 236;
Best Local Similarity 33.3%; Pred. No. 7.2e-15;
Matches 77; Conservative 43; Mismatches 92; Indels 19; Gaps 10;

Qy 4 SESENEKDLKSKSELORNAL-SNLRLQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
Db 17 SQEVAQQDDPDSQHLKSSLVKLNLIYFLYEGDPVTHENVKSDVQLSHDLIYN---VS 73

Qy 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQC--AGGTPNKATACMYGGVTLHDNNRL 119
Db 74 GPYNDKLTKEKQEMATLKFKNVDIYSVEYHYLCVLCENASRSACIYGVTHNENHL 133

Qy 120 TEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDFGGKV 179
Db 134 EIPKIKVKSVIDGIQ-SLSFD-IETNKMTVAQELDYKVRKYLTONKQLYTNGP--SKY 189

Qy 180 QRLGIYFHSSEGSTVSVDLFD----AQGYPTLLRIYRDNTKNTINSENHLI 226
Db 190 ETGYIKRPIPKNKESFWDFPFPEFTQSKY----LMIYKDNLTDSNTSQI 236

RESULT 17
ENSAC1
enterotoxin C-1 precursor - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C;Accession: S06356; A01816
R;Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness b
A;Reference number: S06356; MUID:98038352; PMID:2823067
A;Accession: S06356
A;Molecule type: DNA
A;Residues: 1-266 <BOH>
A;Cross-references: UNIPROT:P01553; UNIPARC:UPI000012A22B; EMBL:X05815; NID:g46566; PIDN
R;Schmidt, J.J.; Spero, L.
J. Biol. Chem. 258, 6300-6306, 1983
A;Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A;Reference number: A01816; MUID:83213327; PMID:6189824
A;Accession: A01816
A;Molecule type: protein
A;Residues: 28-75, 'IL', 78-176, 'N', 178-266 <SCH>
A;Cross-references: UNIPARC:UPI0000173636
C;Genetics:

A;Gene: entC1
C;Superfamily: enterotoxin B
C;Keywords: enterotoxin
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-1 #status experimental <MAT>
F;120-137/Disulfide bonds: #status experimental

Query Match 21.5%; Score 266.5; DB 1; Length 266;
Best Local Similarity 30.5%; Pred. No. 2.6e-14;
Matches 74; Conservative 51; Mismatches 101; Indels 17; Gaps 8;

Qy 1 SEKSEINEKDLKSKSELORNALSNLRLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 27 AESQDPPTDELHKASKF-TGLMNNKVLVYDDHYVSATKVK-SVDKFLAHDLIYNSDKK 84

Qy 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKATACMYGGVTL 113
Db 85 LKNYDKVTLELNEGLAKYKDEVDVYGSNYYVYFSSKDNVGVTKGTCTMYGGITK 144

Qy 114 HNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYN 171
Db 145 HEGNHFNGNLQNLVLRVY-ENKRNITISPE-VQTDKKSVTQAELDIKARNFINKKNLYE 202

Qy 172 SDSFGGKVORGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNTKNTINSENHLIDL 229
Db 203 FNS--SPYETGYIKFTIENNGTFWYDMPPAPGDKFDQSKYLMYNDKNTVDSKSVKIEVH 260

Qy 230 LYT 232
Db 261 LTT 263

RESULT 18
G89968
extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain N31)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G89968
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: G89968
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <KUR>
A;Cross-references: UNIPROT:O85382; UNIPARC:UPI000012A276; GB:BA000018; PID:g13701617; P
A;Experimental source: strain N315
C;Genetics:
A;Gene: seg
C;Superfamily: enterotoxin B

Query Match 20.6%; Score 255.5; DB 2; Length 258;
Best Local Similarity 29.1%; Pred. No. 2e-13;
Matches 71; Conservative 49; Mismatches 83; Indels 41; Gaps 11;

Qy 11 DLKSKSELORN--ALSNLRLQIYY---YNEKAITENKESDDQFLENTLLFKGFFTGHPWYN 65
Db 33 ELNKVSDYKNNKGTGMGNVNNLXTSPPEVGRGVINSR----QFLSHDLIFP---IEYKSYN 85

Qy 66 DLLAVDLGSKDATNKYKGGKVDLYGAYGYQCA-----AGGTPNKATACMYGGVTL 113
Db 86 EVKTELENTLANNYKDKKVDIFGVYFYTCIIPKSEPDINQNFSG-----CMYGGLTTF 140

Qy 114 H--DNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYN 171
Db 141 NSSENER---DKLIITVQVTDNRQSLG--FTITTNKMVTIQELDYKARHWTKEKKLYE 195

Qy 172 SDSFGGKVORGLIVFHSSEGSTVSVDLFDAGQGYPDT---LLRIYRDNTKNTINSENHLIDL 228
Db 196 FD--GSAFESGYIKFTKNTKNTSFWDLPFKKELVPFVPYKFLNIYGDKNVDSKSKIMEV 253

QY 229 YLYT 232
Db 254 FLNT 257

RESULT 19
A26152
streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
N:Alternate names: scarlet fever toxin; SPE type A (speA)
C:Species: Streptococcus sp.
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A26152
R:Johnson, L.P.; I:Italian, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1996
A:Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Staphylococcus aureus exotoxin A
A:Reference number: A26152; MUID:86284313; PMID:3526093
A:Accession: A26152
A:Molecule type: DNA
A:Residues: 1-250 <JOH>
A:Cross-references: UNIPROT:P08095; UNIPARC:UPI0000017021E
A:Superfamily: enterotoxin B
C:Keywords: exotoxin

Query Match 19.8%; Score 245; DB 1; Length 250;
Best Local Similarity 30.7%; Pred. No. 1.3e-12; Mismatches 94; Indels 22; Gaps 9;
Matches 70; Conservative 42

QY 14 KXSELQNALSNLRQIYYNEKA--IT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 70
Db 35 KPSQLQRSNLVKTKIYIFPMRVTLVTHENVKSVQDQLSHDLIYN--VSGPNYDKLKE 91

QY 71 LSKDATNKYKGGKVDLYGAYGYQC-AGTPTNKTAAGTGVTLHDNNRLTEKKVPINL 129
Db 92 LKNQEMATLFDKKNVDIYGVYHLYCYLCENASRACLYGGVTNHEGNHLEIPKKIWKV 151

QY 130 WDGKOT-TVPIDKVTSKKEVTQQLDLQARHLHGKFGLYNSDSFGKGKVGORGLIVFHS 188
Db 152 SDIGIQSLSFDEIQKNG-----NCSRISYTVRKLTNDKQLYNGP--SKYETGIKFP 205

QY 189 SEGSTVSYDLFD----AQGYPTLLRIYRDNKNTINSENHLHDLYLYT 232
Db 206 KNKESPFWFDFPPEPTQSKY----LMYKDNETLDSNTSQIEVLYLT 249

RESULT 20
A89942
hypothetical protein SA1430 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A89942
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogucima, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A89942
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-157 <KUR>
A:Cross-references: UNIPROT:Q99TP7; UNIPARC:UPI000000CAD54; GB:BA0000018; PID:g13701400; E
A:Superfamily: enterotoxin B
C:Keywords: exotoxin

Query Match 16.2%; Score 201; DB 2; Length 157;
Best Local Similarity 35.8%; Pred. No. 2.8e-09; Mismatches 53; Indels 2; Gaps 2;
Matches 42; Conservative 21

QY 1 SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 42 TNSASALEYSDLHHKSKFDSKRLSNK-KMSFINPTQL-ENKNTDRLLKHDLLFHDMFVN 99

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAAGTGVTLHDNNR 118
Db 100 VASKDKFVPEPENEALSKKFINKNDIYAGSYSECHGGATNKTCQSGYGVTLSDNNK 157

RESULT 21
A89969
enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A89969
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogucima, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A89969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <KUR>
A:Cross-references: UNIPROT:Q99T49; UNIPARC:UPI000000CAD54; GB:BA0000018; PID:g13701619; P
A:Superfamily: enterotoxin B
C:Genetics:
A:Gene: yent2

Query Match 15.9%; Score 197; DB 2; Length 136;
Best Local Similarity 34.1%; Pred. No. 5e-09; Mismatches 51; Indels 10; Gaps 5;
Matches 46; Conservative 28

QY 103 KTACMYGGVTLHDNNRLTEKKV--PINLWI--DGKQTTVPIDKVKTSKKEVTVOELDL 157
Db 2 KITCMYGGVTEHDGQIDKKNSTDNHNLILKIVYERNLSLSPD-IPTNKNITAEIDY 60

QY 158 QARHYLHGKFGLYNSDSFGKGKVGORGLIVFHSSEGSTVSVDLFDACQ--YPTDLLRIYRD 215
Db 61 KVRNLLKHLKLYEFNS--SPVETGYIKIEGSHGFWYDLMPESGKFKFYPTKYLIIYND 118

QY 216 NKTINSENHLHDLYL 230
Db 119 NKTVESKSNVVEHL 133

RESULT 22
A30509
exotoxin C precursor - Streptococcus pyogenes
C:Species: Streptococcus pyogenes
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: A30509
R:Goshorn, S.C.; Schlievert, P.M.
Infect. Immun. 56, 2518-2520, 1988
A:Title: Nucleotide sequence of streptococcal pyrogenic exotoxin type C.
A:Reference number: A30509; MUID:88314303; PMID:3045005
A:Accession: A30509
A:Molecule type: DNA
A:Residues: 1-235 <GOS>
A:Cross-references: UNIPROT:P13380; UNIPARC:UPI000017022C; GB:M35514; NID:g153820; PIDN:
A:Superfamily: enterotoxin B
C:Keywords: exotoxin

Query Match 14.8%; Score 183.5; DB 2; Length 235;
Best Local Similarity 25.8%; Pred. No. 1.3e-07; Mismatches 61; Conservative 37; Mismatches 73; Indels 65; Gaps 11;
Matches 61; Conservative 37

QY 47 FLENTLLFKGFFTG-----PW-YNDLLVDLGSKDA-----TNK 79
Db 11 FIITVILISTYFTYHQSDSKDISNVKSDLLVAYTITPYDYKDCRVNFS'THTLNIDTQK 70

QY 80 YKSK-----KVDLYGAYGYQCAGGTPNKTAAGTGVTLHDNNRL 119
Db 71 YRGKDYIISSEMSYEASQKFKRDDHVDVFGFLFILNSHTG-----EYIYGGITPAQNNKV 125

Db 86 -----LLGKD-KDKYKKGLEQNVFVVKELI-----DPNGRLSTVGGV 122

QY 112 TLHDNRLTEKKVPINLWIDGKQTTVPIDKVTSKKEVTQVQELDLQARHYLHGKFGLYN 171

Db 123 TKQNKSSSENTHLFVNK-VYGGNLDASIDSLINKKEVSLKELDPKIRKQLVEKGYLYK 181

QY 172 SDSFGKGQVGLVIFHSSEGSTVSYDLFDAQGGYPTLRLIYRDNKTIINSEN 224

Db 182 -----GTTKYKGTITNLKDEKKEVDLGDK-----LQFERMGVDVLSKDI 221

RESULT 30

G89807

exotoxin 14 [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: G89807

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogino, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: G89807

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-227 <KUR>

A:Cross-references: UNIPROT:Q99WH3; UNIPARC:UPI000000CAB82; GB:BA000018; PID:g13700320; E

A:Experimental source: strain N315

C:Genetics:

A:Gene: set14

C:Superfamily: toxic shock syndrome toxin

Query Match 7.8%; Score 96; DB 2; Length 227;

Best Local Similarity 26.7%; Pred. No. 1.6;

Matches 54; Conservative 28; Mismatches 76; Indels 44; Gaps 9;

QY 8 NEKDLRK--KSELQNALSNLROIYYNEKAITENKESDDQFLENTLLPKGFFTHPWYN 65

Db 33 NQKSNVNHDKREALYR-----YTGKTMEMKNISALKHGKNLRFK--FRGIKIQV 80

QY 66 DLLVDLGSKDATNKYG-----KKVDLYGAYGYQCAGT--PNKTACMGYGVTLHDN 116

Db 81 LLPGNDKSKFQQRSEGLDVFVQEKRDKHDIFY---TVGGVIQNKNTS---GVVSAPI 133

QY 117 NRLTESKKVPINLWIDGKQTTVPIDKVTSKKEVTQVQELDLQARHYLHGKFGLYNSDSFG 176

Db 134 LNISKKEK-----GEDAFVKGYPYIKKEKITLKELDYKURKHLIEKGYLYKTIKSD 184

QY 177 GKVQVGLVIFHSSEGSTVSYDL 198

Db 185 GRVKISL-----KDGsfYNLDL 201

RESULT 31

G86903

cell shape determining protein [imported] - Lactococcus lactis subsp. lactis (strain IL1

C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C:Accession: G86903

R:Boletín, A.; Wincker, P.; Mager, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: G86903

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-291 <STO>

A:Cross-references: UNIPROT:Q9CDI9; UNIPARC:UPI000000C6BFE; GB:AE005176; PID:g12725299; E

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: mreC

Query Match 7.6%; Score 94.5; DB 2; Length 291;

Best Local Similarity 20.7%; Pred. No. 2.8;

Matches 48; Conservative 26; Mismatches 67; Indels 91; Gaps 8;

QY 21 NALSNLROIYYNEKAIT-----ENK-----ESDQFLENTLLPKGFFTHG----- 61

Db 67 NELSNLMDTYQQNQSLKTQLAKSKDDNKLGLSESKELKALKIQTETLDTQTVAANV 126

QY 62 -----PWYNDLVLGLSKDATNKYKGVKVDLYGAYGYQCAGTGNKTACTACMYGVTLHD 115

Db 127 ITRPSSWNTLVIDSGSKD-----CLTTGMIVWANGVV--- 161

QY 116 NNRLTE-----EKKVPINLWIDGKQTTVPIDKVTSKKEVTQVQELDLQ 158

Db 162 -GRVTQVKNSSKVALLSKSGIDNKIPVRIESDGSPIYGLSSYDSQQEAYVYVKNIDSQ 220

QY 159 ARHYLHGKGLYNSDSFGKQVQGLVIFHSSEGSTVSYDLFDAQGGYPTDFTLL 210

Db 221 -----GRFKNGDSVFTSGLGITNSG-----SQGGTPSGLL 249

RESULT 32

S70908

transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB29)

C:Species: Haemophilus influenzae

A:Variety: strain SB29

C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S70908; S73321

R:Loommore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E. Mol. Microbiol. 19, 575-586, 1996

A:Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes

A:Reference number: S70901; MUID:96228706; PMID:8830248

A:Accession: S70908

A:Molecule type: DNA

A:Residues: 1-631 <LOO>

A:Cross-references: UNIPROT:Q48041; UNIPARC:UPI00001783A3; EMBL:U15055

A:Experimental source: strain SB29, clone DS-1090-3-2

R:Loommore, S.M.

A:Reference number: S73320

A:Accession: S73321

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-250, 'I', 252-349, 'RTDATN', 357-631 <LOW>

A:Cross-references: UNIPARC:UPI00000B271A; EMBL:U15055; MID:g1223948; PIDN:AAC43931.1; P1

A:Experimental source: strain SB29, clone DS-1090-3-2

C:Genetics:

A:Gene: tdp2

C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor an

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-631/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 7.6%; Score 94.5; DB 2; Length 631;

Best Local Similarity 20.8%; Pred. No. 7.5;

Matches 52; Conservative 28; Mismatches 55; Indels 115; Gaps 11;

QY 31 YNEKAITENKESDDQFLENTL-----LFGKF-----FTGHPWYNDL----- 67

Db 202 YNRRSAISEDIDN-----LENNKNGAGLTSEFTVNFQTKLTGKLYNERETNNKLQKR 257

QY 68 ----LVDLGSKDATNKYKG-----KVDLYGAYGYQCAGTGNKTACTMY 108

Db 258 KHELYDIDADIYSNRFRGKVPKPTQKDSQHPPTSEGTLEGGFYG-----PNGE--L 308

QY 109 GGVTLLHDNRL-----TEEEKVPINLWIDGKQTTVPIDK-----VKTSKEV 150

Db 309 GKGFLAGDNRFVGFSAKEEETKDKKLSRETLDGKLITFKTKTAKTAANKTDEKNF 368

QY 151 TVQELD-----LQARHYLHG----- 168

Db 369 TTKDIPSGEADYLLIDNYPVPLFPPEINTNDFITSRHHKVGDKTYKVEACKNLSVYKFG 428

QY 169 LYNDSFSGK 178

Db 1194 FQDYQNNNNSLVLKVNFEFSNQSABDYTVFNNGE-----ILLDDINICDYNL 1244

RESULT 36

G90559

tree-like protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C;Species: Mycoplasma pulmonis

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: G90559

R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallieson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001

A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis

A;Reference number: A99512; MUID:21267165; PMID:11353084

A;Accession: G90559

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-853 <KUR>

A;Cross-references: UNIPROT:Q98QH8; UNIPARC:UPI00000045D0; GB:AL445566; PID:g14089797; E

C;Experimental source: strain UAB CTIP

C;Genetics:

A;Gene: MYPU 3830

A;Genetic code: SGC3

Query Match 7.4%; Score 91; DB 2; Length 853;

Best Local Similarity 23.1%; Pred. No. 21;

Matches 56; Conservative 41; Mismatches 97; Indels 48; Gaps 9;

QY 4 SEINEKDLRKK-SELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHP 62

Db 224 SNEIEKISLMKTAGFENFOLSNDVQINLSKINFFKNLELDSEYLENT----- 272

QY 63 WYNDLLVDLGSKDATNKYKGGK-----VDLYGA-YYGYQCAGGTPNKTACMYGGVT 112

Db 273 --NNINENLSKEFEKFEINKKHLKINDYFVNLSQVEEPPFELPGWASNIFKSDSTVI 330

QY 113 LHNNRLTEKKVPIN-LWIDGQTTVP--DKVKTSSKEVTVOELDLQARHYLHGKFGLY 170

Db 331 WHFNSVEEDQAKVLINKAITSRVSINVKXVDIEKEKFIHNFELAKKIAFGKESL- 389

QY 171 NSDSFGKVGQGLIVFHSSEGSTVSDLPDAQGYPTDLLRIYRDNKTINSENLDLYL 230

Db 390 -----KRSSIIIFINK--STNKKDLIKLQNE-----NIKANLINIKINNCL 428

QY 231 YT 232

Db 429 YT 430

RESULT 37

AC1553

B. subtilis YjbK protein homolog lin0964 [imported] - Listeria innocua (strain Clip11262)

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 12-Jul-2004

C;Accession: AC1553

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AC1553

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-194 <GLA>

A;Cross-references: UNIPARC:UPI000000CC3F9; GB:AL592022; PIDN:CAC96195.1; PID:g16413423;

A;Experimental source: strain Clip11262

C;Genetics:

A;Gene: lin0964

C;Superfamily: uncharacterized stand-alone CYTH domain protein, gram-positive bacterial

Query Match 7.3%; Score 90.5; DB 2; Length 194;

Best Local Similarity 22.4%; Pred. No. 3.6;

Matches 53; Conservative 32; Mismatches 89; Indels 63; Gaps 12;

QY 3 KSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHP 62

Db 3 KELEIEFRNLLTYKEEYDR-----LIEDPRIKEDDFEQT-----N 37

QY 63 WYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEE 122

Db 38 FYLD-TADFGKERNALSARIRKLETO-----YQLTLTKTPEARGLM-----ETTQILAAD 85

QY 123 KKVPINLWIDGQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQ 182

Db 86 QATAIT---DG--ANIPVGVPVDTLKEIGINHEDLQV-----FGLSKTIRAEKDYKKG 133

QY 183 LIVFHSS-EGSTVSYDL-----FDAQGOVPTDLLRIYR-----DNKTINSENLDHI 226

Db 134 LVVFDKKNFVGSISDFDLEVEVSDYDKGEIFDKLLKEYQITNHPAENKVARFYN-HV 189

RESULT 38

AI1161

flagellar hook protein FlgE homolog lmo0697 [imported] - Listeria monocytogenes (strain

C;Species: Listeria monocytogenes

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C;Accession: AI1161

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AI1161

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-411 <GLA>

A;Cross-references: UNIPROT:Q92DV7; UNIPARC:UPI000000556A7; GB:NC_003210; PIDN:CAC98775.1;

A;Experimental source: strain EGD-e

C;Genetics:

A;Gene: lmo0697

Query Match 7.3%; Score 90; DB 2; Length 411;

Best Local Similarity 20.9%; Pred. No. 10;

Matches 55; Conservative 39; Mismatches 81; Indels 88; Gaps 14;

QY 32 YNEKAITENKESDDQFLENTL--LFKGFTTG-HPW-----YNDLLVD--LGSKDATNK 79

Db 34 YKQSVYVFN-----DLLYQNTMGSVAGGLYAGTNPMSPGSGSKTGAILTDYTAGSPSTGR 89

QY 80 YKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK----- 123

Db 90 NKDAALQGRGFFIAGNAGG--NIVYTRDGSFAVSDNNYLTTOQGVKVMGYATDKNGNVL 147

QY 124 -----KVPINLWIDGKT-----TVPIDKVTSSKEVTVOELDLQARHYLHGKFG 169

Db 148 NGNLQPIQLPLNSAIPGATKNGSLSGNIPLD---NGEKDTISSELSVY----- 193

QY 170 YNSDSFGG--KVQGLIVFHSSEGSTVSYDL-----FDAQGY--PD 207

Db 194 ---DNAGGKHKLQVNNKAATPDASGNVSVEYEQMDGKALTTPVTGTGLTNYNAQGLTNPD 250

QY 208 TLLRIYRDNKTINSENLDHLDLYL 230

Db 251 ALKNI-QINSTVNGKQVNMGLNL 272

RESULT 39

AI1520

flagellar hook protein FlgE homolog lin0705 [imported] - Listeria innocua (strain Clip11262)

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

Db 556 EHTQSDTASAKISSNKEHLKNLSYIRKXNSNSTFDIATNTQNTSFSGANVALIL 615
QY 114 HDNNRLTEKKVPINLWIDKQTPVDPKVKTSKEVTVOELDQARHYLHGKFLGYNLS- 172
Db 616 ADSNK-----TLAFDRVEADLKG---NALDLKSGRG-NAKFDLYYS 653
QY 173 -----DSFGKG-----VQGLVIFH-SSEGSIVSYDLFPAQOQYPTTLRIYR 214
Db 654 NDNLNVSNIDNLYNEFLQKQAVODG--VFNLISIRKSGLEY--FDGQIDFKNTYV---K 706
QY 215 DNKTINSENLIHD 227
Db 707 DLKGINQLISFID 719
RESULT 52
A45604
major blood-stage surface antigen Pv200 - Plasmodium vivax
C:Species: Plasmodium vivax
C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C:Accession: A45604
R:Gibson, H.L.; Tucker, J.B.; Kaelow, D.C.; Kretzli, A.U.; Collins, W.E.; Kiefer, M.C.;
Mol. Biochem. Parasitol. 50, 325-333, 1992
A:Title: Structure and expression of the gene for Pv200, a major blood-stage surface ant
A:Reference number: A45604; MUID:92158013; PMID:1371329
A:Accession: A45604
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1751 <GIB>
A:Cross-references: UNIPROT:Q26194; UNIPARC:UPI0000083C26; GB:M75674; NID:g160608; PID:9
A:Note: sequence extracted from NCBI backbone (NCBI:83591, NCBI:83592)
C:Superfamily: G surface protein
C:Keywords: surface antigen
Query Match 7.0%; Score 86.5; DB 2; Length 1751;
Best Local Similarity 22.9%; Pred. No. 1.2e+02;
Matches 44; Conservative 30; Mismatches 63; Indels 55; Gaps 8;
QY 2 EKSEINEKND-----LRKKSQLRNALSNLRQIY-----YNEKAITENKESDDQFLE 49
Db 1087 KKNKISNSKDIKKLTSKLNKLRQNLNPTSVLKNYTAFFNKKRETEKKEVENTLKN 1146
QY 50 NTLLPK-----GFFTHPWYNDLLVDLGSKDNTN-----KYK-----GKKVDLYG 89
Db 1147 TEILLKYKARAKYIYGEPPFLKTLSEESQKEDNYLNLEKFRVLSRLGRLGKNIIELEK 1206
QY 90 AYYGYQACGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDKQTPVDPKVKTSKK- 148
Db 1207 ENISYLSG-----LH-HVLTSLKEILKKNKYSGNDHTKNIIVAAVKEALQA 1250
QY 149 -----EVTQVE 154
Db 1251 YQELIPKVTQVE 1262
RESULT 53
S78650
DNA endonuclease a15-alpha - yeast (Saccharomyces cerevisiae) mitochondrion
N:Alternate names: protein Q0070
C:Species: mitochondrion Saccharomyces cerevisiae
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Accession: S78650; S78651; S27138
R:Foury, F.; Roganti, T.; Lecrenier, N.; Purnelle, B.
submitted to the Protein Sequence Database, December 1998
A:Reference number: S78634
A:Accession: S78650
A:Molecule type: DNA
A:Residues: 1-630 <FOU>
A:Cross-references: UNIPROT:Q92ZK1; UNIPARC:UPI0000091C05; EMBL:AJ011856; GSPDB:GN00017;
A:Experimental source: strain FY1679, isogenic derivative of strain S288C
R:Foury, F.; Roganti, T.; Lecrenier, N.; Purnelle, B.
FEBS Lett. 440, 325-331, 1998

A:Title: The complete sequence of the mitochondrial genome of Saccharomyces cerevisiae.
A:Reference number: Z13743; MUID:99087401; PMID:9872396
A:Accession: S78651
A:Molecule type: DNA
A:Residues: 1-630 <POU>
A:Cross-references: UNIPARC:UPI0000091C05; EMBL:AJ011856; NID:g4160362; PIDN:CAA09829.1;
A:Experimental source: strain FY1679, isogenic derivative of strain S288C
R:Hensgens, L.A.M.; Bonen, L.; de Haan, M.; van der Horst, G.; Grivell, L.A.
Cell 32, 379-389, 1983
A:Title: Two intron sequences in yeast mitochondrial COX1 gene: homology among URF-contai
A:Reference number: S27138; MUID:83129428; PMID:6297792
A:Accession: S27138
A:Molecule type: DNA
A:Residues: 241-630 <HEN>
A:Cross-references: UNIPARC:UPI00001787C6; EMBL:J01477
A:Experimental source: strain KLI4-4A
C:Genetics:
A:Gene: SGD:A15 ALPHA; SCA15alpha; MIPS:Q0070
A:Cross-references: SGD:S0007265
A:Genome: mitochondrion
A:Genetic code: SG2
C:Superfamily: DNA endonuclease I-SceII; COI intron 9 protein homology; cytochrome-c oxi
C:Keywords: mitochondrion
F:241-324/Region: cox1 exon 5-alpha encoded
F:325-630/Region: cox1 intron encoded
Query Match 6.9%; Score 86; DB 2; Length 630;
Best Local Similarity 19.5%; Pred. No. 3;
Matches 56; Conservative 35; Mismatches 86; Indels 110; Gaps 14;
QY 2 EKSEINEKDKKKGSELQNALSNLRQIYIYNEKAITENKESDDQFLENTLFPKGFFTGH 61
Db 331 DKNKKNKKLIRNYQKMNW---NMKTYLNNNNMIMWNN-----MYKG----- 370
QY 62 PWYNDLLVDLGSKDNTNKKYKKVDLYGAYGY---QCAG-----GTPNKTAC 106
Db 371 -----NLDIYPRSNRNYIQPNINKELVYGVNLESVCVGMPTTYNIVKHMVGIPNNILY 425
QY 107 MYGGVTLHDNNRLTEKKVPINLWIDKQTPVDPKVKTSKKEV---TVQELDLQAR--- 160
Db 426 IMTGILLTDG-----WID-----YTSKDLDKKTIMEINCRFLKQ 461
QY 161 -----HY-----LHGKFLGYNLSDSFGKVKQVQGL-----IVF 186
Db 462 SMHSEYLMYVFWLISHYCMSPKMKIAKVKGK--SYNQLEF---YTRSLPCFTILRYMF 516
QY 187 HSSEGSTVSYDLFDAQOQYPTDLRIYRDNKNTINSENHIDLIVYTT 233
Db 517 YNGRVKIVPNNLYDLL-NYESLAHIMCDGSFVKGGGLYNLQSF 562
RESULT 54
AG1749
glycosidase homolog lin2540 [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AG1749
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, T.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fsihi, H.;
S. Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefit, J.; Kuhn, M.; Kunst, P.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative Genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1749
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1090 <GLA>
A:Cross-references: UNIPROT:Q928J2; UNIPARC:UPI000000CC8DB; GB:AL592022; PIDN:CAC97767.1;
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin2540

Query Match	6.9%;	Score 86;	DB 2;	Length 1090;	
Best Local Similarity	22.5%;	Pred. No. 73;			
Matches	47;	Conservative 35;	Mismatches 61;	Indels 66; Gaps 14;	
Qy	33	NEKAITENKESDDOLFENTLLFKGFF	-----TGHP-----	WY-NDLLVDLGSKDATNKY 80	
	:	: : : : :	:	: : : : :	
	:	: : : : :	:	: : : : :	
	:	: : : : :	:	: : : : :	
Db	491	DDNTVYEQRDNDEY----	MISQGSADDDGTGAPYVPASQWFGNGILLDFLTNKDAVNMW 546		
Qy	81	KGKK-----	VDLYGAYGVOCAGGTENKTACMYGGVTLHDNNRLTEERKKVPLINLWID 132		
	:	: : : : :	:	: : : : :	
	:	: : : : :	:	: : : : :	
Db	547	TSQREYLLTDVGID-----	GFKTDGG-----	EMWGEDTTFSGEKGQEMR----- 587	
Qy	133	GKQTTVPIDKVT--	SKKEVTVOELDLQARHYLHG--	KFGLYNS-----	DSFGKGQV 180
	:	: : : : :	:	: : : : :	
	:	: : : : :	:	: : : : :	
	:	: : : : :	:	: : : : :	
Db	588	---NRYPTDYVSSYFDPAKSNINPAVSF--	SRSGTSGAKSGKIYWSGGDTSTFDSFQASVK 643		
Qy	181	RGLTVFHSSEGSTVSY----	DLFDAGQGV 206		
	:	: : : : :	:	: : : : :	
	:	: : : : :	:	: : : : :	
	:	: : : : :	:	: : : : :	
Db	644	AGL-----	SASTSGVSYWAWDMAGTGNYP 668		

RESULT 55
T27404
hypothetical protein Y75B8A.22 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T27404
R;Barlow, K.
submitted to the EMBL Data Library, November 1998
A/Reference number: Z20361
A/Accession: T27404
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1353 <WIL>
A/Cross-references: UNIPROT:Q9XW65; UNIPARC:UPI000008241A; EMBL:AL033514; NID:el1343251;
A/Experimental source: clone Y75B8A
C/Genetics:
A/Gene: CESP:Y75B8A.22
A/Introns: 28/1; 79/2; 634/3; 996/1; 1134/1; 1296/3

Query Match	6.9%;	Score 86;	DB 2;	Length 1353;
Best Local Similarity	21.2%;	Pred. No. 96;		
Matches	65;	Conservative 40;	Mismatches 88;	Indels 114; Gaps 15;

Qy	2	EKSEEINEKDLRKKSSELORNALSNLRLQIYYYNEXAITENKESDQDOLENTLLFKGFFTGH	61
Db	452	EHAKEENERPKAKR-----ALEHIVNVEYRELPFIITIKFPSSSVLSNNFLRELVLVLTTH	505
Qy	62	PTYN--DLLVDLGS-KDATNKYKGGKVDLYGAYICYOCAGGTPNKTACM-----YGG	110
Db	506	HYMKLVVERFVKTGALKKVKVYKRA-----TKSKWSEEDVRSRFDG	549
Qy	111	VTLHNNRLTEKK-----VPINLWIDGKQTTVPIDKVTSKSEKVTVQ	153
Db	550	MSKKDLRLMBEESKGLVLQILKEVPEPMGNVPIDSQLD-----VPVDAQOKFAK-LSIQ	603
Qy	154	ELDIQARHYLHGKGLYNS-----DSFGKVQRGLIVFHSEG-----	191
Db	604	R-SURSRGP-PAAVGLYHASRALWPESF-----KRGLTDFQPSGEEDQLBLEQLLKADM	657
Qy	192	-----STVSYDLFDAQG-----QYPTDLLRIYR-----DNKITS	221
Db	658	KYVAKDLKAESCKTCDEDPAYKKYDKMDATALQSLWEQSTDTTLARILSHELPESESISP	717
Qy	222	ENLHIDL	228
Db	718	VNWOLDI	724

RESULT 56
AD1770
arginyl tRNA synthetase [imported] - Listeria innocua (strain Clip11262)

C;Species: *Listeria innocua*
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1770
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H., D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Krest, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maqueno, E.; Maitournam, A.; Matok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1770
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-556 <GLA>
A;Cross-references: UNIPROT:Q927T2; UNIPARC:UPI000013664A; GB:AL592022; PIDN:CACS97932.1;
A;Experimental source: strain Clip1262
C;Genetics:
A;Gene: argS
A;Superfamily: Bacillus arginine-trna ligase

Query Match	6.9%;	Score 85.5;	DB 2;	Length 556;
Best Local Similarity	21.1%;	Pred. No. 34;		
Matches	60;	Conservative 39;	Mismatches 74;	Indels 111; Gaps 15;
Qy	22	ALSNLRQI-YYNEKAITENKESDDO	FLENTLLFKGFFCTGHPYNDLL	YLDLGSKDATNKY 80
Db	275	ALERLENGYIYBQDGATWLRTTDF	EDDKDRLVIKSDGS----	YTFPLDIAYH--LNKL 328
Qy	81	K--GKKVDLYG--YGY-----	QCAGGTENKTACMYGGVTLHD	NNRLTEKKVPIN 128
Db	329	ERGFVDLIDIWGADHHGYIPRMAA	IEALGYSP-----	NOLEVEIQLVH 373
Qy	129	LWIDGKQTTVPIDKVKTSK-----	VOELDLQARHYLHGKFGLYNS	DSF----- 175
Db	374	LFEDGVQ-----	VKMSKRTGKSVTRDRLIEVGL	DATYF---FAMRSSDTHMFDMS 423
Qy	176	-----	GGKVQRGLIVFHSSEGSTV----	SYDLFDAGQGY 205
Db	424	LAKSTNDNPVYVQYAHARISSIL	RSKG--EQGLEVSKDANMSLLE	TEAEYDLLKVLGEF 482
Qy	206	PDPLL-----	RIYRDKNTINSNLHI	226
Db	483	ADVVAEAAVKRAPHRIVRVYNDL	ATAFHRFPYNSKNVLDMDN	LEV 526

RESULT 57

D86342

hypothetical protein F9H16.6 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
C:Accession: D86342

R:Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID: 21016719; PMID:11130712

[illegible]

Best Local Similarity 30.6%; Pred. No. 43; Mismatches 26; Conservative 8; Mismatches 35; Indels 16; Gaps 3;

Qy 74 KDATNKYKGVKVDLYGAYGYQCAGGTPNKTACMYGGVT-----LHDNNRLTEE 122
Db 412 KEGT--YGKKFNVAICHFFGQARGSLPSKFCDDYAVVLGHICVHVLAAAGLNGYMATVTN 469

Qy 123 KKVPINLWIDGKQTTVPIDKVKTSK 147
Db 470 LKSPVKNK---KCGATPITAMTIVK 491

RESULT 58
T10102
diphosphate-fructose-6-phosphate 1-phosphotransferase (EC 2.7.1.90) alpha chain - castor
N;Alternate names: 6-phosphofructokinase (pyrophosphate)
C;Species: Ricinus communis (castor bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10102
R;Todd, J.F.; Blakeley, S.D.; Dennis, D.T.
Gene 152, 181-186, 1995
A;Title: Structure of the genes encoding the alpha- and beta-subunits of castor pyrophosphate
A;Reference number: Z16949; MUID:95137384; PMID:7835697
A;Accession: T10102
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-617 <TOD>
A;Cross-references: UNIPROT:Q41140; UNIPARC:UPI0000013175D; EMBL:Z32849; NID:9483546; PIR:
C;Genetics: 30/3; 88/2; 126/1; 151/1; 189/1; 211/3; 239/3; 257/3; 284/3; 316/1; 340/3; 37
C;Superfamily: pyrophosphate-dependent phosphofructokinase, PfpB type; 6-phosphofructokin
C;Keywords: phosphotransferase

Query Match 6.9%; Score 85; DB 2; Length 617;
Best Local Similarity 30.2%; Pred. No. 43; Mismatches 35; Indels 16; Gaps 3;
Matches 26; Conservative 9;

Qy 74 KDATNKYKGVKVDLYGAYGYQCAGGTPNKTACMYGGVT-----LHDNNRLTEE 122
Db 412 KEGT--YGKKFNVAICHFFGQARGSLPSKFCDDYAVVLGHICVHVLAAAGLNGYMATATN 469

Qy 123 KKVPINLWIDGKQTTVPIDKVKTSK 148
Db 470 LKSNPVNKRCC---AAPITAMTIVKR 492

RESULT 59
B44858
lactococpin (EC 3.4.21.96) precursor [validated] - Lactobacillus paracasei (strain NCDO 1
N;Alternate names: cell-envelope-associated proteinase prtP; serine proteinase lp151
C;Species: Lactobacillus paracasei
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: B44858; C44858; A44850
R;Holck, A.; Naes, H.
J. Gen. Microbiol. 138, 1353-1364, 1992
A;Title: Cloning, sequencing and expression of the gene encoding the cell-envelope-assoc
A;Reference number: A44858; MUID:92381481; PMID:1512565
A;Accession: B44858
A;Molecule type: DNA
A;Residues: 1-1902 <HOL1>
A;Cross-references: UNIPROT:Q02470; UNIPARC:UPI00000130FF0; GB:M83946; NID:g149580; PID:
R;Naes, H.; Nissen-Meyer, J.
J. Gen. Microbiol. 138, 313-318, 1992
A;Title: Purification and N-terminal amino acid sequence determination of the cell-wall-
A;Reference number: A44850; MUID:92226694; PMID:1564442
A;Accession: A44850
A;Status: preliminary

[illegible]

```

Db      393 IKYGGQLYGFYFAALFKFPSSGEMNLKPIV-----DGSIPVTV--AKKDPGSL 446
QY      210 LRIYRN-----KTINGENLHIDLILYLT 232
Db      447 FQ-FNDKDELLFTLYVKEQISVADPNFMNLLRGQNLH-DLELYT 488

RESULT 61
AH1793
ABC transporter, ATP-binding protein homolog lin2894 [imported] - Listeria innocua (stra
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH1793
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Faihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1793
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-573 <GLA>
A;Cross-references: UNIPROT:Q92625; UNIPARC:UPI000000CC9EE; GB:AL592022; PIDN:CAC98120.1;
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2894
C;Superfamily: Becherichia coli ABC transporter mdIA; ATP-binding cassette homology

Query Match      6.8%; Score 84.5; DB 2; Length 573;
Best Local Similarity 23.3%; Pred. No. 43;
Matches 45; Conservative 30; Mismatches 81; Indels 37; Gaps 8;

QY      22 ALSNLRQI--YYNEKAITNKESDDQFLENTLLFKGF-----FTGH--PWYNDLLVD----- 70
Db      298 ALISLRKITEVLETPEDITYNENAPEQDLGTEVFRNVSPKYDGDTPALEDISFRANVG 357
QY      71 --LGSKDATNKYGGKVDLYGAYGYOCAGTGNKTACMGYGGVTLHDNNRLTEBKVPIN 128
Db      358 EMVGIVGATSGSGKSTLAQLIPRLY-----DPTGEVVIIGGTNLKDKINKTLRSTVSFV 410
QY      129 LWIDGKQTTVPIDKVKTSKKEVTQVELD-----LQARHYLHGKFGLYNS-----DSFGG 177
Db      411 LQRAILFSGTIADNLRHGKDKATIDEMEHASKIAQAEFIDKQAKLYEAPVSRGNFSG 470
QY      178 -----KVQGLI 184
Db      471 GQKQRLSITRGVI 483

RESULT 62
D71623
erythrocyte membrane protein pFEMP3 PFB0095c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C;Accession: D71623
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: D71623
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-2441 <GAR>
A;Cross-references: UNIPROT:O96124; UNIPARC:UPI00000082B5E; GB:AE001371; GB:AE001362; NID
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0095c
```

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Query Match      6.8%; Score 84.5; DB 2; Length 2441;
Best Local Similarity 31.6%; Pred. No. 2.6e+02;
Matches 31; Conservative 9; Mismatches 29; Indels 29; Gaps 5;

QY      2 EKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGH 61
Db      853 ENLEEYNETDLAKGKVTNKARENLEE---YNETDLAKGKVTNKARENL----- 899
QY      62 PWYNDLLVDLG-SKDATNK-----YKGKKV 85
Db      900 EYNE--TDLAKGKVTNKARENLEEYNETDLAKGKEV 935

RESULT 63
C89808
exotoxin 15 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89808
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89808
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-227 <KUR>
A;Cross-references: UNIPROT:Q99WG9; UNIPARC:UPI000000CACF0; GB:BA000018; PID:g13700324; P
A;Experimental source: strain N315
C;Genetics:
A;Gene: set15
C;Superfamily: toxic shock syndrome toxin

Query Match      6.8%; Score 84; DB 2; Length 227;
Best Local Similarity 21.2%; Pred. No. 15;
Matches 48; Conservative 42; Mismatches 90; Indels 46; Gaps 10;

QY      6 EINEKDLRKXSELQRN---ALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGH 62
Db      34 EVRSQATDLSLEYKKGFGFELTNVGYKGNKVTFFDINSQOIDVTL-----TG-- 81
QY      63 WYNDLLVDLGSKDATNKYGGKVDLYGAYGYOCAGTGNKTACMGYGGVTLHDNNRLTEE 122
Db      82 --NEKLTVRKDDDEVSN-----VDVFVRGSDKSAITTS-----IGGIT-KTNGTQHKD 127
QY      123 KKVPINLWID--GKOTT-VPIDKVKTSKKEVTQVELDLQARHYLHGKFGLYNSDSFGK 178
Db      128 TVQNVNLSVSKSTGQHTTSVTSEYYSIYKEISLKLDFKLRKHLIDKHDLKYTEPKDCK 187
QY      179 VQRGLIVFHSSEGSTVSYDLFDAQGVDPDTLLRIYRDNKTKTINSEN 224
Db      188 IR-----ITMKNGGYTFEL-----NKKLQPHRMGDTIDSRNI 220

RESULT 64
D86671
transposase of IS1077C [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86671
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: D86671
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-272 <STO>
A;Cross-references: UNIPROT:Q9CII8; UNIPARC:UPI000000C680D; GB:AE005176; PID:g12723243; P
A;Experimental source: strain IL1403
C;Genetics:
```

A:Gene: tra1077C

Query Match 6.8%; Score 84; DB 2; Length 272;
Best Local Similarity 21.5%; Pred. No. 19;
Matches 42; Conservative 30; Mismatches 67; Indels 56; Gaps 7;

QY 5 EEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPWY 64
DB 19 ERNVKDELLEKEMLK-----IRQ-----EHANAGYRPMRELLKQRGTHVNHKKV 62

QY 65 NDLLVDLGSKDATNKYKGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEERK 124
DB 63 QRLMKKGLRVTSYHKSRL-----YNSYKGKGVTAKN-----KLHRRFR----- 103

QY 125 VPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVORGLI 184
DB 104 -----TSIPHQKITDTTPEKYVEDGQKKCYLNPYIALFNSE-----VI 143

QY 185 VFH-SSEGSTVSVDL 198
DB 144 SYHISKQPSYQSIDI 158

RESULT 65
F70339
Glycerol kinase - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: F70339
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.

Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: F70339
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-492 <AQP>
A:Cross-references: UNIPROT:O66746; UNIPARC:UPI0000056365; GB:AE000690; NID:92983100; PI
A:Experimental source: strain VFS
C:Genetics:
A:Gene: glpK
C:Superfamily: xylulokinase

Query Match 6.8%; Score 84; DB 2; Length 492;
Best Local Similarity 25.7%; Pred. No. 39;
Matches 61; Conservative 30; Mismatches 74; Indels 72; Gaps 15;

QY 9 EKDLRKSELQNALSNLRQ---IYYNEKAITENKESDDQFLENTLLFKGFTGHPWYN 65
DB 44 EQDPLELWAVRKSLSSEVIQQVLKEINSIGITNQRE-----TVILWDXETGRPVYN 95

QY 66 DLL-VDLGSKDATNKYKGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEERK 124
DB 96 AILWQDLRTEDIC-----RKLSEYSEYKENT-----GLLLHPYFSASK--- 134

QY 125 VPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGK--FGLYNS-----DSFGK 178
DB 135 --VN-WI-----IENVNGVKKDE-----RGKVIQFTVDTWILMNLTKGK 171

QY 179 VQGRGLIVFHSSEGSTVSVD-LFDAQG-QYPTDLLRIYRONKNTNSP-NLHIDLILYT 232
DB 172 V-----HKTEPSNASRLLFNIRKLEYDDELLKIFRIPKNIIPVNESSLSFGYT 221

RESULT 66
T41863
chitinase chi-A orf126 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C:Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
A:Variety: Isolate T3
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41863
R:Gomi, S.; Majima, K.; Maeda, S.

J. Gen. Virol. 80, 1323-1337, 1999
A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A:Reference number: Z22020; MUID:99281911; PMID:10355780
A:Accession: T41863
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-552 <KAM>
A:Cross-references: UNIPROT:O92482; UNIPARC:UPI00000F4295; EMBL:L33180; NID:g3745835; PI
A:Experimental source: isolate T3
C:Superfamily: Serratia marcescens chitinase

Query Match 6.8%; Score 84; DB 2; Length 552;
Best Local Similarity 24.3%; Pred. No. 45;
Matches 45; Conservative 23; Mismatches 69; Indels 48; Gaps 11;

QY 32 YNEKAI---TENKESDDQFLENTLLFKGFTGHPWYNLLVDLGSKDATNKYKGKVDLY 88
DB 359 YDKIAVNVYAEAKSLDKIFLMTYDFKG-----AWSN---TDLGYQTTVYAFPSWSEELY 410

QY 89 GAYGYQC---AGGTPNKT---ACMYG---CVTLHDN-NRLTEKKVPIN-LWIDGKQT 136
DB 411 TTHYAVDALLEGQVDPNKIIIVGAVYGRWGTGVTNTNGNYFSGTNGPVGSTWEDG--- 467

QY 137 TVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVORGLIIVFHSSEGSTVS 196
DB 468 -----VDYRQIQKDLNNY-----VYTFDS-----AAQASYVFDKSKGDLISF 505

QY 197 DLFDA 201
DB 506 DSVD 510

RESULT 67
T44118
penicillin-binding protein 2 [imported] - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T44118
R:Ito, T.; Katayama, Y.; Hiramatsu, K.
Antimicrob. Agents Chemother. 43, 1449-1458, 1999
A:Title: Cloning and nucleotide sequence determination of the entire mec DNA of pre-meth
A:Reference number: Z22733; MUID:99278010; PMID:10348769
A:Accession: T44118
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-668 <ITO>
A:Cross-references: UNIPROT:Q54113; UNIPARC:UPI00000DA0B7; EMBL:D86934; PIDN:BAA82220.1
A:Experimental source: strain N315
C:Genetics:
A:Note: mecA
C:Superfamily: penicillin-binding protein 2B

Query Match 6.8%; Score 84; DB 2; Length 668;
Best Local Similarity 20.0%; Pred. No. 57;
Matches 63; Conservative 45; Mismatches 87; Indels 120; Gaps 15;

QY 4 SEINEKDLRKSE---LORNALSNLRQIYYNEK-----YDKKLQHEGQYRVITVDNSNTIAHTLIE 39
DB 261 SEELKQKEYKGYKDDAVIGKKGLEKL-----YDKKLQHEGQYRVITVDNSNTIAHTLIE 315

QY 40 NKESDDQFLENTLLFKGFTGHPWYNLLVDLGSKDATNKYKGKVDL-----YGAYGY 94
DB 316 KKKKGKQIQLTIDAK---VQKSIYNNMKNDYGSQTAIHPQTGELLALVSTPSYDV--- 369

QY 95 QCAGGTPNKTACMYGGVTLHDNNRLTEKKVP-INLWIDGKQTTVP--IDKVKTSKKEV 151
DB 370 -----PMY-GMSNEEYNKLTEDKKEPLLKNF---QITTSFGSTQKILTAMIGLN 415

QY 152 VQELDLQARHYLHGKFGLYNSDSFGG----- 177
DB 416 NKTLDKTSYKIDGK-GWQKQKSWGYNVTRVEVNGNIDLKQAISSNIPFARVALEL 474

QY 178 ---KVQGRGLIVFHSSEGSTVSVDLFDQAQ-----GQ-----YPTDLLRI 212

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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:08:30 ; Search time 76.7226 Seconds
(without alignments)
2142.628 Million cell updates/sec

Title: US-09-900-766-7
Perfect score: 1238
Sequence: 1 SEKSEINEKURKKSELOR.....RDKNKTINSENLHIDLXYLTT 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	257	1	ETXE STAAU
2	1023	82.6	257	1	ETXA STAAU
3	1023	82.6	257	1	ETXA STAAU
4	1023	82.6	257	2	O6G7Y7 STAAU
5	1023	82.6	260	2	Q931M4 STAAU
6	1018	82.2	261	2	Q5P8P6 STAAU
7	1013	81.8	257	2	Q6GFA8 STAAU
8	994	80.3	260	2	Q998U3 STAAU
9	971	78.4	219	2	Q6XZB9 STAAU
10	837	67.6	268	2	O761S7 STAAU
11	830	67.0	288	2	O85217 STAAU
12	825	66.6	154	2	Q6R2G0 STAAU
13	663	53.6	258	1	ETXD STAAU
14	496	40.1	152	2	Q6R2F9 STAAU
15	492.5	39.8	234	2	O5HFG0 STAAU
16	490.5	39.6	229	2	O6G8W7 STAAU
17	490.5	39.6	229	2	O8NW97 STAAU
18	461.5	37.3	258	2	Q9EZM4 STAAU
19	461.5	37.3	258	2	Q7A2Q6 STAAU
20	461.5	37.3	258	2	Q7A4X1 STAAU
21	446.5	36.1	251	2	O6YCN3 STAAU
22	446.5	36.1	251	2	O6GFM1 STAAU
23	414	33.4	254	2	O6GFM7 STAAU
24	387.5	31.3	260	2	Q7A4W6 STAAU
25	387.5	31.3	260	2	Q99T46 STAAU
26	387.5	31.3	261	2	Q9EZM8 STAAU
27	381	30.8	179	2	O52075 9ZZZZ
28	366	29.6	217	2	O8RR76 STAAU
29	366	29.6	241	1	ETXH STAAU
30	366	29.6	241	1	ETXH STAAU
31	366	29.6	241	2	Q6VAM8 STAAU

32	366	29.6	241	2	Q6GD45 STAAU	Q6GD45	staphylococ
33	348.5	28.2	242	2	Q7X0E8 STAAU	Q7X0E8	staphylococ
34	348.5	28.2	242	2	Q6GFM9 STAAU	Q6GFM9	staphylococ
35	341.5	27.6	225	2	Q8VVM1 STRPY	Q8VVM1	streptococ
36	340.5	27.5	243	2	Q7X0E7 STAAU	Q7X0E7	staphylococ
37	339.5	27.4	242	2	O5D1J9 STAAU	O5D1J9	staphylococ
38	339.5	27.4	242	2	O8S383 STAAU	O8S383	staphylococ
39	339.5	27.4	242	2	Q7A2Q5 STAAU	Q7A2Q5	staphylococ
40	339.5	27.4	242	2	Q7A4W8 STAAU	Q7A4W8	staphylococ
41	337.5	27.3	218	2	O52T95 STAAU	O52T95	staphylococ
42	337	27.2	240	2	Q9F0L7 STAAU	Q9F0L7	staphylococ
43	337	27.2	240	2	Q7A2N9 STAAU	Q7A2N9	staphylococ
44	337	27.2	240	2	Q7A4K9 STAAU	Q7A4K9	staphylococ
45	336.5	27.2	209	2	O52TA0 STAAU	O52TA0	staphylococ
46	336	27.1	240	2	O8NXJ5 STAAU	O8NXJ5	staphylococ
47	335.5	27.1	210	2	O52T97 STAAU	O52T97	staphylococ
48	335.5	27.1	218	2	Q8RR75 STAAU	Q8RR75	staphylococ
49	335.5	27.1	225	2	Q9L921 STRPY	Q9L921	streptococ
50	334.5	27.0	225	2	Q99Z21 STRPY	Q99Z21	streptococ
51	332.5	26.9	242	2	Q7X0E6 STAAU	Q7X0E6	staphylococ
52	320	25.8	239	2	Q7A4W7 STAAU	Q7A4W7	staphylococ
53	320	25.8	239	2	Q99T47 STAAU	Q99T47	staphylococ
54	319.5	25.8	242	2	O6G7U1 STAAU	O6G7U1	staphylococ
55	319.5	25.8	242	2	O8NVW3 STAAU	O8NVW3	staphylococ
56	318.5	25.7	256	2	Q8VLW7 STAAU	Q8VLW7	staphylococ
57	316.5	25.6	242	2	Q93CC6 STAAU	Q93CC6	staphylococ
58	316.5	25.6	242	2	O5HHJ9 STAAU	O5HHJ9	staphylococ
59	316	25.5	239	2	Q9EZM7 STAAU	Q9EZM7	staphylococ
60	312	25.2	86	2	Q711S9 STAIN	Q711S9	staphylococ
61	310	25.0	242	2	Q6G7U0 STAAU	Q6G7U0	staphylococ
62	310	25.0	242	2	O8NVW2 STAAU	O8NVW2	staphylococ
63	309	25.0	163	2	O6R2F8 STAAU	O6R2F8	staphylococ
64	309	25.0	242	2	O54476 STAAU	O54476	staphylococ
65	309	25.0	242	2	Q93CC5 STAAU	Q93CC5	staphylococ
66	309	25.0	242	2	O5HHK0 STAAU	O5HHK0	staphylococ
67	302	24.4	239	2	Q6GFM8 STAAU	Q6GFM8	staphylococ
68	300.5	24.3	250	2	Q5MAA8 STAAU	Q5MAA8	staphylococ
69	300.5	24.3	266	1	ETXB STAAU	ETXB	staphylococ
70	300.5	24.3	266	2	Q7BBY8 STAAU	Q7BBY8	staphylococ
71	300.5	24.3	266	2	O5HHH9 STAAU	O5HHH9	staphylococ
72	299.5	24.2	239	2	O5MAB7 STAAU	O5MAB7	staphylococ
73	298	24.1	261	2	Q6YCN4 STAAU	Q6YCN4	staphylococ
74	298	24.1	261	2	Q6GFM0 STAAU	Q6GFM0	staphylococ
75	296.5	23.9	256	2	O5XC17 STRP6	O5XC17	streptococ
76	295.5	23.9	251	1	SPEA STRP8	SPEA	streptococ
77	295.5	23.9	251	1	SPEA STRP8	SPEA	streptococ
78	295	23.8	177	2	Q6R1Y7 STAAU	Q6R1Y7	staphylococ
79	294.5	23.8	251	2	Q8K6K5 STRP3	Q8K6K5	streptococ
80	291.5	23.5	261	2	Q6XXM3 STAAU	Q6XXM3	staphylococ
81	290.5	23.5	261	2	Q6XXM5 STAAU	Q6XXM5	staphylococ
82	288.5	23.3	261	2	Q6XXM4 STAAU	Q6XXM4	staphylococ
83	285.5	23.1	239	2	Q06531 STAAU	Q06531	staphylococ
84	285.5	23.1	239	2	O06532 STAAU	O06532	staphylococ
85	285.5	23.1	266	1	ENTC3 STAAU	ENTC3	staphylococ
86	285.5	23.1	266	1	ENTC3 STAAU	ENTC3	staphylococ
87	285.5	23.1	266	1	ENTC3 STAAU	ENTC3	staphylococ
88	285.5	23.1	266	2	O54A76 STAAU	O54A76	staphylococ
89	284.5	23.0	239	2	Q06535 STAAU	Q06535	staphylococ
90	283.5	22.9	239	2	O05157 STAIN	O05157	staphylococ
91	283.5	22.9	266	2	O8NXJ6 STAAU	O8NXJ6	staphylococ
92	282.5	22.8	239	2	O06533 STAAU	O06533	staphylococ
93	281.5	22.7	266	1	ENTC2 STAAU	ENTC2	staphylococ
94	281.5	22.7	266	2	O53X04 STAAU	O53X04	staphylococ
95	280.5	22.7	222	2	Q6XZE6 STAAU	Q6XZE6	staphylococ
96	280.5	22.7	239	2	Q6ST49 STAAU	Q6ST49	staphylococ
97	279.5	22.6	236	2	Q54696 STRPY	Q54696	streptococ
98	279.5	22.6	271	2	Q9F0L6 STAAU	Q9F0L6	staphylococ
99	278.5	22.5	236	2	P97163 STRPY	P97163	streptococ
100	278.5	22.5	239	2	O53678 STAAU	O53678	staphylococ
101	277.5	22.4	222	2	Q938P4 STRPY	Q938P4	streptococ
102	277.5	22.4	222	2	Q985Z4 STRPY	Q985Z4	streptococ
103	277.5	22.4	234	2	Q9R5X4 STAP	Q9R5X4	staphylococ
104	277.5	22.4	236	2	Q54779 STRPY	Q54779	streptococ

105	276.5	22.3	222	2	Q9R931_STRPY	Q9r931 streptococc	178	217	17.5	240	2	Q8P2R5_STRP8	Q8p2r5 streptococc
106	272.5	22.0	236	2	Q57453_STRPY	Q57453 streptococc	179	216	17.4	210	2	Q9K2G9_STRPY	Q9k2g9 streptococc
107	272.5	22.0	239	2	Q06534_STAAU	Q06534 staphylococ	180	214	17.3	234	2	Q76FM2_STRDY	Q76fm2 streptococc
108	269.5	21.8	260	2	Q54971_STRPY	Q54971 streptococc	181	213	17.2	234	2	Q76FM3_STRDY	Q76fm3 streptococc
109	267.5	21.6	260	2	Q54738_STRPY	Q54738 streptococc	182	208	16.8	234	2	Q76FN0_STRREQ	Q76fn0 streptococc
110	267.5	21.6	260	2	Q54739_STRPY	Q54739 streptococc	183	205	16.6	234	2	Q76FM5_STRREQ	Q76fm5 streptococc
111	267.5	21.6	260	2	Q79X14_STRP3	Q79x14 streptococc	184	203	16.4	234	2	Q76FM7_STRREQ	Q76fm7 streptococc
112	266.5	21.5	266	1	ENTC1_STAAU	Q01553 staphylococ	185	201	16.2	257	2	Q7A5A7_STAAU	Q7a5a7 staphylococ
113	264.5	21.4	258	2	Q7X0E4_STAAU	Q7x0e4 staphylococ	186	201	16.2	257	2	Q95TP7_STAAU	Q95tp7 staphylococ
114	264.5	21.4	258	2	Q6GFN2_STAAU	Q6gfn2 staphylococ	187	199	16.1	234	2	Q76FM3_STRREQ	Q76fm3 streptococc
115	262.5	21.2	233	2	Q52T98_STAAU	Q52t98 staphylococ	188	199	16.1	236	2	Q9L920_9STRE	Q9l920 streptococc
116	262.5	21.2	258	2	Q9ZNF2_STAAU	Q9zmf2 staphylococ	189	198	16.0	234	2	Q76FM9_STAAU	Q76fm9 streptococc
117	259.5	21.0	222	2	Q6XZB7_STAAU	Q6xzb7 staphylococ	190	197	15.9	136	2	Q7A4X0_STAAU	Q7a4x0 staphylococ
118	258.5	20.9	258	2	Q5D1K7_STAAU	Q5d1k7 staphylococ	191	197	15.9	136	2	Q99T49_STAAU	Q99t49 staphylococ
119	256.5	20.7	264	2	Q764P6_STAIN	Q764p6 staphylococ	192	197	15.9	195	2	Q6VCN2_STAAU	Q6vcn2 staphylococ
120	256	20.7	209	2	Q9RQ05_STRPY	Q9rq05 streptococc	193	197	15.9	234	2	Q8G9K7_STRREQ	Q8g9k7 streptococc
121	255.5	20.6	233	2	Q8RR77_STAAU	Q8rr77 staphylococ	194	197	15.9	234	2	Q9JRR3_STRREQ	Q9jrr3 streptococc
122	255.5	20.6	258	1	ETXG_STAAU	P0a017 staphylococ	195	197	15.9	236	1	SPEH_STRPY	Q9x5c8 streptococc
123	255.5	20.6	258	1	ETXG_STAAU	P0a018 staphylococ	196	193	15.6	232	2	Q7BAE3_STRPY	Q7bae3 streptococc
124	255.5	20.6	258	2	Q7X0E5_STAAU	Q7x0e5 staphylococ	197	187	15.1	256	2	Q9S1H9_STRPY	Q9s1h9 streptococc
125	255.5	20.6	258	2	Q9EZM3_STRPY	Q9ezm3 staphylococ	198	187	15.1	256	2	Q9X9R8_STRPY	Q9x9r8 streptococc
126	255.5	20.6	258	2	Q5Q043_STRPY	Q5q043 streptococc	199	185	14.9	235	1	SPEC_STRP6	Q5xb82 streptococc
127	253	20.4	209	2	Q9LAD8_STRPY	Q9lad8 streptococc	200	185	14.9	235	1	SPEC_STRP6	Q8nxx2 streptococc
128	253	20.4	209	2	Q9LAE0_STRPY	Q9lae0 streptococc	201	185	14.9	235	1	SPEC_STRPY	Q8nxx2 streptococc
129	253	20.4	209	2	Q76LS8_STAAU	Q76ls8 staphylococ	202	180	14.5	235	2	Q6LD36_STRPY	P13380 streptococc
130	251.5	20.3	259	2	Q9LAC6_STRPY	Q9lac6 streptococc	203	163	13.6	206	2	Q54512_STRPY	Q54512 streptococc
131	251	20.3	209	2	Q9LAD1_STRPY	Q9lad1 streptococc	204	163	13.2	206	2	Q9EZM5_STAAU	Q9ezm5 staphylococ
132	251	20.3	209	2	Q9LAD1_STRPY	Q9lad1 streptococc	205	160.5	13.0	108	2	Q7A5A8_STAAU	Q7a5a8 staphylococ
133	250.5	20.2	258	2	Q79IV2_STAAU	Q79iv2 staphylococ	206	144	11.6	62	2	Q99TP8_STRPY	Q99tp8 staphylococ
134	249	20.1	209	2	Q9LAC4_STRPY	Q9lac4 streptococc	207	144	11.6	62	2	Q99TP8_STAAU	Q99tp8 staphylococ
135	249	20.1	209	2	Q9LAE1_STRPY	Q9lae1 streptococc	208	138	11.1	96	2	Q5XE11_STRP6	Q5xe11 streptococc
136	249	20.1	233	2	Q76WJ7_STRPY	Q76wj7 streptococc	209	135	10.9	259	2	Q70EW3_9STRE	Q70ew3 streptococc
137	248.5	20.1	258	2	Q5D1K4_STAAU	Q5d1k4 staphylococ	210	135	10.9	259	2	Q5W1M5_9STRE	Q5w1m5 streptococc
138	247.5	20.0	220	2	Q79AQ0_STRPY	Q79aq0 streptococc	211	135	10.9	262	2	Q8P0S0_STRP8	Q8p0s0 streptococc
139	247	20.0	209	2	Q9LAC5_STRPY	Q9lac5 streptococc	212	134.5	10.9	98	2	Q5XC18_STRP6	Q5xc18 streptococc
140	247	20.0	223	2	Q52TA2_STAAU	Q52ta2 staphylococ	213	134	10.8	227	2	Q849U3_STRPY	Q849u3 streptococc
141	246	19.9	209	2	Q9LAC7_STRPY	Q9lac7 streptococc	214	134	10.8	262	2	Q70EW2_9STRE	Q70ew2 streptococc
142	245.5	19.8	159	2	Q6R2G1_STAAU	Q6r2g1 staphylococ	215	134	10.8	262	2	Q5W1M4_9STRE	Q5w1m4 streptococc
143	245.5	19.8	214	2	Q6XZE8_STAAU	Q6xze8 staphylococ	216	130	10.5	259	2	Q918J1_9CAUD	Q918j1 temperate p
144	244.5	19.7	258	2	Q7WS59_STAAU	Q7ws59 staphylococ	217	127.5	10.3	62	2	Q8NYV9_STAAU	Q8nyv9 staphylococ
145	244	19.7	209	2	Q9LAD2_STRPY	Q9lad2 streptococc	218	126	10.2	209	2	Q879B0_STRP3	Q879b0 streptococc
146	244	19.7	209	2	Q9LAD6_STRPY	Q9lad6 streptococc	219	126	10.2	233	2	Q849U4_STRPY	Q849u4 streptococc
147	243.5	19.7	191	2	Q4ZJR6_STRPY	Q4zjr6 streptococc	220	123	9.9	132	2	Q9EZM6_STAAU	Q9ezm6 staphylococ
148	243	19.6	207	2	Q7WY99_STRCB	Q7wy99 streptococc	221	123	9.9	133	2	Q7A4W9_STAAU	Q7a4w9 staphylococ
149	243	19.6	233	2	Q6VB17_STRCB	Q6vb17 streptococc	222	123	9.9	133	2	Q99T48_STAAU	Q99t48 staphylococ
150	242	19.5	209	2	Q5Q044_STRPY	Q5q044 streptococc	223	122	9.9	156	2	Q71US9_STRPY	Q71us9 streptococc
151	242	19.5	209	2	Q5Q045_STRPY	Q5q045 streptococc	224	120	9.7	883	2	Q4YAD4_PLABE	Q4yad4 plasmodium
152	242	19.5	209	2	Q9LAD9_STRPY	Q9lad9 streptococc	225	118.5	9.6	156	2	Q7ETR4_STRPY	Q7etr4 streptococc
153	242	19.5	233	2	Q8N289_STRP8	Q8n289 streptococc	226	116.5	9.4	231	2	Q9RN32_STAAU	Q9rn32 staphylococ
154	241	19.5	209	2	Q9LAC4_STRPY	Q9lac4 streptococc	227	116	9.4	231	2	Q9ZFS5_STAAU	Q9zfs5 staphylococ
155	240	19.4	209	2	Q9LAD4_STRPY	Q9lad4 streptococc	228	116	9.4	231	2	Q6GJP2_STAAU	Q6gjp2 staphylococ
156	239	19.3	209	2	Q9LAC3_STRPY	Q9lac3 streptococc	229	115.5	9.3	180	2	Q5XBU3_STRP6	Q5xbu3 streptococc
157	239	19.3	209	2	Q9LAC8_STRPY	Q9lac8 streptococc	230	114.5	9.2	231	2	Q6C58_STAAU	Q6c58 staphylococ
158	239	19.3	258	2	Q5X9R9_STRP6	Q5x9r9 streptococc	231	114.5	9.2	231	2	Q8NY48_STAAU	Q8ny48 staphylococ
159	238	19.2	256	2	Q9S1H8_STRPY	Q9s1h8 streptococc	232	114	9.2	231	2	Q9RN33_STAAU	Q9rn33 staphylococ
160	237.5	19.2	180	2	Q6DTL6_STRPY	Q6dtl6 streptococc	233	113.5	9.2	1400	2	Q86AL1_DICDI	Q86al1 dicyostelli
161	237	19.1	209	2	Q9LAD5_STRPY	Q9lad5 streptococc	234	113	9.1	232	2	Q7A7H2_STAAU	Q7a7h2 staphylococ
162	234	18.9	179	2	Q56D15_STRPY	Q56d15 streptococc	235	113	9.1	232	2	Q99WHA_STAAU	Q99wha staphylococ
163	234	18.9	209	2	Q9LAD7_STRPY	Q9lad7 streptococc	236	112.5	9.1	237	2	Q8P0R9_STRP8	Q8p0r9 streptococc
164	233	18.8	209	2	Q9LAD3_STRPY	Q9lad3 streptococc	237	111.5	9.0	443	2	Q5HL39_STAEP	Q5hl39 staphylococ
165	232	18.7	233	2	Q99XW1_STRPY	Q99xw1 streptococc	238	111.5	9.0	443	2	Q8CMZ5_STAEP	Q8cmz5 staphylococ
166	231.5	18.7	180	2	Q6DTL4_STRPY	Q6dtl4 streptococc	239	111.5	9.0	1158	2	Q4N1Y5_THEPA	Q4n1y5 thelleria p
167	231	18.7	209	2	Q9LAD0_STRPY	Q9lad0 streptococc	240	109.5	8.8	680	2	Q4Z2H5_PLABE	Q4z2h5 plasmodium
168	228	18.4	180	2	Q56D03_STRPY	Q56d03 streptococc	241	109	8.8	232	2	Q9ZFS4_STAAU	Q9zfs4 staphylococ
169	228	18.4	183	2	Q6DTL3_STRPY	Q6dtl3 streptococc	242	109	8.8	232	2	Q6C56_STAAU	Q6c56 staphylococ
170	227	18.3	259	2	Q936G4_STAAU	Q936g4 staphylococ	243	109	8.8	232	2	Q6GJPI_STAAU	Q6gjpi staphylococ
171	226.5	18.3	178	2	Q56D04_STRPY	Q56d04 streptococc	244	109	8.8	232	2	Q5HIP4_STAAC	Q5hip4 staphylococ
172	224	18.1	183	2	Q6DTL5_STRPY	Q6dtl5 streptococc	245	109	8.8	232	2	Q8NY46_STAAU	Q8ny46 staphylococ
173	221	17.9	180	2	Q4ZJR7_STRPY	Q4zjr7 streptococc	246	108.5	8.8	1176	2	Q4U991_THEAN	Q4u991 thelleria a
174	220.5	17.8	131	2	Q7CEP2_STRP3	Q7cep2 streptococc	247	107.5	8.7	234	1	TSST_STAAU	P06886 staphylococ
175	220	17.8	234	1	SPEG_STRP3	Q8k8g7 streptococc	248	107.5	8.5	234	2	Q8RSX9_STAAU	Q8rsx9 staphylococ
176	218	17.6	183	2	Q6DTL1_STRPY	Q6dtl1 streptococc	249	105.5	8.5	234	2	Q54462_STAAU	Q54462 staphylococ
177	217	17.5	234	1	SPEG_STRPY	Q9x5c7 streptococc	250	105.5	8.5	234	2	Q7A2N8_STAAU	Q7a2n8 staphylococ

251	105.5	8.5	234	2	Q7A4K7_STAAN	Q7A4K7 staphylococ	RT	enterotoxin gene."
252	105	8.5	226	2	Q5HIP9_STAAC	O5hip9 staphylococ	RL	J. Bacteriol. 170:2954-2960 (1988).
253	104	8.4	226	2	Q6GC64_STAAS	Q6gc64 staphylococ	RN	[2]
254	104	8.4	226	2	Q8NV54_STAAM	Q8nv54 staphylococ	RP	3D-STRUCTURE MODELING.
255	104	8.4	553	2	Q4N6P4_THEPA	Q4n6p4 thelleria p	RX	MEDLINE=96022987; PubMed=7552730;
256	104	8.4	582	2	Q4XJ33_PLACH	Q4xj33 plasmodium	RA	Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
257	103.5	8.4	2232	2	Q7RRK8_PLAYO	Q7rrk8 plasmodium	RX	"Residues defining V beta specificity in staphylococcal
258	103	8.3	1147	2	Q8KERO_FUSNU	Q8kero fusobacteri	RT	enterotoxins."
259	102.5	8.3	967	2	Q4XZHW_PLACH	Q4xzhw plasmodium	RL	Nat. Struct. Biol. 2:680-686 (1995).
260	102	8.2	232	2	Q8NY47_STAAM	Q8ny47 staphylococ	CC	-!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
261	102	8.2	234	2	Q6GC57_STAAS	Q6gc57 staphylococ	CC	staphylococcal food poisoning syndrome. The illness characterized
262	101.5	8.2	771	2	Q7RG71_PLAYO	Q7rg71 plasmodium	CC	by high fever, hypotension, diarrhea, shock, and in some cases
263	101	8.2	232	2	Q7A7H3_STAAN	Q7a7h3 staphylococ	CC	death.
264	101	8.2	232	2	Q99WH5_STAAM	Q99wh5 staphylococ	CC	-!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
265	101	8.2	238	2	Q8L3E1_STRDY	Q8l3e1 streptococ	CC	for the toxin interaction with MHC class II (By similarity).
266	101	8.2	569	2	Q8I2T6_PLAF7	Q8i2t6 plasmodium	CC	-!- SUBCELLULAR LOCATION: Secreted.
267	100.5	8.1	608	2	Q7R922_PLAYO	Q7r922 plasmodium	CC	-!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
268	100	8.1	279	2	Q4X8R2_PLACH	Q4x8r2 plasmodium	CC	family.
269	100	8.1	2251	2	Q8IKB6_PLAF7	Q8ikb6 plasmodium	CC	-----
270	99.5	8.0	231	2	Q7A7H4_STAAN	Q7a7h4 staphylococ	CC	This Swiss-Prot entry is copyright. It is produced through a collaboration
271	99.5	8.0	231	2	Q99WH6_STAAM	Q99wh6 staphylococ	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
272	99.5	8.0	602	2	Q8IB95_PLAF7	Q8ib95 plasmodium	CC	the European Bioinformatics Institute. There are no restrictions on its
273	99.5	8.0	733	2	Q7R918_PLAYO	Q7r918 plasmodium	CC	use as long as its content is in no way modified and this statement is not
274	99.5	8.0	1811	2	Q8IL76_PLAF7	Q8il76 plasmodium	CC	removed.
275	98.5	8.0	234	2	Q9F0L4_STAAN	Q9f0l4 staphylococ	CC	-----
276	98.5	8.0	468	2	Q4L308_STAHP	Q4l308 staphylococ	DR	EMBL; M21319; AAA26617.1; -; Genomic_DNA.
277	98.5	8.0	611	2	Q4XFQ2_PLACH	Q4xfq2 plasmodium	DR	PIR; A28179; A28179.
278	97.5	7.9	655	2	Q4YMT7_PLABE	Q4ymt7 plasmodium	DR	PDB; 1SBE; Model; @=28-257.
279	97.5	7.9	1636	2	Q4XZ26_PLACH	Q4xz26 plasmodium	DR	InterPro; IPR006177; Bctrl tox.
280	97	7.8	232	2	Q6GC59_STAAS	Q6gc59 staphylococ	DR	InterPro; IPR006123; Stap/Strep toxin.
281	97	7.8	232	2	Q8NY49_STAAM	Q8ny49 staphylococ	DR	InterPro; IPR006126; Stap/Strep tox.
282	97	7.8	463	2	Q7V2X1_PROMP	Q7v2x1 prochloroco	DR	InterPro; IPR006173; Staph tox OB.
283	97	7.8	614	2	Q4YW78_PLABE	Q4yw78 plasmodium	DR	Pfam; PF02876; Stap_Strip_toxin; 1.
284	96.5	7.8	588	2	Q4NRF6_THEPA	Q4nrf6 thelleria p	DR	Pfam; PF01123; Stap_Strip_toxin; 1.
285	96.5	7.8	617	2	Q69W78_ORYSA	Q69w78 oryza sativ	DR	PRINTS; PR00279; BACTELOXIN
286	96.5	7.8	632	2	Q4H333_9CAUD	Q4h333 streptococ	DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
287	96.5	7.8	1100	2	Q55F96_DICDI	Q55f96 dictyosteli	DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
288	96	7.8	227	2	Q6GC55_STAAS	Q6gc55 staphylococ	DR	3D-structure; Antigen; Direct protein sequencing; Enterotoxin;
289	96	7.8	227	2	Q5HIP3_STAAC	O5hip3 staphylococ	KW	Metal-binding; Signal; Superantigen; Toxin; Zinc.
290	96	7.8	227	2	Q7A7H1_STAAN	Q7a7h1 staphylococ	FT	SIGNAL 1 27
291	96	7.8	227	2	Q8NV45_STAAM	Q8nv45 staphylococ	FT	CHAIN 28 257 Enterotoxin type E.
292	96	7.8	227	2	Q99WH3_STAAM	Q99wh3 staphylococ	FT	METAL 211 211 Zinc (By similarity).
293	96	7.8	495	2	Q7RDT5_PLAYO	Q7rdt5 plasmodium	FT	METAL 249 249 Zinc (By similarity).
294	95.5	7.7	150	1	RS19E_THEVO	Q97cu4 thermoplasm	FT	METAL 251 251 Zinc (By similarity).
295	95.5	7.7	1307	2	Q4YVS2_PLABE	Q4yvs2 plasmodium	FT	HELIX 33 35
296	95	7.7	709	2	Q4HM91_CAMLA	Q4hm91 campylobact	FT	HELIX 39 41
297	94.5	7.6	291	2	Q9CDI9_LACIA	Q9cdi9 lactococcus	FT	STRAND 42 42
298	94.5	7.6	402	2	Q5HN31_STAEO	Q5hn31 staphylococ	FT	TURN 46 47
299	94.5	7.6	402	2	Q8CRU1_STAEP	Q8cru1 staphylococ	FT	HELIX 48 51
300	94.5	7.6	820	1	GORK_ARATH	Q94a76 arabidopsis	FT	HELIX 52 54
							FT	STRAND 59 64
							FT	TURN 66 67
							FT	STRAND 69 69
							FT	TURN 73 74
							FT	STRAND 75 79
							FT	TURN 83 84
							FT	STRAND 90 94
							FT	STRAND 98 104
							FT	TURN 105 106
							FT	STRAND 109 113
							FT	STRAND 115 116
							FT	TURN 118 119
							FT	STRAND 128 132
							FT	STRAND 135 137
							FT	TURN 139 140
							FT	STRAND 142 142
							FT	STRAND 152 152
							FT	STRAND 154 155
							FT	TURN 156 157
							FT	STRAND 163 163
							FT	STRAND 171 171
							FT	STRAND 173 175
							FT	HELIX 176 190

ALIGNMENTS

RESULT 1
ETXE_STAAN STANDARD; PRT; 257 AA.
AC P12953;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Enterotoxin type E precursor (SEE).
GN Name-entE;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 28-74.
RC STRAIN=MJB265;
RX MEDLINE=88257005; PubMed=3384800;
RA Couch J.B., Soltis M.T., Betley M.J.;
RT "Cloning and nucleotide sequence of the type E staphylococcal

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FT TURN 191 191
FT STRAND 203 211
FT STRAND 219 221
FT STRAND 227 227
FT STRAND 234 239
FT STRAND 242 244
FT STRAND 245 247
FT STRAND 249 257
SQ SEQUENCE 257 AA; 29358 MW; 27EDA94B97770CE3 CRC64;

Query Match 100.0%; Score 1238; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.2e-93;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSKSELQNALSNLRQIYYNEKAITENKSDDOFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSKSELQNALSNLRQIYYNEKAITENKSDDOFLENTLLFKGFFTG 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYCAGGTPNKTCMYGCVTLHDNNRLT 120
DB 85 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYCAGGTPNKTCMYGCVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTYQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTYQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVPHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLHIDLILYTT 233
DB 205 RGLIVPHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLHIDLILYTT 257

RESULT 2
ETXA STAAU
ID BTA STAAU STANDARD; PRT; 257 AA.
AC POA0L2; P13163;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Enterotoxin type A precursor (SEA).
GN Name=entA;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PRI337;
RX MEDLINE=88086892; PubMed=3335483;
RA Betley M.J., Mekalanos J.J.;
RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
RL J. Bacteriol. 170:34-41(1988).
RN [2]
RP PROTEIN SEQUENCE OF 25-257.
RX MEDLINE=87222293; PubMed=3584106;
RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
RT "Complete amino acid sequence of staphylococcal enterotoxin A.";
RL J. Biol. Chem. 262:7006-7013(1987).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95354648; PubMed=7628431;
RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohlsten M., Kalland T.,
RA Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
RT "Crystal structure of the superantigen staphylococcal enterotoxin type A.";
RL EMBO J. 14:3292-3301(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=97113025; PubMed=8943278; DOI=10.1074/jbc.271.50.32212;
RA Sundstrom M., Hallen D., Svensson A., Schad E., Dohlsten M.,
RA Abrahamson L.;
RT "The Co-crystal structure of staphylococcal enterotoxin type A with Zn2+ at 2.7-A resolution. Implications for major histocompatibility complex class II binding.";
RL J. Biol. Chem. 271:32212-32216(1996).
RN [5]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal enterotoxins.";
RL Nat. Struct. Biol. 2:680-686(1995).
RN [6]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=97334373; PubMed=9191070; DOI=10.1006/jmbi.1997.1023;
RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT "A structural and functional comparison of staphylococcal enterotoxins A and C2 reveals remarkable similarity and dissimilarity.";
RL J. Mol. Biol. 269:270-280(1997).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
CC -!- COPACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary for the toxin interaction with MHC class II.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: This toxin seems to be coded by a bacteriophage.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
DR EMBL; M18970; AAA26681.1; -; Genomic_DNA.
DR PIR; A28664; A28664.
DR PDB; 1DQY; X-ray; A=25-257.
DR PDB; 1ESF; X-ray; A/B=25-257.
DR PDB; 1I4G; X-ray; A/B=25-257.
DR PDB; 1I4H; X-ray; A/B=25-257.
DR PDB; 1LO5; X-ray; D=25-257.
DR PDB; 1SEA; Model; @=25-257.
DR PDB; 1SXT; X-ray; A/B=25-257.
DR SMR; POA0L2; 25-257.
DR InterPro; IPR006177; Bcrl toxin.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR 3D-structure; Antigen; Direct protein sequencing; Enterotoxin;
KW Metal-binding; Signal; Superantigen; Toxin; Zinc.
FT SIGNAL 1 24
FT CHAIN 25 257 Enterotoxin type A.
FT METAL 211 211 Zinc.
FT METAL 249 249 Zinc.
FT METAL 251 251 Zinc.
FT DISULFID 120 130
FT CONFLICT 242 242
FT HELIX 33 35 T -> S (in Ref. 2).
FT HELIX 39 41
FT TURN 44 45
FT HELIX 46 55
FT STRAND 59 65
FT STRAND 75 78
FT TURN 79 80
FT STRAND 90 94
FT STRAND 98 104
FT TURN 105 106
FT STRAND 109 114
FT STRAND 116 116
FT HELIX 117 119

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FT TURN 122 123
FT TURN 126 127
FT STRAND 128 132
FT STRAND 135 137
FT TURN 139 140
FT STRAND 142 148
FT STRAND 151 155
FT TURN 156 157
FT STRAND 158 160
FT TURN 164 165
FT STRAND 168 171
FT STRAND 173 175
FT HELIX 176 191
FT TURN 193 194
FT HELIX 197 199
FT TURN 200 200
FT STRAND 205 211
FT STRAND 218 221
FT TURN 222 223
FT TURN 227 228
FT TURN 230 232
FT TURN 233 237
FT HELIX 238 239
FT TURN 242 244
FT STRAND 246 247
FT TURN 249 255
SQ SEQUENCE 257 AA; ADEBF5BCA1F14677 CRC64;

Query Match      82.6%; Score 1023; DB 1; Length 257;
Best Local Similarity 82.0%; Pred. No. 6e-76;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDOFLNTLIFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDOFLNTLIFKGFFTD 84

QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDFDSKDIDVYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKXEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EEKVPINLWIDGKQNTVPLETVKTKNKNVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDKNKTINSENHLDLYLTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDKNKTINSENHLDIYLYTS 257

RESULT 3
ETXA STAAW STANDARD; PRT; 257 AA.
AC POA0L1; P13163;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Enterotoxin type A precursor (SEA).
GN Name-entA; OrderedLocusNames=MW1889;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases

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CC death (By similarity).
CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; BA000033; BAB95754.1; -; Genomic_DNA.
CC SMR; POA0L1; 25-257.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF02876; Staph_Strip_tox_C; 1.
DR Pfam; PF01123; Staph_Strip_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Antigen; Complete proteome; Enterotoxin; Metal-binding; Signal;
KW Superantigen; Toxin; Zinc.
FT SIGNAL 1 24 By similarity.
FT CHAIN 25 257 Enterotoxin type A.
FT METAL 211 211 Zinc (By similarity).
FT METAL 249 249 Zinc (By similarity).
FT METAL 251 251 Zinc (By similarity).
FT DISULFID 120 130 By similarity.
SQ SEQUENCE 257 AA; 29669 MW; ADEBF5BCA1F14677 CRC64;

Query Match      82.6%; Score 1023; DB 1; Length 257;
Best Local Similarity 82.0%; Pred. No. 6e-76;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDOFLNTLIFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDOFLNTLIFKGFFTD 84

QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDFDSKDIDVYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKXEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EEKVPINLWIDGKQNTVPLETVKTKNKNVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDKNKTINSENHLDLYLTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDKNKTINSENHLDIYLYTS 257

RESULT 4
Q6GY7 STAAW PRELIMINARY; PRT; 257 AA.
AC Q6GY7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enterotoxin type A.
GN OrderedLocusNames=SAS1872;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,

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RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.,
RA "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571857; CAG43678.1; -; Genomic_DNA.
DR SMR; Q6G7Y7; 25-257.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph/Strep_tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 257 AA; 29669 MW; ADEBF5BCA1F14677 CRC64;

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 6e-76;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELORNALSNLQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAKTENKESHDOFLQHTILFKGFFTD 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIVDYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQNTVPLETKNKNVTVOELDLQARRYLQEKYLYNSDVDFGKVKQ 204
QY 181 RGLIVFHSSEGSVSYDLFDAQGYPDTLRIYRDNKTINSENHLHDLYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQGYSTLLRIYRDNKTINSENMMHIDIYLYTS 257

RESULT 5
Q931M4 STAAAM PRELIMINARY; PRT; 260 AA.
AC Q931M4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin P.
GN Names-sep; OrderedLocNames-SAV1948;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE-21311952; PubMed-11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshina K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "whole genome sequencing of methicillin-resistant Staphylococcus
RL Lancet 357:1225-1240(2001).
DR EMBL; BA000017; BAB58110.1; -; Genomic_DNA.
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DR HSSP; PI3163; 1LO5.
DR SMR; Q931M4; 28-260.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 260 AA; 30016 MW; 15C2D36270FA8241 CRC64;

Query Match 82.6%; Score 1023; DB 2; Length 260;
Best Local Similarity 82.0%; Pred. No. 6.1e-76;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELORNALSNLQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 28 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAKTENKESHDOFLQHTILFKGFFTD 87
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT 120
DB 88 HSWYNDLLVDFDSKDIVDYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT 147
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 148 EEKVPINLWIDGKQNTVPLETKNKNVTVOELDLQARRYLQEKYLYNSDVDFGKVKQ 207
QY 181 RGLIVFHSSEGSVSYDLFDAQGYPDTLRIYRDNKTINSENHLHDLYLYTT 233
DB 208 RGLIVFHTSTEPSVNYDLFQAQGYSTLLRIYRDNKTINSENMMHIDIYLYTS 260

RESULT 6
Q5PSP6 STAAU PRELIMINARY; PRT; 261 AA.
AC Q5PSP6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Enterotoxin A (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 13565;
RC Wang L., Zhang S., Yu M.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY827552; AAV84102.1; -; Genomic_DNA.
DR SMR; Q5PSP6; 28-260.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
FT NON TER 261
SQ SEQUENCE 261 AA; 30144 MW; 36B6F7EDFA8AD9B3 CRC64;

Query Match 82.2%; Score 1018; DB 2; Length 261;
Best Local Similarity 81.5%; Pred. No. 1.6e-75;
Matches 190; Conservative 18; Mismatches 25; Indels 0; Gaps 0;
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QY 1 SEKSEINEKDLRKKSLOALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 60
DB 28 SEKSEINEKDLRKKSLOALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTD 87
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 88 HSWYNDLLVDFDSKDIIVDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 147
QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 148 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 207
QY 181 RGLIVHSSSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLHIDLYLYTT 233
DB 208 RGLIVHTSTEPSVYDLFDAQOQYPTLLRIYRDNKTINSENHMHIDLYLYTS 260
RESULT 7
Q6GFA8 STAA
ID Q6GFA8 STAA PRELIMINARY; PRT; 257 AA.
AC Q6GFA8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Enterotoxin type A.
GN OrderedLocusNames=SA2043;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG41028.1; -; Genomic_DNA.
DR SNR; Q6GFA8; 25-257.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
SQ SEQUENCE 257 AA; 29674 MW; 56B0A6D952EDFED4 CRC64;
Query Match 81.8%; Score 1013; DB 2; Length 257;
Best Local Similarity 81.5%; Pred. No. 4e-75;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSLOALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSLOALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTN 84
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIIVDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
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QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVHSSSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLHIDLYLYTT 233
DB 205 RGLIVHTSTEPSVYDLFDAQOQYPTLLRIYRDNKTINSENHMHIDLYLYTS 257
RESULT 8
Q99SU3 STAA
ID Q99SU3 STAA PRELIMINARY; PRT; 260 AA.
AC Q99SU3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin P.
GN Names=ep; OrderedLocusNames=SA1761;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekinizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Shiba T.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Hiramatsu K.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL; BA000018; BAB43036.1; -; Genomic_DNA.
DR FIK; C89984; C89984.
DR HSSP; P13163; 1SXT.
DR SNR; Q99SU3; 28-260.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
SQ SEQUENCE 260 AA; 29708 MW; 087C5B4EC028CFDB CRC64;
Query Match 80.3%; Score 994; DB 2; Length 260;
Best Local Similarity 79.0%; Pred. No. 1.5e-73;
Matches 184; Conservative 17; Mismatches 32; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSLOALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 60
DB 28 SEKSEINEKDLRKKSLOALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTN 87
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 88 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 147
QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 148 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 207
QY 181 RGLIVHSSSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLHIDLYLYTT 233
DB 208 RGLIEFHPSSGDSVGVLDLFAQOQYPTQLRIYRDNKTIKSKNMHIDLYLYTT 260
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RESULT 9
Q6XZ9 STAAU PRELIMINARY; PRT; 219 AA.
AC Q6XZ9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enterotoxin sea variant (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=3208;
RX MEDLINE=22943091; PubMed=14580397; DOI=10.1016/S0890-8508(03)00058-6;
RA Leteire C., Perelle S., Dillasser F., Fach P.;
RT "A strategy based on 5' nuclease multiplex PCR to detect enterotoxin
RT genes sea to sej of Staphylococcus aureus.";
RL Mol. Cell. Probes 17:227-235(2003).
RL EMBL; AF196686; AAP37183.1; -; Genomic_DNA.
DR SMR; Q6XZ9; 2-219.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
FT NON TER 219
SQ SEQUENCE 219 AA; 25264 MW; DE8F38AEB652FC89 CRC64;

Query Match 78.4%; Score 971; DB 2; Length 219;
Best Local Similarity 82.6%; Pred. No. 9.4e-72;
Matches 180; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

QY 9 EKDLRKSELQNALNRLQIYYNEKAITENKESDDQFLNTLLFKGFFTGHPWYNDLL 68
DB 2 EKDLHKSELQVALNRLQIYYHNGKAITENKESDQFLQHTLFPNGFFTDHPWYNDLL 61

QY 69 VDLGSKDATNKYKGVLDLYGAYGYQCAGGTPTNKACMYGGVTLHDNNRLTEKKVPIN 128
DB 62 VDPFDSKVLADKYKGVLDLYGAYGYQCAGGTPTNKACMYGGVTLHDNNRLTEKKVPIN 121

QY 129 LMTDGKQTVPTDKVTSKEVTQELDQARHLHGKFLGYNLSDSFGGKVGRLIVFHS 188
DB 122 LMLDGGKQTVPLETVTKNKKEVTQELDQARHLHGKFLGYNLSDTFDGKVGRLIVFHT 181

QY 189 SEGTSVSYDLFDAQGYPTTLRIYRDNKTINSENHLI 226
DB 182 STEPSVNYDLFGAGQGYNTLLRIYRDNKTINSENHI 219

RESULT 10
Q76LS7 STAAU PRELIMINARY; PRT; 268 AA.
AC Q76LS7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Enterotoxin J.
GN Name=sej;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KSI1410;
RX MEDLINE=99052098; PubMed=9835033;
RA Zhang S., Iandolo J.J., Stewart G.C.;
RT "The enterotoxin D plasmid of Staphylococcus aureus encodes a second
RT enterotoxin determinant (sej).";
RL FEMS Microbiol. Lett. 168:227-233(1998).
DR EMBL; AF053140; AAC78590.1; -; Genomic_DNA.
DR HSSP; P13163; IESP.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Plasmid.
SQ SEQUENCE 268 AA; 31230 MW; ACSF3546060ACE22 CRC64;

Query Match 67.0%; Score 830; DB 2; Length 268;
Best Local Similarity 65.4%; Pred. No. 1.3e-60;
Matches 151; Conservative 38; Mismatches 42; Indels 0; Gaps 0;

DR EMBL; AB075606; BAC97796.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 268 AA; 31237 MW; 016E5346079D3E20 CRC64;

Query Match 67.6%; Score 837; DB 2; Length 268;
Best Local Similarity 65.4%; Pred. No. 1.3e-60;
Matches 151; Conservative 38; Mismatches 42; Indels 0; Gaps 0;

QY 3 KSEINEKDLRKSELQNALNRLQIYYNEKAITENKESDDQFLNTLLFKGFFTGHP 62
DB 27 KNETIKERNLHKSELSSITLNLRIHYFFNEKGISEKIMTEDQFLDYTLFLKSFIFHS 86

QY 63 WYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPTNKACMYGGVTLHDNNRLTBE 122
DB 87 QINDLLVQFDSKETVWPKGQVDLYGSYGFQCSGKGNKTACMYGGVTLHENNQLYDT 146

QY 123 KKVPINLMTDGKQTVPTDKVTSKEVTQELDQARHLHGKFLGYNLSDSFGGKVGORG 182
DB 147 KKIPINLMTDSIRTVVPLDIVTKNKKVTIQELDQARYYLLHKQYNLYNPSFTGGKIQKG 206

QY 183 LIVFHSSEGTSVSYDLFDAQGYPTTLRIYRDNKTINSENHLIDLILYTT 233
DB 207 LIVFHSKEPLVSYDLFVWVGQYPKLLKIYQDNKIIESENHHIDILYLS 257

RESULT 11
O85217 STAAU PRELIMINARY; PRT; 268 AA.
AC O85217;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin J.
GN Name=sej;
OS Staphylococcus aureus.
OG Plasmid p18485.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KSI1410;
RX MEDLINE=99052098; PubMed=9835033;
RA Zhang S., Iandolo J.J., Stewart G.C.;
RT "The enterotoxin D plasmid of Staphylococcus aureus encodes a second
RT enterotoxin determinant (sej).";
RL FEMS Microbiol. Lett. 168:227-233(1998).
DR EMBL; AF053140; AAC78590.1; -; Genomic_DNA.
DR HSSP; P13163; IESP.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Plasmid.
SQ SEQUENCE 268 AA; 31230 MW; ACSF3546060ACE22 CRC64;

Query Match 67.0%; Score 830; DB 2; Length 268;
```

Best Local Similarity 64.9%; Pred. No. 4.8e-60;
Matches 150; Conservative 38; Mismatches 43; Indels 0; Gaps 0;

QY 3 KSEINEKDLRKSELOALNSLRQIYYNKAITENKESDDQFLENTLLKGFPTGHP 62
DB 27 KNETIKERLKHKKSELSITLNNRHLYFPNEKIGSEKIMTBDQFLDYTLFLKSPFISHS 86
QY 63 WYNDLLVLDGSKDATNKYKGVKQVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRLTBE 122
DB 87 QYNDLLVQFDSKETVKNFKGVKQVDLYGSGYGFQCSGKFNKTACMYGGVTLHNNQLYDT 146
QY 123 KKVPINLWIDGQTTVPIDKVKTSKEVTVQELDLQARHLYHGKFGLYNSDSFGGKVGQK 182
DB 147 KKIPINLWIDSRTVVPIDKVKTSKEVTVQELDLQARHLYHGKFGLYNSDSFGGKVGQK 206
QY 183 LIVFHSSEGSTVSYDLFDAQGGVPTLLRIYRDNKTINSNLHIDLILYLT 233
DB 207 LIVFHTSKEPLSYDLFNVIGVYFDKLLIYQDNKIIESNHNHIDILYLT 257

RESULT 12
QY Q6R2G0 STAAU PRELIMINARY; PRT; 154 AA.
AC Q6R2G0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Enterotoxin E (Fragment).
OS Staphylococcus aureus subsp. aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=46170;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 27664;
RX PubMed=1513181; DOI=10.1128/JCM.42.5.2134-2143.2004;
RA Sergeev N., Volokhov D., Chizhikov V., Rasooly A.;
RT "Simultaneous analysis of multiple staphylococcal enterotoxin genes by
an oligonucleotide microarray assay";
J. Clin. Microbiol. 42:2134-2143 (2004).
DR EMBL; AY518387; AAR99635.1; -; Genomic_DNA.
DR HSSP; PI3380; 1AN8.
DR SMR; Q6R2G0; 3-154.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 154
FT NON_TER 154
SQ SEQUENCE 154 AA; 17390 MW; 10D2329E23F0C74F CRC64;

Query Match 66.6%; Score 825; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 6.3e-60;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 ATNKYGGKVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 135
DB 1 ATNKYGGKVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 60
QY 136 TTVPIDKVKTSKEVTVQELDLQARHLYHGKFGLYNSDSFGGKVGQGLIVFHSSEGSTVS 195
DB 61 TTVPIDKVKTSKEVTVQELDLQARHLYHGKFGLYNSDSFGGKVGQGLIVFHSSEGSTVS 120
QY 196 YDLFDAQGGVPTLLRIYRDNKTINSNLHIDLILYLT 229
DB 121 YDLFDAQGGVPTLLRIYRDNKTINSNLHIDLILYLT 154

RESULT 13
ETXD STAAU STANDARD; PRT; 258 AA.
AC P20723;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Enterotoxin type D precursor (SED).
GN Name=entD;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89359112; PubMed=2549000;
RA Bayles K.W., Tandolo J.J.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal
enterotoxin D";
J. Bacteriol. 171:4799-4806 (1989).
RN [2]
RP NUCLEOTIDE SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC STRAIN=ATCC 23235;
RX MEDLINE=97157473; PubMed=9003758;
RA Sundstroem M., Abrahmsen L., Antonsson P., Mehindate K., Mourad W.,
Dohlieten M.;
RT "The crystal structure of staphylococcal enterotoxin type D reveals
Zn2+-mediated homodimerization";
EMBO J. 15:6832-6840 (1996).
RL
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
staphylococcal food poisoning syndrome. The illness characterized
by high fever, hypotension, diarrhea, shock, and in some cases
death.
CC -!- SUBUNIT: Homodimer; zinc-dependent.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC EMBL; M28521; AAB06195.1; -; Genomic_DNA.
DR PIR; A33953; A33953.
DR HSSP; PI3183; LSXT.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Antigen; Enterotoxin; Metal-binding; Signal; Superantigen; Toxin;
Zinc
FT SIGNAL 1 25
FT CHAIN 26 258 Enterotoxin type D.
FT METAL 212 212 Zinc.
FT METAL 250 250 Zinc.
FT METAL 252 252 Zinc.
FT VARIANT 114 114 P -> A (in strain ATCC 23235).
SQ SEQUENCE 258 AA; 29746 MW; 4F7C6A28D42597FD CRC64;

Query Match 53.6%; Score 663; DB 1; Length 258;
Best Local Similarity 54.5%; Pred. No. 2.5e-46;
Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNKAITENKESDDQFLENTLLKGFPTG 60
DB 26 NENIDSVKRELKHKSELSSTALNNMKHSYADKNPIIGENKSTGDDQFLENTLLKGFPTD 85

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QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLT 120
Db 86 LINFEDLLFNFSKEMQAQFKQNDVPIRISYNCYGGEIDRTACTYGGVTPHEGNKLUK 145
QY 121 EEKQVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 146 ERKKIPINLWINGVQKEVSLDKVQTDKKNVTQVELDAQARRYLQKDLKLYNNDTLGGKIQ 205
QY 181 RGLIVFHSSEGSTVSYDLFDAGQVPTDLLRIYRDNKTINSENHLHIDLILY 231
Db 206 RKGIEFSSDGSKVSVDLFDVKGDFPEKQLRIYSDNKTLSLTHELHIDLILY 256

RESULT 14
Q6R2F9 STAAU PRELIMINARY; PRT; 152 AA.
AC Q6R2F9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Enterotoxin D (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NTCC 16656;
RX PubMed=1513181; DOI=10.1128/JCM.42.5.2134-2143.2004;
RA Sergeev N., Velokhov D., Chizhikov V., Rasooly A.;
RT "Simultaneous analysis of multiple staphylococcal enterotoxin genes by
an oligonucleotide microarray assay.";
RL Clin Microbiol. 42:2134-2143(2004).
DR EMBL; AY518386; AAR95636.1; -; Genomic_DNA.
DR HSSP; F13380; IAN8.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 152
SQ SEQUENCE 152 AA; 17514 MW; F0354318924CB739 CRC64;

Query Match 40.1%; Score 496; DB 2; Length 152;
Best Local Similarity 59.9%; Pred. No. 7.3e-33;
Matches 91; Conservative 22; Mismatches 39; Indels 0; Gaps 0;

QY 80 YKGGKVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLTEKKVPIINLWIDGKQTTVP 139
Db 1 FSKKNVDVVAIRYSYNCYGGEIDRTACTYGGVTPHEGNKLERKKIPINLWINGVQKEVS 60
QY 140 IDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQKGLIVFHSSEGSTVSYDLF 199
Db 61 LDKVQTDKKNVTVQELDAQARRYLQKDLKLYNNDTLGGKIQKIEFSSDGSKVSVDLFD 120
QY 200 DAQGOYPTDLLRIYRDNKTINSENHLHIDLILY 231
Db 121 DVKGDFFPEKQLRIYSDNKTLSLTHELHIDLILY 152

RESULT 15
QSHFG0 STAAC PRELIMINARY; PRT; 234 AA.
AC QSHFG0;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
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DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Enterotoxin type A, putative.
GN OrderedLocusNames=SACOL1657;
OS Staphylococcus aureus (strain COL).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=93062;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA Ravel J.R., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA Haddon R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,
RA Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA Hance I.R., Nelson K.E., Fraser C.M.;
RT "Insights on evolution of virulence and resistance from the complete
genome analysis of an early methicillin-resistant Staphylococcus
RT aureus strain and a biofilm-producing methicillin-resistant
RT Staphylococcus epidermidis strain.";
RL J. Bacteriol. 187:2426-2438(2005).
DR EMBL; CP000046; AAW38273.1; -; Genomic_DNA.
DR TIGR; SACOL1657; -.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 234 AA; 27337 MW; 16613BEFEF94AF1D CRC64;

Query Match 39.8%; Score 492.5; DB 2; Length 234;
Best Local Similarity 39.8%; Pred. No. 2.4e-32;
Matches 92; Conservative 48; Mismatches 86; Indels 5; Gaps 3;

QY 1 SEKSEINEKDLRKKSELRNALSRLRIYYNYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 7 TNSASAIYSYDLHLHKSKFDSKRLSNAK-MSFINPTQL-ENKNTNDRLLKHDLFDHMFVN 64
QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLT 120
Db 65 DWWKDDFKVEFENEALSKKFINKDIDIFAGNYGYGCHGATNKTQCSYGGVILSDNNKYD 124
QY 121 EEKQVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 125 DYKNIPCNLWIDGHQTEIETAVTKTKKIVTTQELVQLRNLNKKYKLYEQ---GGDIV 181
QY 181 RGLIVFHSSEGSTVSYDLFDAGQVPTDLLRIYRDNKTINSENHLHIDLILY 231
Db 182 KGYVKYNDDEQNVDFYNLNGEYGREVLKMYADNKTINSDKLHLDIYLF 232

RESULT 16
Q6G8W7 STAA PRELIMINARY; PRT; 229 AA.
AC Q6G8W7;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Putative enterotoxin.
GN OrderedLocusNames=SAS1538;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
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DR InterPro: IPR0061126; Staph/Strept tox.
DR InterPro: IPR0061173; Staph_tox_OB.
DR Pfam: PF01123; Staph_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 229 AA; 26728 MW; AD3DAF9EAAAE3677 CRC64;

Query Match          39.6%; Score 490.5; DB 2; Length 229;
Best Local Similarity 39.4%; Pred.No. 3,4e-32;
Matches 91; Conservative 48; Mismatches 87; Indels 5; Gaps 3;

QY      1 SEKSEINEKDLRKSKSELQRNALSNLRQIYYVNEKAITENKESDDQFLENTLLFKGFFFTG 60
DB      2 TNSASAIEYSDDLHHKSKFDSKLSNAK-MSPINPTQL-ENKNVNDRLHKDLLFHDHMFVN 59

QY     61 HPWYNLDLVLGSKOATNKYKGKKVDLYGAYGYQCAGTTPNKTACMYGGVTUHDNNRLT 120
DB      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
DB     60 DDWKDKDFKEFEANEALSKEFPINKIDIFAGNYGYGCHGATNKTQCSYGVTILSDNNKYD 119

QY    121 EEKVPIINLIWDGKQTTPVIDKVKTSKKEVTYQELDLQARHYHLHGKFLGNYSDFSFGKVKQ 180
DB    120 DYKNIIFCNLIWDGHQAIEILTAVTKTKKIIVTIQELDVQLRYNLNEYKVLQEY---GGDIV 176

QY    181 RGLIVPHSEGSTVSVDLFDAQOQYPDTLLRIYRDNKTINSENLHIDLVIYL 231
DB    177 KGVYKHNDDEQNIYFNFYNLANGEYGEVLEKMVADNKTINSCKLHDIYLF 227

RESULT 18
Q9EZM4_STAAB PRELIMINARY; PRT; 258 AA.
ID Q9EZM4;
AC Q9EZM4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SFN.
GN Names-en;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]

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MEDLINE=20571956; PubMed=11123352;
RX Jarraud S., Peyrat M.A., Lim A., Tristan A., Bes M., Mougel C.,
RA Etienne J., Vandenesch F., Bonneville M., Lina G.;
RA "egc, a highly prevalent operon of enterotoxin gene, forms a putative
RT nursery of superantigens in Staphylococcus aureus.";
RT J. Immunol. 166:669-677(2001).
RL ENBL; AF285760; AAG36956.1; -; Genomic_DNA.
DR PIR; H89968; H89968.
DR HSSP; Q03585; 1F77.
DR GO; GO:000576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006117; Bcrl tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Stap_Strep_toxin; 1.
DR Pfam; PF02876; Stap_Strep_tox C; 1.
DR PRINTS; PR00279; BACTELTOXIN
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE .258 AA; 29676 MW; 8A6C074F3E1F82D2 CRC64;

Query Match 37.3%; Score 461.5; DB 2; Length 258;
Best Local Similarity 41.2%; Pred.No. 9.6e-30;
Matches 96; Conservative 45; Mismatches 77; Indels 15; Gaps 6;
QY 6 EINEKDLRKXSELQRNALGNLRQIYYNYNEKAIT-----ENKESDDQFLENTLLFKGFFTG 60

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Db 32 EVDKKDLKKSDSDSKLFNLTS--YYTD--ITWQLDENKISTDQLLNTILKNIDIS 87
Qy 61 HPWYNLLVDLGSKDATNKYGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 88 VLKTSLSLKVEFNSSDLANQFKGNIDYGLYFGNKCGLTEKTSCLYGGVTHDGNQLD 147
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 148 EEKVGIVNFKDGVQOEGFV--IKTKAKVTVQELDTKVRFKLENLYKYNKDT--GNIQ 203
Qy 181 RGLIVFHS--SEGSTVSYDLFDAQQGVPTDLLRIYRDNKTINSENHLIDLYL 231
Db 204 KGCIFPHSHNQDSFYDLYNVKSGVGAEFFQFYSDNRTVSSSNHYDVFY 256

RESULT 19
Q7A2Q6 STAAH
ID Q7A2Q6 STAAH PRELIMINARY; PRT; 258 AA.
AC Q7A2Q6_2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Enterotoxin.
GN Name=sen; OrderedLocusNames=SAV1825;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; BA000017; BAB57987.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strep toxin; 1.
DR Pfam; PF02876; Staph Strep tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29676 MW; 8A6C074F3E1F82D2 CRC64;

Query Match 37.3%; Score 461.5; DB 2; Length 258;
Best Local Similarity 41.2%; Pred. No. 9.6e-30;
Matches 96; Conservative 45; Mismatches 77; Indels 15; Gaps 6;

Qy 6 EINEKLRKKSBLQRNALSRLRIYYNEKAIT-----ENKESDDQFLENTLLFKGFFTG 60
Db 32 EVDKKDLKKSDSDSKLFNLTS--YYTD--ITWQLDENKISTDQLLNTILKNIDIS 87
Qy 61 HPWYNLLVDLGSKDATNKYGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 88 VLKTSLSLKVEFNSSDLANQFKGNIDYGLYFGNKCGLTEKTSCLYGGVTHDGNQLD 147
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 148 EEKVGIVNFKDGVQOEGFV--IKTKAKVTVQELDTKVRFKLENLYKYNKDT--GNIQ 203
Qy 181 RGLIVFHS--SEGSTVSYDLFDAQQGVPTDLLRIYRDNKTINSENHLIDLYL 231
Db 204 KGCIFPHSHNQDSFYDLYNVKSGVGAEFFQFYSDNRTVSSSNHYDVFY 256

RESULT 21
Q6YCN3 STAAU
ID Q6YCN3 STAAU PRELIMINARY; PRT; 251 AA.
AC Q6YCN3_2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Enterotoxin SEN variant.
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Db 204 KGCIFPHSHNQDSFYDLYNVKSGVGAEFFQFYSDNRTVSSSNHYDVFY 256

RESULT 20
Q7A4X1 STAAH
ID Q7A4X1 STAAH PRELIMINARY; PRT; 258 AA.
AC Q7A4X1_2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Enterotoxin Sen.
GN Name=sen; OrderedLocusNames=SA1643;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; BA000018; BAB42911.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strep toxin; 1.
DR Pfam; PF02876; Staph Strep tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29676 MW; 8A6C074F3E1F82D2 CRC64;

Query Match 37.3%; Score 461.5; DB 2; Length 258;
Best Local Similarity 41.2%; Pred. No. 9.6e-30;
Matches 96; Conservative 45; Mismatches 77; Indels 15; Gaps 6;

Qy 6 EINEKLRKKSBLQRNALSRLRIYYNEKAIT-----ENKESDDQFLENTLLFKGFFTG 60
Db 32 EVDKKDLKKSDSDSKLFNLTS--YYTD--ITWQLDENKISTDQLLNTILKNIDIS 87
Qy 61 HPWYNLLVDLGSKDATNKYGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 88 VLKTSLSLKVEFNSSDLANQFKGNIDYGLYFGNKCGLTEKTSCLYGGVTHDGNQLD 147
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 148 EEKVGIVNFKDGVQOEGFV--IKTKAKVTVQELDTKVRFKLENLYKYNKDT--GNIQ 203
Qy 181 RGLIVFHS--SEGSTVSYDLFDAQQGVPTDLLRIYRDNKTINSENHLIDLYL 231
Db 204 KGCIFPHSHNQDSFYDLYNVKSGVGAEFFQFYSDNRTVSSSNHYDVFY 256

RESULT 21
Q6YCN3 STAAU
ID Q6YCN3 STAAU PRELIMINARY; PRT; 251 AA.
AC Q6YCN3_2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Enterotoxin SEN variant.
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OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=382F;
RX MEDLINE=22692404; PubMed=12807452;
RX DOI=10.1046/j.1365-2672.2003.01957.x;
RA Letetire C., Perelle S., Dilasser F., Fach P.;
RT "Identification of a new putative enterotoxin SEU encoded by the egc
RT cluster of Staphylococcus aureus.";
RL J. Appl. Microbiol. 95:38-43(2003).
DR EMBL; AY158703; AA017733.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH STREP TOXIN 1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 251 AA; 28806 MW; 1E2966FBBF86BA40 CRC64;

Query Match 36.1%; Score 446.5; DB 2; Length 251;
Best Local Similarity 39.5%; Pred. No. 1.6e-28;
Matches 92; Conservative 49; Mismatches 77; Indels 15; Gaps 6;

QY 6 EINEKDLRKSEIQRNLSNLRQIYYNEKAIT-----ENKESDDQPLENTLFFKGFFTG 60
Db 25 DVDKNDLKKKSDIDSSKLFNLTS--YYTD--ITWQDESINKISTDQLLNNTIILKIDIS 80
QY 61 HPWYNLLVDLGSKDATNKYKGVLDYGYVQCAGGTPNKTACWGGVTLHNNRLT 120
Db 81 VLKTSLSKVEFNSSDLANQFKGNIDYGLYGNKCVGLTEKTSCLYGGVTIYDGNQD 140
QY 121 EEKKVPINLWIDGKQTTPIDKVKTSKKEVTQELDQARHYLHGKFGLYNSDSFGKVK 180
Db 141 EERVIGNVFQDGIQEGFV--IKTKAKVTQVELDTKVRFKLENLYKIYKNT--GNIQ 196
QY 181 RGLIVFHSS--EGSTVSVDLFDAGQGVPTDLLRIYRDNKTINSENLHIDLYLY 231
Db 197 KGCIFHSHNNHQNSFYVDLYNKGSGAEFFQFYSNDRVTSSNVHIDVFLY 249

RESULT 22
Q6GFN1 STAAAR PRELIMINARY; PRT; 251 AA.
AC Q6GFN1;
DT 05-JUL-2004 (T-EMBLrel. 27, Created);
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update);
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update);
DE Enterotoxin.
GN OrderedLocusNames=SAR1917;
OS Staphylococcus aureus (strain MSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.04025211101;
RX Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RX Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RX Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RX Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RX Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RX James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RX Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RX Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG40903.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH STREP TOXIN 1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 251 AA; 28806 MW; 1E2966FBBF86BA40 CRC64;

Query Match 36.1%; Score 446.5; DB 2; Length 251;
Best Local Similarity 39.5%; Pred. No. 1.6e-28;
Matches 92; Conservative 49; Mismatches 77; Indels 15; Gaps 6;

QY 6 EINEKDLRKSEIQRNLSNLRQIYYNEKAIT-----ENKESDDQPLENTLFFKGFFTG 60
Db 25 DVDKNDLKKKSDIDSSKLFNLTS--YYTD--ITWQDESINKISTDQLLNNTIILKIDIS 80
QY 61 HPWYNLLVDLGSKDATNKYKGVLDYGYVQCAGGTPNKTACWGGVTLHNNRLT 120
Db 81 VLKTSLSKVEFNSSDLANQFKGNIDYGLYGNKCVGLTEKTSCLYGGVTIYDGNQD 140
QY 121 EEKKVPINLWIDGKQTTPIDKVKTSKKEVTQELDQARHYLHGKFGLYNSDSFGKVK 180
Db 141 EERVIGNVFQDGIQEGFV--IKTKAKVTQVELDTKVRFKLENLYKIYKNT--GNIQ 196
QY 181 RGLIVFHSS--EGSTVSVDLFDAGQGVPTDLLRIYRDNKTINSENLHIDLYLY 231
Db 197 KGCIFHSHNNHQNSFYVDLYNKGSGAEFFQFYSNDRVTSSNVHIDVFLY 249

RESULT 22
Q6GFN1 STAAAR PRELIMINARY; PRT; 251 AA.
AC Q6GFN1;
DT 05-JUL-2004 (T-EMBLrel. 27, Created);
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update);
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update);
DE Enterotoxin.
GN OrderedLocusNames=SAR1917;
OS Staphylococcus aureus (strain MSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.04025211101;
RX Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RX Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RX Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RX Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RX Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RX James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RX Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RX Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";

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QY 59 TGHFW-----YNDLLVGLGSKDATNKYKKVLDLYGAYGYQCAGGTPNKTACMYGV 111
Db 85 ---NWLDDGISAEPKOLKVEFSSAISKEFLGKTVDYGVYKAKHGEHQVDFTACTYGV 141
QY 112 TLHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTQBELDQARHYLHGKFLYN 171
Db 142 TPHNNKLSPEKNGVAVYKDNVNVNFTFI--VTDDKKVTAQBELDKVRTLNNAYKLY- 198
QY 172 SDSFGKVGKGLVHFSSSEGSTVS--YDLFDAQGVDPDTLLRIRYRDNKTINSNLHIDLY 229
Db 199 -DRMTSDVQKGYIKFHSHEKSFYVDLYFIKGNLPDQVLYQNDKNTIDSSDYHIDVY 257
QY 230 LYT 232
Db 258 LFT 260

RESULT 26
Q9EZM8 STAAU PRELIMINARY; PRT; 261 AA.
AC Q9EZM8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SEO.
GN Name=seo;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A900322;
RX MEDLINE=20571956; PubMed=11123352;
RA Jarraud S., Peyrat M.A., Lim A., Tristan A., Bes M., Mougel C.,
RA Etienne J., Vandenesch F., Bonneville M., Lina G.;
RT "egc, a highly prevalent operon of enterotoxin gene, forms a putative
RT nursery of superantigens in Staphylococcus aureus.";
RL J. Immunol. 166:669-677(2001).
DR EMBL; AF285760; AAG36951.1; -; Genomic_DNA.
DR HSSP; Q54971; 1BXT.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 261 AA; 29949 MW; 24DA4DD766288EC CRC64;

Query Match 31.3%; Score 387.5; DB 2; Length 261;
Best Local Similarity 39.9%; Pred. No. 1.2e-23;
Matches 97; Conservative 31; Mismatches 86; Indels 29; Gaps 8;

QY 8 NEKD-----LRKKSLEQNALSLRQIYYNE----KAITENKESDDQFLENTLLFKGPF 58
Db 30 NEEDPKIESLCKSSVDPTALHNDYINRRTTVKSIIVSTTE---KFLDPDLLFKSI- 85
QY 59 TGHFW-----YNDLLVGLGSKDATNKYKKVLDLYGAYGYQCAGGTPNKTACMYGV 111
Db 86 ---NWLDDGISAEPKOLKVEFSSAISKEFLGKTVDYGVYKAKHGEHQVDFTACTYGV 142
QY 112 TLHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTQBELDQARHYLHGKFLYN 171
Db 143 TPHNNKLSPEKNGVAVYKDNVNVNFTFI--VTDDKKVTAQBELDKVRTLNNAYKLY- 199
QY 172 SDSFGKVGKGLVHFSSSEGSTVS--YDLFDAQGVDPDTLLRIRYRDNKTINSNLHIDLY 229
Db 200 -DRMTSDVQKGYIKFHSHEKSFYVDLYFIKGNLPDQVLYQNDKNTIDSSDYHIDVY 258
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QY 230 LYT 232
Db 259 LFT 261

RESULT 27
Q52075 92ZZZ PRELIMINARY; PRT; 179 AA.
ID Q52075;
AC Q52075;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin D.
GN Name=virc2;
OS Plasmid pIB485.
OG Plasmid pIB485.
OC other sequences; plasmids.
OX NCBI_TaxID=2565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89359112; PubMed=2549000;
RA Bayles K.W., Tandolo J.J.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal
RT enterotoxin D.";
RL J. Bacteriol. 171:4799-4806(1989).
DR EMBL; M94872; AAA98133.1; -; Genomic_DNA.
DR HSSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin_C; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
KW Plasmid.
SQ SEQUENCE 179 AA; 20564 MW; 579FFE811BC08747 CRC64;

Query Match 30.8%; Score 381; DB 2; Length 179;
Best Local Similarity 48.7%; Pred. No. 2.6e-23;
Matches 73; Conservative 24; Mismatches 53; Indels 0; Gaps 0;

QY 1 SEKSEBINEKDLRKKSLEQNALSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 26 NENIDSVKEKELKKSSELSSTALNNMKHSYADKNPIIGENKSTGDOFLENTLLYKKFFTD 85
QY 61 HPWYNDLLVGLGSKDATNKYKKVLDLYGAYGYQCAGGTPNKTACMYGVTLHNNRLT 120
Db 86 LINFEDLLINFNSKEMAQHFKSNVDVYPIRYSINCYGGEIDKTACTYGGVTPHEGNLKL 145
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEV 150
Db 146 ERKKIPINLWINGVQKEVSLDKVQTDKKNL 175

RESULT 28
Q8RR76 STAAU PRELIMINARY; PRT; 217 AA.
ID Q8RR76;
AC Q8RR76;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin H (Fragment).
GN Name=seh;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21871379; PubMed=11880405; DOI=10.1128/JCM.40.3.857-862.2002;
RA Onoe K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shinagawa K.;
RT "Detection of seg, seh, and sel genes in Staphylococcus aureus
RT isolates and determination of the enterotoxin productivities of S.
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RT aureus isolates Harboring seg, seh, or sel genes.";
RL J. Clin. Microbiol. 40:857-862(2002).
DR EMBL; AB060536; BAB85990.1; -, Genomic_DNA.
DR HSSP; Q53585; IEWC.
DR SMR; Q8RR76; 2-213.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF011123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STRP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 217 AA; 25143 MW; A8A44E23F1DE80D CRC64;

Query Match 29.6%; Score 366; DB 2; Length 217;
Best Local Similarity 37.9%; Pred. No. 5.6e-22;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY 10 KDLRKSELQNALNLRIQYIYNEKAITENKESDDQPLENTLLPKGFTGHPWYNDLLV 69
Db 1 EDLHDKSELTDLALAN--AYGQYNHPFIKENIKSDEISGEKDLIFRN--QGDSG-NDLRV 55
QY 70 DLGSKDATNKYKGVKVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINL 129
Db 56 KPATADLAQKFNKNVDIYGASFYKCEKISENISECLYGGTTL-NSEKLAQERVIGANV 114
QY 130 WIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGRLIVFHS 189
Db 115 WVDGIQKETEL--IRTNKNVTLQELDIKIRKILSDKYKIYKDS---EISKGLIEFDMK 169

QY 190 EGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENL-HIDLXYLT 232
Db 170 TPRDYSFDIYDLKGENDYEDIKYEDNKTILKSDDISHDVNLVT 213

RESULT 29
ETXH_STAAN
ID ETXH_STAAN STANDARD; PRT; 241 AA.
AC P0A0L9; Q53585;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Enterotoxin type H precursor (SEH).
GN Name=entH; Synonyms=seh;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE, PARTIAL PROTEIN SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=D4508;
RX MEDLINE=95053699; PubMed=7964453; DOI=10.1084/jem.180.5.1675;
RA Pen K., Bannan J.D., Pancholi V., Cheung A.L., Robbins J.C.,
RA Fischetti V.A., Zabriskie J.B.;
RT "Characterization and biological properties of a new staphylococcal
RT exotoxin.";
RL J. Exp. Med. 180:1675-1683(1994).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.69 ANGSTROMS).
RX PubMed=10986116; DOI=10.1006/jmbi.2000.4093;
RA Haekansson M., Petersson K., Nilsson H., Forsberg G., Bjoerk P.,
RA Antonsson P., Svensson L.A.;
RT "The crystal structure of staphylococcal enterotoxin H: implications
RT for binding properties to MHC class II and TcR molecules.";
RL J. Mol. Biol. 302:527-537(2000).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II.
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RT acquired MRSA.";
RL Lancelot 359:1819-1827(2002).
CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death (By similarity).
CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BA000033; BAB93916.1; -; Genomic_DNA.
DR SMR; P0A0L9; 26-237.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Antigen; Complete proteome; Enterotoxin; Metal-binding; Signal;
KW Superantigen; toxin; zinc.
FT SIGNAL 1 24 By similarity.
FT CHAIN 25 241 Enterotoxin type H.
FT METAL 230 230 Zinc (By similarity).
FT METAL 232 232 Zinc (By similarity).
FT DISULFID 106 116 By similarity.
FT SEQUENCE 241 AA; 27859 MW; 70f77985877616CE CRC64;

Query Match 29.6%; Score 366; DB 1; Length 241;
Best Local Similarity 37.9%; Pred. No. 6.4e-22;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY 10 KDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTGHPWYNDLLV 69
DB 25 EDLHDKSELTDLAN--AYQYNHPFIKENIKSDEISGEKDLIFRN--QGDG-NDLRV 79

QY 70 DLGSKDATNKYKGVLDYGVYGYQCAGGTPNKTACMGVTLHDNNRLTEKKVPINL 129
DB 80 KFTADLAQKFKNVVDIYGASFYKCEKISENISECLYGGTTL-NSEKLAQERVIGANV 138

QY 130 WIDGKQTTVPIDKVTSKSEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQVORGLIVPHSS 189
DB 139 WVDGIQKETEL--IRTNKNVTLQELDKIRKILSKDKYIYKDS---EISKGLIEFDMK 193

QY 190 EGSTVSYDLFDAQGYQPTDLLRIYRDNKNTINSENL-HIDLVLVLT 232
DB 194 TPRDYSFDIYDLKGENYDEIKYIYEDNKTLKSDSHIDVNLVLT 237

RESULT 31
Q6VAM8 STAAU PRELIMINARY; PRT; 241 AA.
AC Q6VAM8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Enterotoxin H precursor.
GN Name=seh;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.

Q6VAM8 STAAU PRELIMINARY; PRT; 241 AA.
AC Q6VAM8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Enterotoxin H precursor.
GN Name=seh;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=FRI 137;
RA Gul'ko L.B., Voyushin K.E., Fluer F.S., Okorokova N.A., Krivenko M.S.,
RA Veiko V.P., Debabov V.G.;
RT "The Obtaining of the Tumor-Addressed Genetically Engineered Drug for
RT Cancer Immunotherapy. II. Cloning a Gene of the pro-Enterotoxin H (seh)
RT from Staphylococcus aureus, its Expression in Escherichia coli.
RT Investigation of the Enterotoxin H Secretion by E. coli Cells.";
RL Biotechnologia 6:72-78(2003).
DR EMBL; AY345144; AAQ63188.1; -; Genomic_DNA.
DR SMR; O6VAM8; 26-237.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT SIGNAL 1 24 Enterotoxin H.
FT CHAIN 25 241
FT SEQUENCE 241 AA; 27831 MW; 70EBA8418C9ECCFE CRC64;

Query Match 29.6%; Score 366; DB 2; Length 241;
Best Local Similarity 37.9%; Pred. No. 6.4e-22;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY 10 KDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTGHPWYNDLLV 69
DB 25 EDLHDKSELTDLAN--AYQYNHPFIKENIKSDEISGEKDLIFRN--QGDG-NDLRV 79

QY 70 DLGSKDATNKYKGVLDYGVYGYQCAGGTPNKTACMGVTLHDNNRLTEKKVPINL 129
DB 80 KFTADLAQKFKNVVDIYGASFYKCEKISENISECLYGGTTL-NSEKLAQERVIGANV 138

QY 130 WIDGKQTTVPIDKVTSKSEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQVORGLIVPHSS 189
DB 139 WVDGIQKETEL--IRTNKNVTLQELDKIRKILSKDKYIYKDS---EISKGLIEFDMK 193

QY 190 EGSTVSYDLFDAQGYQPTDLLRIYRDNKNTINSENL-HIDLVLVLT 232
DB 194 TPRDYSFDIYDLKGENYDEIKYIYEDNKTLKSDSHIDVNLVLT 237

RESULT 32
Q6GD45 STAAU PRELIMINARY; PRT; 241 AA.
AC Q6GD45;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Enterotoxin H.
GN Name=seh; OrderedLocusNames=SAS0051;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571857; CAG41819.1; -; Genomic_DNA.

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DR SMR; Q6GD45; 26-237.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 241 AA; 27858 MW; 70F77985877616CE CRC64;

Query Match 29.6%; Score 366; DB 2; Length 241;
Best Local Similarity 37.9%; Pred. No. 6.4e-22;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY 10 KDLRKSELRNLSLRQIYYNEKAITENKESDDQFLNTLLPKGFPTGHPWYNDLLV 69
DB :||| ||||| ||||| :||| ||||| ||||| :||| ||||| ||||| :||| ||||| |||||
25 EDLHDKSELITDLALAN--AYQYNHFFIKENIKSDISEKDLIFRN--QGDSG-NDLRV 79
QY 70 DLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLTEKKVPINL 129
DB :||| :||| ||||| ||||| :||| :||| ||||| ||||| :||| :||| ||||| |||||
80 KFTADLAQKFKKNQVDIYGASPYKCEKISENSECLYGGTTL-NSEKLAQERVIGANV 138
QY 130 WIDGKQTTVPIDKVTSKKEVTVQELDLQARHLYHGKFGLYNSDSFGGKVQRGLIVFHS 189
DB :||| ||||| ||||| :||| ||||| ||||| :||| ||||| ||||| :||| ||||| |||||
139 WVDGIQKETEL--IRTNKKNVTQLQELDIKIRKTLSDKYIYKDS---EISKGLIFDMK 193
QY 190 EGSTVSVDLFDAGQYDPDTLLRIRYDNKNTINSENLL-HIDLXYLT 232
DB :||| :||| ||||| ||||| :||| ||||| ||||| :||| ||||| ||||| :||| ||||| |||||
194 TPRDVSFDIYDLKGENDYIDKIYEDNKTLKSDISHIDVNLXYT 237

RESULT 33
Q7X0E8 STAAU PRELIMINARY; PRT; 242 AA.
AC Q7X0E8; Q6VCN5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Enterotoxin type I (Enterotoxin type Iv) (Enterotoxin SEI variant).
DE Name=seiv;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB-8802;
RX PubMed=15357721; DOI=10.1111/j.1365-2672.2004.02349.x;
RA Blalotta G., Ercolini D., Pennacchia C., Fusco V., Casaburi A., Pepe O., Villani F.;
RT "PCR detection of staphylococcal enterotoxin genes in Staphylococcus spp. strains isolated from meat and dairy products. Evidence for new variants of seG and sei in S. aureus AB-8802.";
RL J. Appl. Microbiol. 97:719-730(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB-8802, OM562a, A2812/98, ATCC 25923, and 7645a;
RX PubMed=15357721; DOI=10.1111/j.1365-2672.2003.01957.x;
RA Blalotta G., Fusco V., Villani F., von Eiff C., Becker K.;
RT "Detection and characterization of the Staphylococcus aureus enterotoxin gene cluster (egc) in strains isolated from different source (human, veterinary, food and reference).";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=382F;
RX MEDLINE=22692404; PubMed=12807452;
RA DOI=10.1046/j.1365-2672.2003.01957.x;
RA Letetere C., Perelle S., Dillasser F., Fach P.;
RT "Identification of a new putative enterotoxin SEU encoded by the egc cluster of Staphylococcus aureus.";

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RL J. Appl. Microbiol. 95:38-43 (2003).
DR EMBL; AY291444; AAP78524.2; -; Genomic DNA.
DR EMBL; AY920264; AAX11328.1; -; Genomic DNA.
DR EMBL; AY920265; AAX11329.1; -; Genomic DNA.
DR EMBL; AY920269; AAX11333.1; -; Genomic DNA.
DR EMBL; AY158703; AAO17731.1; -; Genomic DNA.
DR EMBL; AY920263; AAX11327.1; -; Genomic DNA.
DR HSSP; PI3380; 1AN8.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF02876; Staph_Strp_toxin_C; 1.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 242 AA; 27950 MW; 5935658E21C4C89C CRC64;

Query Match 28.2%; Score 348.5; DB 2; Length 242;
Best Local Similarity 36.6%; Pred. No. 1.8e-20;
Matches 87; Conservative 37; Mismatches 77; Indels 37; Gaps 9;

QY 8 NEKDLRKSELRN-ALSNLRQIY----YYNEKAITENKESDDQFLNTLLPKGFPTGHP 62
DB :||| ||||| ||||| :||| ||||| ||||| :||| ||||| ||||| :||| ||||| |||||
17 NIKDL---SYAOGDIGVGNLRNFYTKYDIDLKGVTDKNLPANQLE-----FSTG-- 64
QY 63 WYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLTEE 122
DB :||| :||| ||||| ||||| :||| :||| ||||| ||||| :||| :||| ||||| |||||
65 -TNDLISENNWDEISKPKGKMDLFGIDYNGPC-----KTKYMYGGATL-SGQYLNSA 116
QY 123 KKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHLYHGKFGLYNSDSFG-GK--- 178
DB :||| ||||| ||||| :||| ||||| ||||| :||| ||||| ||||| :||| ||||| |||||
117 RKIPINLWINGKHKTISTDKIATNKKLVTAQELDKVLRRYLQEEYNIYGHNNNGKKEYG 176
QY 179 -----VQRGLIVFHSSEGSTVSYDLFDAGQYDPDTLLRIRYDNKNTINSENLLHIDL 228
DB :||| ||||| ||||| :||| ||||| ||||| :||| ||||| ||||| :||| ||||| |||||
177 YKSKFYSGFNKGKVLPHLNDEKSFYDLFTYTGDLGVSLFKIYEDNKIIESEKFLHDLV 234

RESULT 34
Q6GFM9 STAAU PRELIMINARY; PRT; 242 AA.
AC Q6GFM9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enterotoxin.
GN OrderedLocusNames=SAR1919;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J., Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A., Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L., Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K., James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K., Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M., Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G., Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains: evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG40905.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph tox_OB.

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AC Q7A205;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Extracellular enterotoxin type I.
GN Name=sei; OrderedLocNames=SAV1828;
OS Staphylococcus aureus (strain MU50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of meticillin-resistant Staphylococcus aureus.";
RT aureus.
RL Lancet 357:1225-1240(2001).
DR EMBL; BA000017; BAB57990.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPRO06177; Bctrl tox.
DR InterPro; IPRO06123; Staph/Strep toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 242 AA; 27863 MW; C5CB4ACEE5414A8 CRC64;

Query Match 27.4%; Score 339.5; DB 2; Length 242;
Best Local Similarity 35.6%; Pred. No. 9.7e-20;
Matches 79; Conservative 36; Mismatches 74; Indels 33; Gaps 7;

QY 23 LSNLRQIY----YNEKAITENKESDDQFLENTLLFKGFTGHPWYNDLVLGSKDATN 78
DB 30 VGNLRFYTKHDYIDLKGVTDKNLPTANQLE-----FSTG---TNDLISESNNWDEIS 79

QY 79 KYGKKVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTV 138
DB 80 KFKGKKLDFGIDYNGPC-----KSKYMGGATL-SGQYLSARKIPINLWNGKHKTI 132

QY 139 PIDKVKTSKEVTQVQLDQARHYLHGKFLYNSDSFG-GK-----VORGILVF 186
DB 133 STDKIATNKKLVTAQEDVLRRLQEEYNIYHNNTGKGKEYGKSKFYSGFNNGKVLV 192

QY 187 HSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIDL 228
DB 193 HLNNEKFSYDLYFTGDLGVSPFLKIYEDNKIIESEKPHLDV 234

RESULT 41
Q52T95 STAAU PRELIMINARY; PRT; 218 AA.
ID Q52T95 STAAU PRELIMINARY; PRT; 218 AA.
AC Q52T95;
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Enterotoxin type I (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FC35, and FC30;
RA Fernandez M.M., De Marzi M.C., Berquer P., Burzyn D., Langley R.J.,
RA Piazzon I., Mariusz R.A., Malchiodi E.L.;
RT "Binding of natural variants of staphylococcal superantigens SEG and SEI to TCR and MHC class II molecules.";
RL Mol. Immunol. 0:0-0(2005).
DR EMBL; AY961387; AAX84816.1; -; Genomic DNA.
DR EMBL; AY961381; AAX84810.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPRO06177; Bctrl tox.
DR InterPro; IPRO06123; Staph/Strep toxin.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 1
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DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 240 AA; 27478 MW; 85CD62DA731C3D95 CRC64;

Query Match 27.1%; Score 336; DB 2; Length 240;
Best Local Similarity 35.3%; Pred. No. 1.9e-19;
Matches 78; Conservative 37; Mismatches 72; Indels 34; Gaps 6;

QY 25 NLRLQIY-----YNEKAITENKESDDQFLENTLLFKGFFTGHPWYND-LLVLDLGSKDATNK 79
DB 32 NLRNFYTKYEVNLRKVKDKNSPESHRL-----YSKNDTLVAEFNVEYISD 80
QY 80 YKGKVDLYGAYGYQCAGTGNKTAACMGVGVTLHDNNRLTEKKVPINLWIDGKQTTVP 139
DB 81 LKGKNDVFGISKY-----GSNRT--IYGVTKAENKLDSPRIIPINLIINGKHQTTV 134
QY 140 IDKVTSKKEVTVQELDQARHYLHGKFGLY-----NSDSFGKVGQVGLIVFH 187
DB 135 TKSVSVDKMWTAQIEDVKLRKYLQDEFNIYGHNDTGKKEYGTSSKFYSFGDKGSWFH 194
QY 188 SSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLIDL 228
DB 195 INDGNSFSYDLFTYGTGLPESFLKIYDKNKTVDSTQFHLDV 235

RESULT 47
Q52T97 STAAU PRELIMINARY; PRT; 210 AA.
AC Q52T97;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Enterotoxin type I (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=rc65;
RA Fernandez M.M., De Marzi M.C., Berquer P., Burzyn D., Langley R.J.,
RA Piazon I., Mariuza R.A., Malchiodi E.L.;
RT "Binding of natural variants of staphylococcal superantigens SEG and
RT SEI to TCR and MHC class II molecules.";
RL Mol. Immunol. 0:0-0(2005).
DR EMBL; AY961385; AX84814.1; -; Genomic_DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006173; Bctrl tox.
DR InterPro; IPR006173; Staph_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 210
SQ SEQUENCE 210 AA; 24082 MW; 15A1E489513EBB8E CRC64;

Query Match 27.1%; Score 335.5; DB 2; Length 210;
Best Local Similarity 35.9%; Pred. No. 1.7e-19;
Matches 79; Conservative 39; Mismatches 67; Indels 35; Gaps 8;

QY 26 LRQIYYNEK-----AITENKESDDQFLENTLLFKGFFTGHPWYNDLLVLDLGSKDATNKY 80
DB 1 LKFLYKHDSIDSKGLDKNLPANQ-LE-----FSTG---INDLISESNWNDEISKF 49
QY 81 KGGKVDLYGAYGYQCAGTGNKTAACMGVGVTLHDNNRLTEKKVPINLWIDGKQTTVP 140
DB 50 KGGKLDIFGIDYNGPC-----KSKYMGYGGATL-SGQYLSARKIPINLWVNGKHKTIST 102
QY 141 DKVTSKKEVTVQELDQARHYLHGKFGLYNSDSFG-GK-----VQRGGLIVFHS 188
DB 103 DKISTNKLVTAEIDVKLRRLYQEEYNIYGHNSTGKKEYGYSKFSYGFNKGKVLHL 162

QY 189 SSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLIDL 228
DB 163 NDEKSFSDYDLFTYGDGVPVSFLKIYEDNKIIESEKFHLDV 202

RESULT 48
Q8RR75 STAAU PRELIMINARY; PRT; 218 AA.
ID Q8RR75;
AC Q8RR75;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin I (Fragment).
GN Name=sei;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21871379; PubMed=11880405; DOI=10.1128/JCM.40.3.857-862.2002;
RA Omoe K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shinagawa K.;
RT "Detection of seg, seh, and sei genes in Staphylococcus aureus
RT isolates and determination of the enterotoxin production activities of S.
RT aureus isolates Harboring seg, seh, or sei genes.";
RL J. Clin. Microbiol. 40:857-862(2002).
DR EMBL; AB060537; BAB85991.1; -; Genomic_DNA.
DR HSSP; P13380; IKTK.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 218 AA; 24909 MW; 1017728FB71BF662 CRC64;

Query Match 27.1%; Score 335.5; DB 2; Length 218;
Best Local Similarity 35.1%; Pred. No. 1.8e-19;
Matches 78; Conservative 37; Mismatches 74; Indels 33; Gaps 7;

QY 23 LSNLRQIY----YNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVLDLGSKDATN 78
DB 6 VGNLRFYTKHYDIDKLGVTDKNLPANQLE-----FSTG---INDLISESNWNDEIS 55
QY 79 KYGKVDLYGAYGYQCAGTGNKTAACMGVGVTLHDNNRLTEKKVPINLWIDGKQTTV 138
DB 56 KFKGKKLDIFGIDYNGPC-----KSKYMGFGATL-SGQYLSARKIPINLWVNGKHKT 108
QY 139 PIDKVTSKKEVTVQELDQARHYLHGKFGLYNSDSFG-GK-----VQRGGLIVF 186
DB 109 STDKIATNKLVTAEIDVKLRRLYQEEYNIYGHNTGKKEYGYSKFSYGFNNGKVLV 168
QY 187 HSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLIDL 228
DB 169 HLNNEKSFSDYDLFTYGDGLPVSFLKIYEDNKIIESEKFHLDV 210

RESULT 49
Q9L921 STRE PRELIMINARY; PRT; 225 AA.
ID Q9L921;
AC Q9L921;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 25.7 kDa protein.
OS Streptococcus equi.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1336;
RN [1]
RP NUCLEOTIDE SEQUENCE.


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QY 23 LSNLRQIY-----YYNEKAITENKESDDQFLENTLLFKGFTGHPWYNDLLVLDGSKDATN 78
DB 30 VGNLRFYTKHDYIDLKGVTDKNLPANQLE-----FSTG---TNDLISESNWNDEIS 79

QY 79 KYGKVDLYGAYYGQACGTPNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTV 138
DB 80 KFKGKLDIFGIDYNGFC-----KSKYMYGGATL-SGQYLSARKIPINLWNGXGKHTI 132

QY 139 PIDKVKTSKEVTVQBLDQARHYLHGKFLGYNDSFG-GK-----VQRLGIVF 186
DB 133 STDKIATNKKLVTAQEIADVLRRLQOEYNIYGHNTGKGYKSKFYSGFNNGKVLV 192

QY 187 HSSEGSTVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLIDL 228
DB 193 HLNNEKSFYDLFYTGHGLPVSLFKIYEDNTIIESEKFLHDV 234

RESULT 52
Q7A4W7 STAA
ID Q7A4W7 STAA PRELIMINARY; PRT; 239 AA.
AC Q7A4W7;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Enterotoxin SEM.
GN Name-sem; OrderedLocusNames=SA1647;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekiizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Hara Y., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of meticillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; BA000018; BAB42915.1; -; Genomic_DNA.
DR HSSP; P13380; IAN8.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
SQ SEQUENCE 239 AA; 27370 MW; 5F29665125705600 CRC64;
Query Match 25.8%; Score 320; DB 2; Length 239;
Best Local Similarity 33.0%; Pred. No. 3.8e-18;
Matches 72; Conservative 40; Mismatches 78; Indels 28; Gaps 6;

QY 25 NLRIYYNEKAITENK--ESDDQFLENTLLFKGFTGHPWYNDLLVLDGSKDATNKYKG 82
DB 28 NLRN--YGYSPYEDHQINPENNHLHQVLS-----MDNSTVTAEFKVDDVKFKN 79

QY 83 KKVLDYGAYYGQACGTPNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
DB 80 HAVDVYGLSYSGYCL-----KNKYIYGGVTL-AGDYLEKSRRIPINLWNGEHQTISTDK 133

QY 143 VKTSKEVTVQBLDQARHYLHGKFLGY-----NSDSFGKVGQRLIVFHSSE 190
DB 134 VSTNKKLVTAQEIADTKRLRYLQOEYNIYGFNDTNKGRNYGNKSKFSSGFGNAGKILFHLND 193

QY 191 GSTVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLIDL 228
DB 194 GGSFSDYDLFDTGTGQAESFLKIYNDKNTVETEKFLHDV 231

RESULT 54
Q6G7UL STAA
ID Q6G7UL STAA PRELIMINARY; PRT; 242 AA.
AC Q6G7UL;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Enterotoxin.
GN Name-sem; OrderedLocusNames=SAV1829;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekiizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Hara Y., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of meticillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; BA000017; BAB57991.1; -; Genomic_DNA.
DR PIR; D89969; D89969.
DR HSSP; Q3RQ05; 1ET6.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
SQ SEQUENCE 239 AA; 27370 MW; 5F29665125705600 CRC64;
Query Match 25.8%; Score 320; DB 2; Length 239;
Best Local Similarity 33.0%; Pred. No. 3.8e-18;
Matches 72; Conservative 40; Mismatches 78; Indels 28; Gaps 6;

QY 25 NLRIYYNEKAITENK--ESDDQFLENTLLFKGFTGHPWYNDLLVLDGSKDATNKYKG 82
DB 28 NLRN--YGYSPYEDHQINPENNHLHQVLS-----MDNSTVTAEFKVDDVKFKN 79

QY 83 KKVLDYGAYYGQACGTPNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
DB 80 HAVDVYGLSYSGYCL-----KNKYIYGGVTL-AGDYLEKSRRIPINLWNGEHQTISTDK 133

QY 143 VKTSKEVTVQBLDQARHYLHGKFLGY-----NSDSFGKVGQRLIVFHSSE 190
DB 134 VSTNKKLVTAQEIADTKRLRYLQOEYNIYGFNDTNKGRNYGNKSKFSSGFGNAGKILFHLND 193

QY 191 GSTVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLIDL 228
DB 194 GGSFSDYDLFDTGTGQAESFLKIYNDKNTVETEKFLHDV 231

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DR GO: 0009405; P: pathogenesis; IEA.
DR InterPro: IPR006177; Bc1r1 tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR008375; Staph exotoxin.
DR InterPro: IPR006173; Staph tox OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PRINTS: PR01800; STAPHSTREP_TOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 256 AA; 29794 MW; 9E2F13790823A7DF CRC64;

Query Match 25.7%; Score 318.5; DB 2; Length 256;
Best Local Similarity 33.8%; Pred. No. 5.5e-18;
Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;

QY 25 NLRQIY--YYNEK--AITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKY 80
DB 46 NLRNFYANPEPEKLGQVSSGNFSTSHQLE---YIDGKYTLYSQFH-----NEY 90

QY 81 KKGK-----KVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTBEEKVPINLWIDGKQ 135
DB 91 EAKRLXDKHKVDIFGISVSGLC-----NTKYMGGITLANQN-LDKPRNIPINLWNGKQ 143

QY 136 TTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYN-----SDSFGKQVORGL 183
DB 144 NTISTDKVSTQKKEVTAQIDIKRLKYLQNEVNIYGFNKTGKQGYQSKFNSGFNKGK 203

QY 184 IVFHSSEGSTVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLIDL 228
DB 204 ITPHLNNEPSFYDLYFTGTGQAESFLKIYDNDKNTIDAEHFHLDV 248

RESULT 57
O93CC6 STAAU PRELIMINARY; PRT; 242 AA.
AC O93CC6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Seq.
GN Names=seq;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=COL;
RX MEDLINE=21935388; PubMed=11821418; DOI=10.1074/jbc.M111661200;
RA Yarwood J.M., McCormick J.K., Paustian M.L., Orwin P.M., Kapur V.,
RA Schlievert P.M.;
RT "Characterization and expression analysis of Staphylococcus aureus
RT pathogenicity island 3. Implications for the evolution of
RT staphylococcal pathogenicity islands.";
RL J. Biol. Chem. 277:13138-13147(2002).
DR EMBL; AF410775; AAL04146.1; -; Genomic_DNA.
DR HSP; P13380; 1KTK.
DR GO: 0005576; C: extracellular region; IEA.
DR GO: 0009405; P: pathogenesis; IEA.
DR InterPro: IPR006177; Bc1r1 tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR008375; Staph exotoxin.
DR InterPro: IPR006173; Staph tox OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PRINTS: PR01800; STAPHSTREP_TOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 242 AA; 28184 MW; F6EED4AF8C30D85 CRC64;

Query Match 25.6%; Score 316.5; DB 2; Length 242;
Best Local Similarity 33.8%; Pred. No. 7.6e-18;
Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;

QY 25 NLRQIY--YYNEK--AITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKY 80
DB 32 NLRNFYANPEPEKLGQVSSGNFSTSHQLE---YIDGKYTLYSQFH-----NEY 76

QY 81 KKGK-----KVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTBEEKVPINLWIDGKQ 135
DB 77 EAKRLXDKHKVDIFGISVSGLC-----NTKYMGGITLANQN-LDKPRNIPINLWNGKQ 129

QY 136 TTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYN-----SDSFGKQVORGL 183
DB 130 NTISTDKVSTQKKEVTAQIDIKRLKYLQNEVNIYGFNKTGKQGYQSKFNSGFNKGK 189

QY 184 IVFHSSEGSTVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLIDL 228
DB 190 ITPHLNNEPSFYDLYFTGTGQAESFLKIYDNDKNTIDAEHFHLDV 234

RESULT 58
Q5HHJ9 STAAC PRELIMINARY; PRT; 242 AA.
AC Q5HHJ9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Staphylococcal enterotoxin type I.
GN Names=sei; OrderedLocuNames=SACOL0887;
OS Staphylococcus aureus (strain COL)
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=93062;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,
RA Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA Hance I.R., Nelson K.E., Fraser C.M.;
RT "Insights on evolution of virulence and resistance from the complete
RT genome analysis of an early methicillin-resistant Staphylococcus
RT aureus strain and a biofilm-producing methicillin-resistant
RT Staphylococcus epidermidis strain.";
RL J. Bacteriol. 187:2426-2438(2005).
DR EMBL; CP000046; AAW36440.1; -; Genomic_DNA.
DR TIGR; SACOL0887; -.
DR GO: 0005576; C: extracellular region; IEA.
DR GO: 0009405; P: pathogenesis; IEA.
DR InterPro: IPR006177; Bc1r1 tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR008375; Staph exotoxin.
DR InterPro: IPR006173; Staph tox OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PRINTS: PR01800; STAPHSTREP_TOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 242 AA; 28184 MW; F6EED4AF8C30D85 CRC64;

Query Match 25.6%; Score 316.5; DB 2; Length 242;
Best Local Similarity 33.8%; Pred. No. 7.6e-18;
Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;

QY 25 NLRQIY--YYNEK--AITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKY 80
DB 32 NLRNFYANPEPEKLGQVSSGNFSTSHQLE---YIDGKYTLYSQFH-----NEY 76

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[illegible][illegible]

117 KGKITFHLNNEPSTFYDLFTGTGQAESFLKIYEDNKNTVESEKFHLD 163


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Qy 23 LSNLRQIYYNEKAITENKSDDDQFLENTLLFKGFFTGCHPWNLDLLVDLGSKDATNKYKG 82
Db 29 IDNLRNFTYTKDFDLKDVNDNTPIANQLQF-----SNESY-DLISESKDFNKFNSFKG 82
Qy 83 KYVDLYGAYGYCQAGGTPNKTAGYGVTLHDNNRLTEKKVPIINLWIDGKQTTVPIDK 142
Db 83 KKLDFVGISYNGQC-----NTKYIYGGVTA-TNEYLDKGRNIPINIWINGNHKTISTNK 135
Qy 143 VKTSKKEVTYQELDLQARHYLHGKFGLY-----NSDSFGGK-----VORGIVFHSSE 190
Db 136 VSTNKKFVTAQEIIVKLRLQBEYNIYGHNGTKKGEYGHKSFKYSGFNIGKVTFFLNN 195
Qy 191 GSTVSYDLF-DAQQYQPTLLRIYRDNKTINSENHLIDL 228
Db 196 NDTFSYDLFTGDDGLPKSFLKIYEDNKTVESEKFHLDV 234

RESULT 67
Q6GFM8 STAA8
ID Q6GFM8 STAA8 PRELIMINARY; PRT; 239 AA.
AC Q6GFM8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enterotoxin.
GN OrderedLocusNames=SAR1920;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jørgensen K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG40906.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 239 AA; 27410 MW; 74ABCTAEAF3FBF CRC64;

Query Match 24.4%; Score 302; DB 2; Length 239;
Best Local Similarity 33.0%; Pred. No. 1.2e-16;
Matches 72; Conservative 40; Mismatches 78; Indels 28; Gaps 7;

Qy 25 NLRQIYYNEKAIT--ENKESDDQFLENTLLFKGFFTGCHPWNLDLLVDLGSKDATNKYKG 82
Db 28 NLRN--YVGSYPIDHQINPNNRLSHQLVFS-----KDNSTVTAEFKNVEDVKFKFN 79
Qy 83 KYVDLYGAYGYCQAGGTPNKTAGYGVTLHDNNRLTEKKVPIINLWIDGKQTTVPIDK 142
Db 80 RAVDVYGLSYSGYCL-----KNKYMYGGVTL-AGDYLEKSRICIPINLWVNGLNKLTISTDK 133
Qy 143 VKTSKKEVTYQELDLQARHYLHGKFGLYNSD-----SFGGK-----VORGIVFHSSE 190
Db 134 VSTNKKIVTAQEIITKLRLYLOEYNIYGFNDTNKGRNYGTYSKFFSGFTGKISFHLND 193
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Qy 191 GSTVSYDLFPAQQYQPTLLRIYRDNKTINSENHLIDL 228
Db 194 GTSFSDYDLFTGTGQAESFLKIYDNKNKTIVETDKFHLDV 231

RESULT 68
Q5MAA8 STAAU
ID Q5MAA8 STAAU PRELIMINARY; PRT; 250 AA.
AC Q5MAA8;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Enterotoxin B (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=CMCC 26075;
RA Wang L., Zhang S., Yu M.;
RT "Nucleotide sequence of enterotoxin b gene from Staphylococcus
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY856382; AAW21709.1; -; Genomic DNA.
DR SNR; Q5MAA8; 12-250.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; UNKNOWN_1.
FT NON_TER
SQ SEQUENCE 250 AA; 29489 MW; DB64A76A441B952 CRC64;

Query Match 24.3%; Score 300.5; DB 2; Length 250;
Best Local Similarity 33.6%; Pred. No. 1.6e-16;
Matches 82; Conservative 47; Mismatches 96; Indels 19; Gaps 8;

Qy 1 SEKSEINEKDLRKKSQELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 11 AESQPPKPDDELHKSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYDLIYSIKDTK 68
Qy 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKTCMYGG 110
Db 69 LGNYDNNRVFEKKNLADKDYKVDVFGANYYYQCYFSKKTNDINSHQTDKRTCMYGG 128
Qy 111 VTLDNNRLTEKKVPIINLWIDGKQTTVPIDKVKTSKKEVTYQELDLQARHYLHGKFGLY 170
Db 129 VTEHNGQLDKYSITVRVVEDGK-NLLSFD-VQTNKKKVTAEQELDYLTRHYLVKNKKLY 186
Qy 171 NSDSFGKQVORGIVFHSSEGSTVSYDLFPAQQYQPT--TLLRIYRDNKTINSENHLIDL 228
Db 187 EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDKNKVMYDVKVIEV 243
Qy 229 YLYT 232
Db 244 YLYT 247

RESULT 69
ETXB STAAU
ID ETXB STAAU STANDARD; PRT; 266 AA.
AC P01552;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Enterotoxin type B precursor (SEB).
```

GN Name=entB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86168029; PubMed=3957869;
RA Jones C.L., Khan S.A.;
RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.";
RL J. Bacteriol. 166:29-33 (1986).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 40-91.
RX MEDLINE=85298255; PubMed=3898073;
RA Ranelli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
RT "Molecular cloning of staphylococcal enterotoxin B gene in Escherichia coli and Staphylococcus aureus.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854 (1985).
RN [3]
RP PROTEIN SEQUENCE OF 28-266 (S-6).
RX MEDLINE=71007902; PubMed=5470821;
RA Huang I.-Y., Bergdoll M.S.;
RT "The primary structure of staphylococcal enterotoxin B. 3. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence.";
RL J. Biol. Chem. 245:3518-3525 (1970).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=93063291; PubMed=1436058; DOI=10.1038/359801a0;
RA Swaminathan S., Pusey W.F. Jr., Fletcher J., Sax M.;
RT "Crystal structure of staphylococcal enterotoxin B, a superantigen.";
RL Nature 359:801-806 (1992).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
RX MEDLINE=94203282; PubMed=8152483; DOI=10.1038/368711a0;
RA Jardezy T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G., Chi Y.I., Stauffer C., Strominger J.L., Wiley D.C.;
RT "Three-dimensional structure of a human class II histocompatibility molecule complexed with superantigen.";
RL Nature 368:711-718 (1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
RX MEDLINE=9906298; PubMed=9881971; DOI=10.1016/S1074-7613(00)80846-9;
RA Li H., Llera A., Tsuchiya D., Leder L., Ysern X., Schlievert P.M., Karjalainen K., Mariuzza R.A.;
RT "Three-dimensional structure of the complex between a T cell receptor beta chain and the superantigen staphylococcal enterotoxin B.";
RL Immunity 9:807-816 (1998).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=98181012; PubMed=9514739; DOI=10.1006/jmbi.1997.1577;
RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;
RT "Crystal structure of microbial superantigen staphylococcal enterotoxin B at 1.5-A resolution: Implications for superantigen recognition by MHC class II molecules and T-cell receptors.";
RL J. Mol. Biol. 277:61-79 (1998).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-- the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
CC ENBL; M11118; AAA89550.1; -; Genomic_DNA.
DR PIR; S27360; ENSAB6.
DR PDB; 1DSM; X-ray; C=28-266.

DR PDB; 1DSX; X-ray; C=28-266.
DR PDB; 1DSZ; X-ray; C=28-266.
DR PDB; 1D6E; X-ray; C=28-266.
DR PDB; 1GOZ; X-ray; A/B=28-266.
DR PDB; 1SBB; X-ray; B/D=28-266.
DR PDB; 1SE3; X-ray; @=28-266.
DR PDB; 1SE4; X-ray; @=28-266.
DR PDB; 1SEB; X-ray; D/H=29-262.
DR PDB; 1SEB; X-ray; D=28-266.
DR PDB; 1SEB; X-ray; @=28-266.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRILTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW 3D-structure; Antigen; Direct protein sequencing; Enterotoxin; Signal;
KW Superantigen; Toxin.
FT SIGNAL 1 27 Enterotoxin type B.
FT CHAIN 28 266
FT DISULFID 120 140 DDN -> NND (in Ref. 3).
FT CONFLICT 56 58 DQFLYFDLI -> NEFFDLIYL (in Ref. 3).
FT CONFLICT 69 77 Missing (in Ref. 3).
FT CONFLICT 118 118 DIN -> NID (in Ref. 3).
FT CONFLICT 128 130 QTD -> ENT (in Ref. 3).
FT CONFLICT 133 135 NG -> GN (in Ref. 3).
FT CONFLICT 149 150 Y -> YY (in Ref. 3).
FT CONFLICT 156 156 QE -> EQ (in Ref. 3).
FT CONFLICT 185 186 D -> N (in Ref. 3).
FT CONFLICT 233 233 DN -> ND (in Ref. 3).
FT CONFLICT 246 247
FT STRAND 29 29
FT HELIX 41 43
FT STRAND 44 44
FT TURN 48 48
FT HELIX 49 52
FT HELIX 53 55
FT STRAND 60 66
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 78
FT TURN 83 85
FT STRAND 90 94
FT HELIX 98 104
FT TURN 105 106
FT STRAND 108 113
FT TURN 116 116
FT TURN 118 119
FT TURN 127 128
FT STRAND 138 142
FT STRAND 145 147
FT TURN 149 150
FT STRAND 152 165
FT TURN 166 167
FT STRAND 168 179
FT STRAND 181 183
FT HELIX 184 199
FT TURN 209 218
FT TURN 219 220
FT STRAND 221 226
FT STRAND 232 232
FT HELIX 237 241
FT HELIX 242 246
FT STRAND 249 251
FT TURN 252 254
FT STRAND 255 263
SQ SEQUENCE 266 AA; 31436 MW; B6D417F61CF018B0 CRC64;
Query Match 24.3%; Score 300.5; DB 1; Length 266;
Best Local Similarity 33.6%; Pred. No. 1.8e-16;

Matches		82; Conservative	47; Mismatches	96; Indels	19; Gaps	8;
Qy	1	SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG	60			
Db	27	ABSQDPKPELHKSKF-TGLMENMKVLYDDNHVSAT-NVKSIDQFLYDLIYSIKDTK	84			
Qy	61	HPWYNDLLVLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGG	110			
Db	85	LGNVDNVRVEFKNKLADKYKVDVFGVANYQCYFSKKTNDINSHQTDKRTCMYGG	144			
Qy	111	VTLHDNNRLTEEEKVPIINLWDGQTTVPIDKVKTSKKEVTQVELDQARHYLHGKFGY	170			
Db	145	VTEHNGNQLDKYRSITVRVFDGK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVNKKLY	202			
Qy	171	NSDSFGGKVGRLIVFHSSEGSTVSYDLFDAQGYPD--TLRLYRNKNTINSNLHIDL	228			
Db	203	EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNQVDSKDVKIEV	259			
Qy	229	YLYT 232				
Db	260	YLT 263				
RESULT 70						
ID	Q7BBY8	STAAU PRELIMINARY;	PRT;	266	AA.	
AC	Q7BBY8					
DT	10-MAY-2005	(Tremblrel. 30, Created)				
DT	10-MAY-2005	(Tremblrel. 30, Last sequence update)				
DT	10-MAY-2005	(Tremblrel. 30, Last annotation update)				
DE	Seb.					
GN	Names=seb;					
OC	Staphylococcus aureus					
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus					
OX	NCBI_TaxID=1280;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=COL;					
RX	MSDLN=21935389; PubMed=11821418; DOI=10.1074/jbc.M111661200;					
RA	Yarwood J.M., McCormick J.K., Paustian M.L., Orwin P.M., Kapur V.,					
RA	Schlievert P.M.;					
RT	"Characterization and expression analysis of Staphylococcus aureus					
RT	pathogenicity island 3. Implications for the evolution of					
RT	staphylococcal pathogenicity islands."					
RL	J. Biol. Chem. 277:13138-13147(2002).					
DR	EMBL; AF410775; AAJ04126.1 -; Genomic DNA.					
SQ	SEQUENCE 266 AA; 31436 MW; B6D417F61CF018B0 CRC64;					
Query Match						
Best Local Similarity		24.3%; Score 300.5; DB 2; Length 266;				
Matches		82; Conservative	47; Mismatches	96; Indels	19; Gaps	8;
Qy	1	SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG	60			
Db	27	ABSQDPKPELHKSKF-TGLMENMKVLYDDNHVSAT-NVKSIDQFLYDLIYSIKDTK	84			
Qy	61	HPWYNDLLVLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGG	110			
Db	85	LGNVDNVRVEFKNKLADKYKVDVFGVANYQCYFSKKTNDINSHQTDKRTCMYGG	144			
Qy	111	VTLHDNNRLTEEEKVPIINLWDGQTTVPIDKVKTSKKEVTQVELDQARHYLHGKFGY	170			
Db	145	VTEHNGNQLDKYRSITVRVFDGK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVNKKLY	202			
Qy	171	NSDSFGGKVGRLIVFHSSEGSTVSYDLFDAQGYPD--TLRLYRNKNTINSNLHIDL	228			
Db	203	EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNQVDSKDVKIEV	259			
Qy	229	YLYT 232				
Db	260	YLT 263				
RESULT 72						
ID	Q5MAB7	STAAU PRELIMINARY;	PRT;	239	AA.	
AC	Q5MAB7					
DT	01-FEB-2005	(Tremblrel. 29, Created)				

Matches		82; Conservative	47; Mismatches	96; Indels	19; Gaps	8;
Qy	1	SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG	60			
Db	27	ABSQDPKPELHKSKF-TGLMENMKVLYDDNHVSAT-NVKSIDQFLYDLIYSIKDTK	84			
Qy	61	HPWYNDLLVLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGG	110			
Db	85	LGNVDNVRVEFKNKLADKYKVDVFGVANYQCYFSKKTNDINSHQTDKRTCMYGG	144			
Qy	111	VTLHDNNRLTEEEKVPIINLWDGQTTVPIDKVKTSKKEVTQVELDQARHYLHGKFGY	170			
Db	145	VTEHNGNQLDKYRSITVRVFDGK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVNKKLY	202			
Qy	171	NSDSFGGKVGRLIVFHSSEGSTVSYDLFDAQGYPD--TLRLYRNKNTINSNLHIDL	228			
Db	203	EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNQVDSKDVKIEV	259			
Qy	229	YLYT 232				
Db	260	YLT 263				
RESULT 71						
ID	Q5HHH9	STAAU PRELIMINARY;	PRT;	266	AA.	
AC	Q5HHH9					
DT	10-MAY-2005	(Tremblrel. 30, Created)				
DT	10-MAY-2005	(Tremblrel. 30, Last sequence update)				
DT	10-MAY-2005	(Tremblrel. 30, Last annotation update)				
DE	Staphylococcal enterotoxin B.					
GN	Name=seb; OrderedLocusNames=SACOL0907;					
OS	Staphylococcus aureus (strain COL)					
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus					
OX	NCBI_TaxID=93062;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]					
RX	PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;					
RA	Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,					
RA	Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,					
RA	Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,					
RA	Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,					
RA	Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,					
RA	Hance I.R., Nelson K.E., Fraser C.M.;					
RT	"Insights on evolution of virulence and resistance from the complete					
RT	genome analysis of an early methicillin-resistant Staphylococcus					
RT	aureus strain and a biofilm-producing methicillin-resistant					
RT	Staphylococcus epidermidis strain."					
RL	J. Bacteriol. 187:2426-2438(2005).					
DR	EMBL; CP000046; AAW37877.1; -; Genomic_DNA.					
DR	SMR; Q5HHH9; 28-266.					
DR	TIGR; SACOL0907; -.					
DR	GO; GO:0005576; C:extracellular region; IEA.					
DR	GO; GO:0009405; P:pathogenesis; IEA.					
DR	InterPro; IPR006177; Bctrl tox.					
DR	InterPro; IPR006123; Staph/Strep. toxin.					
DR	InterPro; IPR006126; Staph/Strep. tox.					
DR	Pfam; PF01123; Staph Strep toxin; 1.					
DR	Pfam; PF02876; Staph Strep toxin; 1.					
DR	PRINTS; PR00279; BACTRLTOXIN.					
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN 1.					
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; UNKNOWN 1.					
KW	Complete proteome.					
SQ	SEQUENCE 266 AA; 31436 MW; B6D417F61CF018B0 CRC64;					
Query Match						
Best Local Similarity		24.3%; Score 300.5; DB 2; Length 266;				
Matches		82; Conservative	47; Mismatches	96; Indels	19; Gaps	8;
Qy	1	SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG	60			
Db	27	ABSQDPKPELHKSKF-TGLMENMKVLYDDNHVSAT-NVKSIDQFLYDLIYSIKDTK	84			
Qy	61	HPWYNDLLVLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGG	110			
Db	85	LGNVDNVRVEFKNKLADKYKVDVFGVANYQCYFSKKTNDINSHQTDKRTCMYGG	144			
Qy	111	VTLHDNNRLTEEEKVPIINLWDGQTTVPIDKVKTSKKEVTQVELDQARHYLHGKFGY	170			
Db	145	VTEHNGNQLDKYRSITVRVFDGK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVNKKLY	202			
Qy	171	NSDSFGGKVGRLIVFHSSEGSTVSYDLFDAQGYPD--TLRLYRNKNTINSNLHIDL	228			
Db	203	EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNQVDSKDVKIEV	259			
Qy	229	YLYT 232				
Db	260	YLT 263				
RESULT 72						
ID	Q5MAB7	STAAU PRELIMINARY;	PRT;	239	AA.	
AC	Q5MAB7					
DT	01-FEB-2005	(Tremblrel. 29, Created)				

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DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Enterotoxin B (Fragment).
GN Name=seb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 14458;
RA Kamboj D.V., Nena V., Singh L.;
RT "Enterotoxin B gene (seb) sequence of Staphylococcus aureus strain ATCC14458.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY852244; AAM19659.1; -; Genomic_DNA.
DR SMR; Q5MAB7; 1-239.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRUTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 239 AA; 28368 MW; AD5566B24A2E2750 CRC64;

Query Match 24.2%; Score 299.5; DB 2; Length 239;
Best Local Similarity 33.7%; Pred. No. 1.9e-16;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;

Qy 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITE--NKESDDQFLENTLLPKGFPTGH 61
Db 1 ESQDDPKPDELRKSKF-TGLMENKVLVDNHSVAI-NVKSIDQFDYFDIYIKDTKL 58

Qy 62 PWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQC-----AGTPTNKTCMYGGV 111
Db 59 GNYDNRVFEQNKDLADKYDKYVDVFGANYYYCYFSKKTINDINSHQTDKRTCMYGGV 118

Qy 112 TLHNNRLTEBKVPINLWIDGKQTTVPIDKVTSKKEVTVDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSTVRVFEDGK-NLLSFD-VQTNKKKVTAEQLDYLTRHYLVKNKKLYE 176

Qy 172 SDSFGKVGRLIVFHSEGSTVSYDLFDAQGYPD--TLRIYEDNKNTINSENHLIDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMWPAPGDKFDQSKYLLMYNDNMVDSKDVKIEVY 233

Qy 230 LYT 232
Db 234 LTT 236

RESULT 73
Q6YCN4 STAAU
ID Q6YCN4 STAAU PRELIMINARY; PRT; 261 AA.
AC Q6YCN4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Enterotoxin SEU variant.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=382F;
RX MEDLINE=22692404; PubMed=12807452;
RX DOI=10.1046/j.1365-2672.2003.01957.x;
RA Leterre C., Perelle S., Dillasser F., Fach P.;
RT "Identification of a new putative enterotoxin SEU encoded by the egc

cluster of Staphylococcus aureus.";
J. Appl. Microbiol. 95:38-43(2003).
EMBL; AY158703; AA017732.1; -; Genomic_DNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR006123; Staph/Strep_toxin.
InterPro; IPR006126; Staph/Strep_tox.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF01123; Staph_Strp_toxin; 1.
Pfam; PF02876; Staph_Strp_tox_C; 1.
PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 261 AA; 30547 MW; A407E960CC5974B0 CRC64;

Query Match 24.1%; Score 298; DB 2; Length 261;
Best Local Similarity 31.5%; Pred. No. 2.8e-16;
Matches 80; Conservative 49; Mismatches 79; Indels 46; Gaps 13;

Qy 3 KSEEINEKDLRKSELQNALSNLRQIYYNEKAITE--NKESDDQFLENTLLPKGFPTGH 61
Db 25 KPEQLN-----KASEF-TGLMDNMR--YLYDDKHVSEINIKAEKFLQHDLLFK----- 70

Qy 62 PWYNDLLVDLGSK-----DATNKYKGVLDLYGAYGYCAGGTPN-----K 103
Db 71 --INGSKID-GSKILKTEFNNSLSUDKYKNKIDLFGTNYYYCYFSADNMELNDGRLE 127

Qy 104 TACMYGGVTLHDNNRLTEERKV--PINLWI---DGKQTTVPIDKVTSKKEVTVDLQ 158
Db 128 KTCMYGGVTEHDGQIDKNNSTONSHILIKVFENRNSLSFD-IPNKKNITAEIDYK 186

Qy 159 ARHYLHGKFGLYNSDSFGKVGRLIVFHSEGSTVSYDLFDAQGO--YPTLLRIYRDN 216
Db 187 VRNYLLKHKLIEFNS--SPYETGYIKFIENGSHFWDMPESGEKFPYPTKYLIIYNDN 244

Qy 217 KTINSENHLIDLY 230
Db 245 KTVESKINSINVEVHL 258

RESULT 74
Q6GFNO STAAU
ID Q6GFNO STAAU PRELIMINARY; PRT; 261 AA.
AC Q6GFNO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Enterotoxin.
GN OrderedLocusNames=SAR1918;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Mouton R., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG40904.1; -; Genomic_DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
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DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 261 AA; 30547 MW; A407B960CC5974B0 CRC64;

Query Match      24.1%; Score 298; DB 2; Length 261;
Best Local Similarity 31.5%; Pred. No. 2.8e-16;
Matches 80; Conservative 49; Mismatches 79; Indels 46; Gaps 13;

OY 3 KSEINEKDLKKSELQNALNLRLQIYYNYNEKAITE--YDDEKRVSEINIKAEKFLQHLLEFK----- 70
DB 25 KPEQLN-----KASEF-TGLMDNMR--YLDDKRVSEINIKAEKFLQHLLEFK----- 70
OY 62 PTWYNDLLVLDGSK-----DATNKYKGGKVDLYGAYTYGYOCAGGTPN-----K 103
DB 71 --INGSKID--GSKILKTEFNNSLSDKYKKNIDLFCTNYNYQCYPSADNMELNDGRLIE 127
OY 104 TACMYGGVTLHNNRLTEKKV--PINLMI---DGKQTTVPIDKVKTSKKEVTVQELDLQ 158
DB 128 KTCMYGGVTEHDGNQIDKNNSTONSHNLIKVFENERNLSFD-IPTNKKNITAEQIDYK 186
OY 159 ARVYLGKFGLYNSDSFGGKVGQRLIVFHSSEGSTVSYDLFDAQGO--YPTULLRIYRDN 216
DB 187 VRNYLLKHKNLDFEFS--SPYETGYIRFIEGNHGSFWYDMPPSGEKFYPTKYLLIYNDN 244
OY 217 KTINSENHLHIDLVL 230
DB 245 KTVESKSINVEVHL 258

RESULT 75
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ID Q5XCI7 STRP6 PRELIMINARY; PRT; 256 AA.
AC Q5XCI7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE SpeA variant.
GN OrderedLocNames=M6_Spy0741;
OS Streptococcus pyogenes (serotype M6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=301450;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MGAS10394;
RX PubMed=15272401; DOI=10.1086/422697;
RA Banks D.J., Porcella S.F., Barbican K.D., Beres S.B., Phillips L.E.,
RA Voyich J.M., Deleo F.R., Martin J.M., Somerville G.A., Musser J.M.;
RT "Progress toward characterization of the group A Streptococcus
RT metagenome: complete genome sequence of a macrolide-resistant serotype
RT M6 strain."
RL J. Infect. Dis. 190:727-738 (2004).
DR EMBL; CP000003; AAT86876.1; -; Genomic_DNA.
DR SMR; Q5XCI7; 36-256.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN_
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 256 AA; 29981 MW; 4A473337FDE2E3F4 CRC64;

Query Match      23.9%; Score 296.5; DB 2; Length 256;
Best Local Similarity 33.9%; Pred. No. 3.6e-16;
Matches 79; Conservative 43; Mismatches 100; Indels 11; Gaps 7;
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:18:35 ; Search time 17.7646 Seconds
(without alignments)
1084.369 Million cell updates/sec

Title: US-09-900-766-7

Perfect score: 1238

Sequence: 1 SEKSEINEKURKKSELR.....RDNKTINSENHLDLYLTYT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1238	100.0	257	2	US-08-486-099-112
3	1238	100.0	257	2	US-08-360-107A-122
4	1238	100.0	257	2	US-08-484-223B-112
5	1238	100.0	257	2	US-08-919-597-112
6	1238	100.0	257	2	US-08-475-668A-112
7	1238	100.0	257	2	US-08-485-551A-112
8	1238	100.0	257	2	US-08-471-913A-112
9	1238	100.0	257	2	US-08-485-264A-112
10	1238	100.0	257	2	US-08-474-349A-112
11	1238	100.0	257	2	US-08-470-896-112
12	1238	100.0	257	2	US-08-485-546A-112
13	1238	100.0	257	2	US-08-487-266A-112
14	1238	100.0	257	2	US-08-484-741-112
15	1202	97.1	254	2	US-09-350-841A-1598
16	1171	94.6	226	2	US-08-896-933-24
17	1171	94.6	226	2	US-09-314-235-24
18	1171	94.6	226	2	US-09-708-008B-24
19	1023	82.6	233	2	US-08-695-692B-7
20	1023	82.6	257	2	US-08-486-099-113
21	1023	82.6	257	2	US-08-360-107A-123
22	1023	82.6	257	2	US-08-484-223B-113
23	1023	82.6	257	2	US-08-919-597-113
24	1023	82.6	257	2	US-08-475-668A-113
25	1023	82.6	257	2	US-08-485-551A-113
26	1023	82.6	257	2	US-08-471-913A-113
27	1023	82.6	257	2	US-08-485-264A-113

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29	1023	82.6	257	2	US-08-470-896-113	Sequence 113, App
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32	1023	82.6	257	2	US-08-484-741-113	Sequence 113, App
33	1019	82.3	233	1	US-08-446-918A-4	Sequence 4, Appli
34	1019	82.3	233	1	US-08-580-806-4	Sequence 4, Appli
35	1003.5	81.1	232	2	US-08-896-933-23	Sequence 23, Appl
36	1003.5	81.1	232	2	US-09-314-235-23	Sequence 23, Appl
37	1003.5	81.1	232	2	US-09-708-008B-23	Sequence 23, Appl
38	1000	80.8	257	2	US-09-144-776B-2	Sequence 2, Appli
39	1000	80.8	257	2	US-08-882-431B-2	Sequence 2, Appli
40	996	80.5	233	2	US-09-144-776B-4	Sequence 4, Appli
41	996	80.5	233	2	US-08-882-431B-4	Sequence 4, Appli
42	926.5	74.8	252	2	US-09-350-841A-1599	Sequence 1599, Ap
43	657	53.1	228	2	US-08-896-933-25	Sequence 25, Appl
44	657	53.1	228	2	US-09-314-235-25	Sequence 25, Appl
45	657	53.1	228	2	US-09-708-008B-25	Sequence 25, Appl
46	457	36.9	82	2	US-09-144-776B-19	Sequence 19, Appl
47	457	36.9	82	2	US-08-882-431B-19	Sequence 19, Appl
48	399	32.2	82	2	US-09-144-776B-17	Sequence 17, Appl
49	399	32.2	82	2	US-08-882-431B-17	Sequence 17, Appl
50	300	24.2	255	1	US-08-446-918A-2	Sequence 2, Appli
51	300	24.2	255	1	US-08-580-806-2	Sequence 2, Appli
52	296.5	23.9	221	2	US-08-896-933-29	Sequence 29, Appl
53	296.5	23.9	221	2	US-09-314-235-29	Sequence 29, Appl
54	296.5	23.9	221	2	US-09-708-008B-29	Sequence 29, Appl
55	294.5	23.8	251	2	US-08-973-391C-13	Sequence 13, Appl
56	294.5	23.8	251	2	US-10-625-221-13	Sequence 13, Appl
57	294.5	23.8	251	2	US-09-308-830B-13	Sequence 13, Appl
58	293.5	23.7	240	2	US-09-555-115A-4	Sequence 4, Appli
59	293.5	23.7	240	2	US-09-144-776B-6	Sequence 6, Appli
60	293.5	23.7	266	2	US-08-882-431B-6	Sequence 6, Appli
61	292.5	23.6	239	2	US-08-896-933-26	Sequence 26, Appl
62	292.5	23.6	239	2	US-09-314-235-26	Sequence 26, Appl
63	292.5	23.6	239	2	US-09-708-008B-26	Sequence 26, Appl
64	292.5	23.6	266	2	US-09-414-276-8	Sequence 8, Appli
65	291.5	23.5	221	2	US-08-973-391C-14	Sequence 14, Appl
66	291.5	23.5	221	2	US-10-625-221-14	Sequence 14, Appl
67	291.5	23.5	221	2	US-09-308-830B-14	Sequence 14, Appl
68	289.5	23.4	251	2	US-09-144-776B-16	Sequence 16, Appl
69	289.5	23.4	251	2	US-08-882-431B-16	Sequence 16, Appl
70	288.5	23.3	239	2	US-09-144-776B-10	Sequence 10, Appl
71	288.5	23.3	239	2	US-08-882-431B-10	Sequence 10, Appl
72	288.5	23.3	240	2	US-09-555-115A-3	Sequence 3, Appli
73	287.5	23.2	240	2	US-09-555-115A-6	Sequence 6, Appli
74	285.5	23.1	240	2	US-09-555-115A-5	Sequence 5, Appli
75	283.5	22.9	240	2	US-09-555-115A-2	Sequence 2, Appli
76	282.5	22.8	266	2	US-09-144-776B-8	Sequence 8, Appli
77	282.5	22.8	266	2	US-08-882-431B-8	Sequence 8, Appli
78	281.5	22.7	238	2	US-08-896-933-28	Sequence 28, Appl
79	281.5	22.7	238	2	US-09-314-235-28	Sequence 28, Appl
80	281.5	22.7	238	2	US-09-708-008B-28	Sequence 28, Appl
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82	276.5	22.3	240	2	US-09-555-115A-8	Sequence 8, Appli
83	267.5	21.6	239	2	US-08-896-933-27	Sequence 27, Appl
84	267.5	21.6	239	2	US-09-314-235-27	Sequence 27, Appl
85	267.5	21.6	239	2	US-09-708-008B-27	Sequence 27, Appl
86	265.5	21.4	240	2	US-09-555-115A-1	Sequence 1, Appli
87	260.5	21.0	239	2	US-08-896-933-21	Sequence 21, Appl
88	260.5	21.0	239	2	US-09-314-235-21	Sequence 21, Appl
89	260.5	21.0	239	2	US-09-708-008B-21	Sequence 21, Appl
90	258.5	20.9	266	2	US-09-144-776B-14	Sequence 14, Appl
91	258.5	20.9	266	2	US-08-882-431B-14	Sequence 14, Appl
92	245	19.8	220	2	US-08-896-933-20	Sequence 20, Appl
93	245	19.8	220	2	US-09-314-235-20	Sequence 20, Appl
94	245	19.8	220	2	US-09-708-008B-20	Sequence 20, Appl
95	215	17.4	82	2	US-09-144-776B-18	Sequence 18, Appl
96	215	17.4	82	2	US-08-882-431B-18	Sequence 18, Appl
97	191	15.4	45	1	US-08-220-378-1	Sequence 1, Appli
98	191	15.4	45	1	US-08-696-012-1	Sequence 1, Appli
99	183.5	14.8	235	2	US-08-336-036-2	Sequence 2, Appli
100	183.5	14.8	235	2	US-09-308-829-2	Sequence 2, Appli

101	181.5	14.7	208	2	US-08-896-933-30	Sequence 30, Appl	174	93	7.5	28	2	US-09-314-235-22	Sequence 22, Appl
102	181.5	14.7	208	2	US-09-314-235-30	Sequence 30, Appl	175	93	7.5	28	2	US-09-708-008B-22	Sequence 22, Appl
103	181.5	14.7	208	2	US-09-708-008B-30	Sequence 30, Appl	176	92.5	7.5	337	2	US-09-248-798A-16723	Sequence 16723, A
104	137.5	11.1	89	2	US-09-144-776B-20	Sequence 20, Appl	177	92.5	7.5	1183	2	US-09-532-310B-5	Sequence 5, Appl
105	137.5	11.1	89	2	US-08-882-431B-20	Sequence 20, Appl	178	89.5	7.2	36	2	US-08-838-413A-7	Sequence 7, Appl
106	129	10.4	28	1	US-08-220-378-2	Sequence 2, Appl	179	89.5	7.2	36	2	US-09-355-581-7	Sequence 8, Appl
107	129	10.4	28	1	US-08-696-012-2	Sequence 2, Appl	180	89.5	7.2	38	2	US-08-838-413A-8	Sequence 8, Appl
108	127	10.3	24	2	US-08-838-413A-22	Sequence 22, Appl	181	89.5	7.2	38	2	US-09-355-581-8	Sequence 8, Appl
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112	124	10.0	29	1	US-08-220-378-6	Sequence 6, Appl	185	89	7.2	317	2	US-09-134-001C-3300	Sequence 3300, Ap
113	124	10.0	29	1	US-08-696-012-6	Sequence 6, Appl	186	89	7.2	317	2	US-09-248-796A-19212	Sequence 19212, A
114	121	9.8	79	2	US-09-144-776B-24	Sequence 24, Appl	187	89	7.2	631	1	US-08-487-890A-115	Sequence 115, App
115	121	9.8	79	2	US-08-882-431B-24	Sequence 24, Appl	188	89	7.2	631	1	US-08-478-435-115	Sequence 115, App
116	120	9.7	22	1	US-08-220-378-4	Sequence 4, Appl	189	89	7.2	631	1	US-08-337-483-115	Sequence 115, App
117	120	9.7	22	1	US-08-696-012-4	Sequence 4, Appl	190	89	7.2	631	1	US-08-478-373-115	Sequence 115, App
118	112.5	9.1	89	2	US-09-144-776B-22	Sequence 22, Appl	191	89	7.2	631	1	US-08-474-671-115	Sequence 115, App
119	112.5	9.1	89	2	US-09-144-776B-23	Sequence 23, Appl	192	89	7.2	631	2	US-08-483-577A-115	Sequence 115, App
120	112.5	9.1	89	2	US-08-882-431B-22	Sequence 22, Appl	193	89	7.2	631	2	US-08-897-438-115	Sequence 115, App
121	112.5	9.1	89	2	US-08-882-431B-23	Sequence 23, Appl	194	89	7.2	631	2	US-08-637-654-115	Sequence 115, App
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124	110	8.9	23	1	US-08-220-378-10	Sequence 10, Appl	197	87	7.0	286	2	US-09-134-001C-4103	Sequence 4103, Ap
125	110	8.9	23	1	US-08-696-012-10	Sequence 10, Appl	198	86.5	7.0	258	2	US-09-107-532A-4002	Sequence 4002, Ap
126	109	8.8	27	2	US-08-896-933-34	Sequence 34, Appl	199	86.5	7.0	834	1	US-08-471-033-21	Sequence 21, Appl
127	109	8.8	27	2	US-09-314-235-34	Sequence 34, Appl	200	86.5	7.0	834	1	US-08-471-044-21	Sequence 21, Appl
128	109	8.8	27	2	US-09-708-008B-34	Sequence 34, Appl	201	86.5	7.0	834	1	US-08-463-483A-21	Sequence 21, Appl
129	109	8.8	193	2	US-08-896-933-31	Sequence 31, Appl	202	86.5	7.0	834	1	US-08-471-046A-21	Sequence 21, Appl
130	109	8.8	193	2	US-09-314-235-31	Sequence 31, Appl	203	86.5	7.0	834	1	US-08-470-566B-21	Sequence 21, Appl
131	109	8.8	193	2	US-09-708-008B-31	Sequence 31, Appl	204	86.5	7.0	834	1	US-08-469-334-21	Sequence 21, Appl
132	109	8.8	229	2	US-09-350-841A-1597	Sequence 1597, Ap	205	86.5	7.0	834	1	US-09-300-529-21	Sequence 21, Appl
133	107.5	8.7	234	2	US-08-486-099-111	Sequence 111, App	206	85	6.9	17	2	US-08-896-933-10	Sequence 10, Appl
134	107.5	8.7	234	2	US-08-360-107A-131	Sequence 121, App	207	85	6.9	17	2	US-09-314-235-10	Sequence 10, Appl
135	107.5	8.7	234	2	US-08-484-223B-111	Sequence 111, App	208	85	6.9	17	2	US-09-708-008B-10	Sequence 10, Appl
136	107.5	8.7	234	2	US-08-919-597-111	Sequence 111, App	209	85	6.9	17	2	US-09-555-115A-34	Sequence 34, Appl
137	107.5	8.7	234	2	US-08-475-668A-111	Sequence 111, App	210	84.5	6.8	228	2	US-09-710-279-1166	Sequence 1166, Ap
138	107.5	8.7	234	2	US-08-485-551A-111	Sequence 111, App	211	84.5	6.8	351	2	US-10-087-013-9	Sequence 9, Appl
139	107.5	8.7	234	2	US-08-471-913A-111	Sequence 111, App	212	84.5	6.8	406	2	US-09-134-000C-3752	Sequence 3752, Ap
140	107.5	8.7	234	2	US-08-485-264A-111	Sequence 111, App	213	84.5	6.8	1588	4	PCT-US93-07261-11	Sequence 11, Appl
141	107.5	8.7	234	2	US-08-474-349A-111	Sequence 111, App	214	84.5	6.8	1663	4	PCT-US93-07261-16	Sequence 16, Appl
142	107.5	8.7	234	2	US-08-470-896-111	Sequence 111, App	215	84	6.8	366	2	US-09-134-001C-4412	Sequence 4412, Ap
143	107.5	8.7	234	2	US-08-485-546A-111	Sequence 111, App	216	84	6.8	558	2	US-09-902-540-14971	Sequence 14971, A
144	107.5	8.7	234	2	US-08-487-266A-111	Sequence 111, App	217	84	6.8	675	2	US-09-134-001C-4547	Sequence 4547, Ap
145	107.5	8.7	234	2	US-08-484-741-111	Sequence 111, App	218	84	6.8	1014	2	US-09-762-724-2	Sequence 2, Appl
146	106.5	8.6	29	1	US-08-220-378-9	Sequence 9, Appl	219	83.5	6.7	251	2	US-09-543-681A-6514	Sequence 6514, Ap
147	106.5	8.6	29	1	US-08-696-012-9	Sequence 9, Appl	220	83.5	6.7	752	2	US-09-710-279-1138	Sequence 1138, Ap
148	106	8.6	28	1	US-08-220-378-7	Sequence 7, Appl	221	83.5	6.7	767	2	US-09-134-001C-4023	Sequence 4023, Ap
149	106	8.6	28	1	US-08-696-012-7	Sequence 7, Appl	222	83	6.7	442	2	US-09-248-796A-21400	Sequence 21400, A
150	105.5	8.5	89	2	US-09-144-776B-21	Sequence 21, Appl	223	82.5	6.7	356	2	US-08-887-534A-72	Sequence 72, Appl
151	105.5	8.5	89	2	US-08-882-431B-21	Sequence 21, Appl	224	82.5	6.7	356	2	US-09-527-431-72	Sequence 72, Appl
152	105.5	8.5	194	1	US-08-446-918A-6	Sequence 6, Appl	225	82.5	6.7	356	2	US-09-446-861-72	Sequence 72, Appl
153	105.5	8.5	194	1	US-08-580-806-6	Sequence 6, Appl	226	82.5	6.7	363	2	US-08-956-171E-5237	Sequence 5237, Ap
154	105	8.5	25	1	US-08-220-378-3	Sequence 3, Appl	227	82.5	6.7	363	2	US-08-781-986A-5237	Sequence 5237, Ap
155	105	8.5	25	1	US-08-696-012-3	Sequence 3, Appl	228	82	6.6	168	2	US-09-134-000C-4049	Sequence 4049, Ap
156	104.5	8.4	234	2	US-09-144-776B-12	Sequence 12, Appl	229	82	6.6	287	2	US-09-270-767-3363	Sequence 3363, A
157	104.5	8.4	234	2	US-08-882-431B-12	Sequence 12, Appl	230	82	6.6	287	2	US-09-270-767-48480	Sequence 48480, A
158	100.5	8.1	234	1	US-08-152-456A-2	Sequence 2, Appl	231	82	6.6	627	2	US-10-071-035-452	Sequence 452, App
159	100.5	8.1	234	1	US-08-440-221-2	Sequence 2, Appl	232	82	6.6	627	2	US-10-206-576-452	Sequence 452, App
160	100	8.1	28	1	US-08-220-378-8	Sequence 8, Appl	233	82	6.6	696	2	US-09-134-000C-4874	Sequence 4874, Ap
161	100	8.1	28	1	US-08-696-012-8	Sequence 8, Appl	234	82	6.6	932	2	US-09-248-796A-19128	Sequence 19128, A
162	94.5	7.6	402	2	US-09-134-001C-4674	Sequence 4674, Ap	235	82	6.6	1028	2	US-09-583-110-4290	Sequence 4290, Ap
163	93.5	7.6	631	1	US-08-487-890A-111	Sequence 111, App	236	82	6.6	1030	2	US-09-107-433-2786	Sequence 2786, Ap
164	93.5	7.6	631	1	US-08-478-435-111	Sequence 111, App	237	82	6.6	1313	2	US-09-071-033-454	Sequence 450, App
165	93.5	7.6	631	1	US-08-337-483-111	Sequence 111, App	238	82	6.6	1313	2	US-09-071-035-454	Sequence 454, App
166	93.5	7.6	631	1	US-08-478-373-111	Sequence 111, App	239	82	6.6	1313	2	US-10-206-576-450	Sequence 450, App
167	93.5	7.6	631	2	US-08-474-671-111	Sequence 111, App	240	82	6.6	1313	2	US-10-206-576-454	Sequence 454, App
168	93.5	7.6	631	2	US-08-483-578A-111	Sequence 111, App	241	81.5	6.6	229	2	US-09-631-616-13	Sequence 13, Appl
169	93.5	7.6	631	2	US-08-897-438-111	Sequence 111, App	242	81.5	6.6	616	2	US-09-393-529-2	Sequence 2, Appl
170	93.5	7.6	631	2	US-08-637-654-111	Sequence 111, App	243	81.5	6.6	616	2	US-09-396-149-7	Sequence 7, Appl
171	93.5	7.6	631	2	US-08-649-518-111	Sequence 111, App	244	81.5	6.6	1017	2	US-10-104-047-2312	Sequence 2312, Ap
172	93	7.5	16	2	US-08-695-692B-20	Sequence 20, Appl	245	81	6.5	14	2	US-08-896-933-1	Sequence 1, Appl
173	93	7.5	28	2	US-08-896-933-22	Sequence 22, Appl	246	81	6.5	14	2	US-08-896-933-9	Sequence 9, Appl


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/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE: 07-JUN-1995
/ APPLICATION NUMBER: US/08/486,099
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-031
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 112:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-486-099-112

Query Match 100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELRNALSRLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELRNALSRLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNRLLT 120
Db 85 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNRLLT 144

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204

QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLIDLTYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLIDLTYTT 257

RESULT 3
US-08-360-107A-122
/ Sequence 122, Application US/08360107A
/ Patent No. 6017536
/ GENERAL INFORMATION:
/ APPLICANT: Bolognesi, Dani P.
/ APPLICANT: Matthews, Thomas J.
/ APPLICANT: Wild, Carl T.
/ APPLICANT: Barney, Shawn O.
/ APPLICANT: Lambert, Dennis M.
/ APPLICANT: Petteway, Stephen R.
/ APPLICANT: Langlois, Alphonse J.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
/ TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
/ NUMBER OF SEQUENCES: 149
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:

/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE: 07-JUN-1995
/ APPLICATION NUMBER: US/08/486,099
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-031
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 112:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-486-099-112

Query Match 100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELRNALSRLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELRNALSRLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNRLLT 120
Db 85 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNRLLT 144

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204

QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLIDLTYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLIDLTYTT 257

RESULT 4
US-08-484-223B-112
/ Sequence 112, Application US/08484223B
/ Patent No. 6020459
/ GENERAL INFORMATION:
/ APPLICANT: Bolognesi, Dani P.
/ APPLICANT: Matthews, Thomas J.
/ APPLICANT: Wild, Carl T.
/ APPLICANT: Barney, Shawn O.
/ APPLICANT: Lambert, Dennis M.
/ APPLICANT: Petteway, Stephen R.
/ APPLICANT: Langlois, Alphonse J.
/ TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
/ TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
/ NUMBER OF SEQUENCES: 245
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-484-223B-112

Query Match 100.0%; Score 1238; DB 2; Length 257;

Best Local Similarity 100.0%; Pred. No. 2e-118;

Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGPFFTG 60

DB 25 SEKSEINEKDLRKKSSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGPFFTG 84

QY 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLLHNNRLT 120

DB 85 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLLHNNRLT 144

QY 121 EEKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180

DB 145 EEKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 181 RGLIVFHSSEGSVSYDLFDAQOQYPTLLRIYRDKNKTINSENLHIDLILYTT 233

DB 205 RGLIVFHSSEGSVSYDLFDAQOQYPTLLRIYRDKNKTINSENLHIDLILYTT 257

RESULT 5

US-08-919-597-112

Sequence 112, Application US/08919597

Patent No. 6054265

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/919,597

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/470,896

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-020

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-919-597-112

Query Match 100.0%; Score 1238; DB 2; Length 257;

Best Local Similarity 100.0%; Pred. No. 2e-118;

Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGPFFTG 60

DB 25 SEKSEINEKDLRKKSSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGPFFTG 84

QY 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLLHNNRLT 120

DB 85 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLLHNNRLT 144

QY 121 EEKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180

DB 145 EEKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 181 RGLIVFHSSEGSVSYDLFDAQOQYPTLLRIYRDKNKTINSENLHIDLILYTT 233

DB 205 RGLIVFHSSEGSVSYDLFDAQOQYPTLLRIYRDKNKTINSENLHIDLILYTT 257

RESULT 6

US-08-475-668A-112

Sequence 112, Application US/08475668A

Patent No. 6060065

GENERAL INFORMATION:

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,668A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-475-668A-112

Query Match 100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 25 SEKSEINEKDLRKSELRNALSRLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
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DB 145 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
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DB 205 RGLIVFHSSEGTSVSYDLFDAQGYPTDLLRIYRDNKTINSENHLHIDLTYTT 257

RESULT 7
US-08-485-551A-112
; Sequence 112, Application US/0848551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,551A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-023
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-551A-112

Query Match 100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELRNALSRLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELRNALSRLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGTSVSYDLFDAQGYPTDLLRIYRDNKTINSENHLHIDLTYTT 233
DB 205 RGLIVFHSSEGTSVSYDLFDAQGYPTDLLRIYRDNKTINSENHLHIDLTYTT 257

RESULT 8
US-08-471-913A-112
; Sequence 112, Application US/08471913A
; Patent No. 6093794
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSSTEIN-BARR VIRUS
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,913A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

```
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-471-913A-112

Query Match      100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELRNALSRLRQIYYINEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELRNALSRLRQIYYINEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHLDLYLYTT 257

RESULT 9
US-08-485-264A-112
; Sequence 112, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; STRANDEDNESS:
; TOPOLOGY: unknown

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-485-264A-112

Query Match      100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELRNALSRLRQIYYINEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELRNALSRLRQIYYINEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHLDLYLYTT 257

RESULT 10
US-08-474-349A-112
; Sequence 112, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
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; MOLECULE TYPE: protein
US-08-474-349A-112

Query Match      100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQGYPDPTLLRIYRDNKNTINSENHIDLYLTT 233
DB 205 RGLIVFHSSEGSTSVSYDLFDAQGYPDPTLLRIYRDNKNTINSENHIDLYLTT 257

RESULT 11
US-08-470-896-112
; Sequence 112, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonsse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,896
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELEPHONE: (212) 990-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-470-896-112

Query Match      100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQGYPDPTLLRIYRDNKNTINSENHIDLYLTT 233
DB 205 RGLIVFHSSEGSTSVSYDLFDAQGYPDPTLLRIYRDNKNTINSENHIDLYLTT 257

RESULT 12
US-08-485-546A-112
; Sequence 112, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonsse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EFSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELEPHONE: (212) 990-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-485-546A-112

Query Match      100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SEKSEINEKDLRKKSSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 HPWYNDLLVDLGSKDATNKYKGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 204
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQOYPTDLLRIYRDKNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHSSEGSTSVSYDLFDAQOYPTDLLRIYRDKNKTINSENHLDLYLYTT 257
RESULT 13
US-08-487-266A-112
; Sequence 112, Application US/08487266A
; Patent No. 6824783
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,266A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-487-266A-112
Query Match 100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNDLLVDLGSKDATNKYKGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQOYPTDLLRIYRDKNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHSSEGSTSVSYDLFDAQOYPTDLLRIYRDKNKTINSENHLDLYLYTT 257
RESULT 14
US-08-484-741-112
; Sequence 112, Application US/08484741
; Patent No. 6951717
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,741
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-08-484-741-112
Query Match 100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

Db 85 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLHIDLTYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLHIDLTYTT 257
RESULT 15
US-09-350-841A-1598
; Sequence 1598, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jeffs, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350,841A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1598
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1598

Query Match 97.1%; Score 1202; DB 2; Length 254;
Best Local Similarity 98.3%; Pred. No. 9.6e-115;
Matches 230; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
QY 1 SEKSEINEKDLRKXSELQARNLSNLRIQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 22 SEKSEINEKDLRKXSELQARNLSNLRIQIYYNEKAITENKESDDQFLENTLLFKGFFTG 81
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 120
Db 82 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 141
QY 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 142 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 200
QY 181 RGLIVFHSSEG-STVSVDLFDAGQYPTDLLRIYRDNKTINSENHLHIDLTYTT 233
Db 201 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLHIDLTYTT 254

RESULT 16
US-08-896-933-24
; Sequence 24, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-24

Query Match 94.6%; Score 1171; DB 2; Length 226;
Best Local Similarity 95.7%; Pred. No. 1.2e-111;
Matches 220; Conservative 4; Mismatches 2; Indels 4; Gaps 1;
QY 4 SEINEKDLRKXSELQARNLSNLRIQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 63
Db 1 SEINEKDLRKXSELQARNLSNLRIQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 60
QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLTEEK 123
Db 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLTEE- 119
QY 124 KVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 183
Db 120 ---VBKWIWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 176
QY 184 IVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLHIDLTYTT 233
Db 177 IVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENMHIDIYLYTT 226
RESULT 17
US-09-314-235-24
; Sequence 24, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-24

Query Match 94.6%; Score 1171; DB 2; Length 226;
Best Local Similarity 95.7%; Pred. No. 1.2e-111;
Matches 220; Conservative 4; Mismatches 2; Indels 4; Gaps 1;
QY 4 SEINEKDLRKXSELQARNLSNLRIQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 63
Db 1 SEINEKDLRKXSELQARNLSNLRIQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 60
QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLTEEK 123
Db 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLTEE- 119
QY 124 KVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 183
Db 120 ---VBKWIWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 176
QY 184 IVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLHIDLTYTT 233
Db 177 IVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENMHIDIYLYTT 226


```
RESULT 18
US-09-708-008B-24
; Sequence 24, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-708-008B-24

Query Match          94.6%; Score 1171; DB 2; Length 226;
Best Local Similarity 95.7%; Pred. No. 1.2e-111;
Matches 220; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 4 SEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 63
Db 1 SEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 60
QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATACMYGGVTLHDNNRLTEK 123
Db 61 YNDLLVDKGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATACMYGGVTLHDNNRLTEE- 119
QY 124 KVPINLWIDGKQTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGL 193
Db 120 --VBKWIDGKQTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGL 176
QY 184 IVFHSSEGSTSVSYDLFDAQGYQPTLLRIYRDKNKTINSENHLDLYLTT 233
Db 177 IVFHSSEGSTSVSYDLFDAQGYQPTLLRIYRDKNKTINSENHLDLYLTT 226

RESULT 19
US-08-695-692B-7
; Sequence 7, Application US/08695692B
; Patent No. 6514498
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; APPLICANT: Johan Hansson, Terje Kalland, Lars
; APPLICANT: Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; TITLE OF INVENTION: AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692B
; FILING DATE: August 12, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9601245-5

;
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-695-692B-7

Query Match          82.6%; Score 1023; DB 2; Length 233;
Best Local Similarity 82.0%; Pred. No. 1.8e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATACMYGGVTLHDNNRLT 120
Db 61 HSWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATACMYGGVTLHDNNRLT 120
QY 121 EEKQVPINLWIDGKQTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQ 180
Db 121 EEKQVPINLWIDGKQTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQ 180
QY 181 RGLIVFHSSEGSTSVSYDLFDAQGYQPTLLRIYRDKNKTINSENHLDLYLTT 233
Db 181 RGLIVFHSSEGSTSVSYDLFDAQGYQPTLLRIYRDKNKTINSENHLDLYLTT 233

RESULT 20
US-08-486-099-113
; Sequence 113, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-486-099-113

Query Match      82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELORNALSNIHQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELORNALSNIHQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFPSKDIIVDKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EEKVPINLWIDGKQTTVPIDKVTTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVPHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLHIDLTYTT 233
DB 205 RGLIVPHSTEPSVNYDLFAGQGYNTLLRIYRDNKTINSENHMDIYLYTS 257

RESULT 21
US-08-360-107A-123
; Sequence 123, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Stephen R.
; APPLICANT: Petteway, Dennis M.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-360-107A-123

Query Match      82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELORNALSNIHQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELORNALSNIHQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFPSKDIIVDKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EEKVPINLWIDGKQTTVPIDKVTTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVPHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLHIDLTYTT 233
DB 205 RGLIVPHSTEPSVNYDLFAGQGYNTLLRIYRDNKTINSENHMDIYLYTS 257

RESULT 22
US-08-484-223B-113
; Sequence 113, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
```

;
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-484-223B-113

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELOALSNLRQIYYVNEKAITENKESDDOPLNTLLPKGFTG 60
Db 25 SEKSEINEKDLRKSELOALSNLRQIYYVNEKAITENKESDDOPLNTLLPKGFTD 84
Qy 61 HPWYNLLVLDGSKDNTKYGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLGNSDSFGKVV 180
Db 145 EEKVPINLWIDGQNTVPLETVKTNKKNVTQVQELDLQARRYLQEKYNLNSDVDFGKVV 204
Qy 181 RGLIVHSSSGTSVSYDLFPAQGYPTLLRIYRDNKTINSENHLDLYLTT 233
Db 205 RGLIVHTSTEPSVNYDLFPAQGYSTLLRIYRDNKTINSENHLDLYLTS 257

RESULT 23

US-08-919-597-113
; Sequence 113, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,896
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-919-597-113

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELOALSNLRQIYYVNEKAITENKESDDOPLNTLLPKGFTG 60
Db 25 SEKSEINEKDLRKSELOALSNLRQIYYVNEKAITENKESDDOPLNTLLPKGFTD 84
Qy 61 HPWYNLLVLDGSKDNTKYGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLGNSDSFGKVV 180
Db 145 EEKVPINLWIDGQNTVPLETVKTNKKNVTQVQELDLQARRYLQEKYNLNSDVDFGKVV 204
Qy 181 RGLIVHSSSGTSVSYDLFPAQGYPTLLRIYRDNKTINSENHLDLYLTT 233
Db 205 RGLIVHTSTEPSVNYDLFPAQGYSTLLRIYRDNKTINSENHLDLYLTS 257

RESULT 24

US-08-475-668A-113
; Sequence 113, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-475-668A-113

Db 25 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAKTENKESHDPLOHTILFKGFFTD 84
QY 61 HPWYNLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVHSSSEGSTSVSYDLFDAQOQYPTTLRIYRDNKTINSENHLDLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQOQYSNTLLRIYRDNKTINSENHLDLYLTS 257

RESULT 27
US-08-485-264A-113
; Sequence 113, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-264A-113

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAKTENKESHDPLOHTILFKGFFTD 60
Db 25 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAKTENKESHDPLOHTILFKGFFTD 84
QY 61 HPWYNLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

Db 85 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVHSSSEGSTSVSYDLFDAQOQYPTTLRIYRDNKTINSENHLDLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQOQYSNTLLRIYRDNKTINSENHLDLYLTS 257

RESULT 28
US-08-474-349A-113
; Sequence 113, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-474-349A-113

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAKTENKESHDPLOHTILFKGFFTD 60
Db 25 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAKTENKESHDPLOHTILFKGFFTD 84
QY 61 HPWYNLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKGLYNSDSFGKQV 180
DB 145 EEKKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARRYLOEKYINLYNSDVFQKQV 204
QY 181 RGLIVPHSSEGSTVSVDLFDAGQYPTDLLRIYRDKNKTINSENHLHIDLXYTT 233
DB 205 RGLIVPHTSTEPSVNYDLFGAQQYSNTLLRIYRDKNKTINSENMHIDIYLYTS 257

RESULT 29
US-08-470-896-113
; Sequence 113, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,896
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-470-896-113

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKXSELQGTALGNLKQIYYNEKAKTENKESHDFLOHTILFKGFFTD 84
QY 61 HPWYNLLVDLGSKDATNKKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKGLYNSDSFGKQV 180
DB 145 EEKKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARRYLOEKYINLYNSDVFQKQV 204

QY 181 RGLIVPHSSEGSTVSVDLFDAGQYPTDLLRIYRDKNKTINSENHLHIDLXYTT 233
DB 205 RGLIVPHTSTEPSVNYDLFGAQQYSNTLLRIYRDKNKTINSENMHIDIYLYTS 257

RESULT 30
US-08-485-546A-113
; Sequence 113, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-485-546A-113

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKXSELQGTALGNLKQIYYNEKAKTENKESHDFLOHTILFKGFFTD 84
QY 61 HPWYNLLVDLGSKDATNKKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKGLYNSDSFGKQV 180
DB 145 EEKKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARRYLOEKYINLYNSDVFQKQV 204
QY 181 RGLIVPHSSEGSTVSVDLFDAGQYPTDLLRIYRDKNKTINSENHLHIDLXYTT 233

Db 205 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNKTNSNHNHDIYLYTS 257

RESULT 31

US-08-487-266A-113

; Sequence 113, Application US/08487266A

; Patent No. 6824783

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/487,266A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-025

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 113:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-487-266A-113

Query Match 82.6%; Score 1023; DB 2; Length 257;

Best Local Similarity 82.0%; Pred. No. 2e-96;

Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60

Db 25 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTD 84

QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNRLT 120

Db 85 HSWYNLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180

Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 181 RGLIVHSSSGSTVSYDLFDAQGYPTLLRIYRDNKTNSNHNHDIYLYTT 233

Db 205 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNKTNSNHNHDIYLYTS 257

RESULT 32

US-08-484-741-113

; Sequence 113, Application US/08484741

; Patent No. 6951717

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/484,741

FILING DATE: 07-Jun-1995

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-022

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 113:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 113:

US-08-484-741-113

Query Match 82.6%; Score 1023; DB 2; Length 257;

Best Local Similarity 82.0%; Pred. No. 2e-96;

Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60

Db 25 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTD 84

QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNRLT 120

Db 85 HSWYNLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180

Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 181 RGLIVHSSSGSTVSYDLFDAQGYPTLLRIYRDNKTNSNHNHDIYLYTT 233

Db 205 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNKTNSNHNHDIYLYTS 257

RESULT 33

US-08-446-918A-4

; Sequence 4, Application US/08446918A

```
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmelle, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,918A
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 552
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-918A-4

Query Match      82.3%; Score 1019; DB 1; Length 233;
Best Local Similarity 81.9%; Pred. No. 4.5e-96;
Matches 190; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY      2 EKSEINEKDLRKSELRNALSNIHQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      2 EKSEINEKDLRKSELRNALSNIHQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      62 PWYNDLLVGLSGKADTKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      62 SWYNDLLVDFDSKIDVYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      122 EKKVPINLWIDGKOTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVOR 181
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      122 EKKVPINLWIDGKOTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVOR 181
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      182 GLIVFHSSSGSTVSVDLFDAGQGYPTDRLRIYRDNKTINSNLHIDLILYTT 233
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      182 GLIVFHTSTSPSVNYDLFCAQGYSTNLLRIYRDNKTINSNLHIDLILYTT 233
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 34
US-08-580-806-4
; Sequence 4, Application US/08580806
; Patent No. 5935568
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmelle, Robyn E.
; APPLICANT: Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado

; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmelle, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-580-806-4

Query Match      82.3%; Score 1019; DB 1; Length 233;
Best Local Similarity 81.9%; Pred. No. 4.5e-96;
Matches 190; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY      2 EKSEINEKDLRKSELRNALSNIHQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      2 EKSEINEKDLRKSELRNALSNIHQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
        |||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      62 PWYNDLLVGLSGKADTKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      62 SWYNDLLVDFDSKIDVYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      122 EKKVPINLWIDGKOTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVOR 181
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      122 EKKVPINLWIDGKOTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVOR 181
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      182 GLIVFHSSSGSTVSVDLFDAGQGYPTDRLRIYRDNKTINSNLHIDLILYTT 233
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      182 GLIVFHTSTSPSVNYDLFCAQGYSTNLLRIYRDNKTINSNLHIDLILYTT 233
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 35
US-08-896-933-23
; Sequence 23, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-896-933-23

Query Match      81.1%; Score 1003.5; DB 2; Length 232;
Best Local Similarity 81.5%; Pred. No. 1.7e-94;
Matches 190; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

QY      1 SEKSEINEKDLRKSELRNALSNIHQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
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Db 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHQDPL-HTILFKGFFTD 59
QY 61 HPWYNLLVLDGSKDATNKYKGGVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 60 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 119
QY 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVK 180
Db 120 EEKVPINLWLDGKQNTVPLETKNKNVTQELDPQARRYLQEKYKLYNSDVFQKVK 179
QY 181 RGLIVHSSSGSTVSYDLFPAQOQYPTLLRIYRDKNKTINSENLHLDLYTT 233
Db 180 RGLIVFHTSTEPSVNYDLFQAQOQYSNTLLRIYRDKNKTINSENNHIDIYLYTS 232
```

RESULT 36

US-09-314-235-23

; Sequence 23, Application US/09314235

; Patent No. 6338845

; GENERAL INFORMATION:

; APPLICANT: Terman, David S.

; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

; FILE REFERENCE: 09629/005004

; CURRENT APPLICATION NUMBER: US/09/314,235

; EARLIER FILING DATE: 1999-05-18

; EARLIER APPLICATION NUMBER: 08/896,933

; EARLIER FILING DATE: 1997-07-18

; EARLIER FILING DATE: 1994-06-02

; EARLIER FILING DATE: 1992-06-01

; EARLIER FILING DATE: 1991-01-17

; EARLIER FILING DATE: 1990-01-17

; EARLIER FILING DATE: 1989-10-03

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 23

; LENGTH: 232

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-09-314-235-23

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Query Match 81.1%; Score 1003.5; DB 2; Length 232;
Best Local Similarity 81.5%; Pred. No. 1.7e-94;
Matches 190; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHQDPL-HTILFKGFFTD 60
Db 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHQDPL-HTILFKGFFTD 59
QY 61 HPWYNLLVLDGSKDATNKYKGGVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 60 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 119
QY 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVK 180
Db 120 EEKVPINLWLDGKQNTVPLETKNKNVTQELDPQARRYLQEKYKLYNSDVFQKVK 179
QY 181 RGLIVHSSSGSTVSYDLFPAQOQYPTLLRIYRDKNKTINSENLHLDLYTT 233
Db 180 RGLIVFHTSTEPSVNYDLFQAQOQYSNTLLRIYRDKNKTINSENNHIDIYLYTS 232
```

RESULT 37

US-09-708-008B-23

; Sequence 23, Application US/09708008B

; Patent No. 6692746

; GENERAL INFORMATION:

```
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-708-008B-23
```

```
Query Match 81.1%; Score 1003.5; DB 2; Length 232;
Best Local Similarity 81.5%; Pred. No. 1.7e-94;
Matches 190; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHQDPL-HTILFKGFFTD 60
Db 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHQDPL-HTILFKGFFTD 59
QY 61 HPWYNLLVLDGSKDATNKYKGGVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 60 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 119
QY 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVK 180
Db 120 EEKVPINLWLDGKQNTVPLETKNKNVTQELDPQARRYLQEKYKLYNSDVFQKVK 179
QY 181 RGLIVHSSSGSTVSYDLFPAQOQYPTLLRIYRDKNKTINSENLHLDLYTT 233
Db 180 RGLIVFHTSTEPSVNYDLFQAQOQYSNTLLRIYRDKNKTINSENNHIDIYLYTS 232
```

RESULT 38

US-09-144-776B-2

; Sequence 2, Application US/09144776B

; Patent No. 6399332

; GENERAL INFORMATION:

; APPLICANT: Robert G. Ulrich,

; Mark A. Olson

; Sina Bavari

; TITLE OF INVENTION: Bacterial Superantigen

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Charles H. Harris

; STREET: US Atty MRC -504 Scott Street

; MCMR-JA (Charles H. Harris-Patent

; Atty)

; CITY: FORT DETRICK

; STATE: MARYLAND

; COUNTRY: USA

; ZIP: 21702-5012

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 7.5

; SOFTWARE: Microsoft Word 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/144,776B

; FILING DATE: 01-Sep-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/882,431

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Charles H. Harris

STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-144-776B-4

Query Match 80.5%; Score 996; DB 2; Length 233;
Best Local Similarity 80.6%; Pred. No. 1e-93;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGSPFTGH 61
DB 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGSPFTDH 61
QY 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLTE 121
DB 62 SWNDLLVDFDSKDIYDKYKGGKVDLYGAYAGYQCAGGTPNKTCACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR 181
DB 122 EKKVPINLWDGKQNTVPLETVKTKNKNVTQVQLDLQARRYLOEKYNLYNSDVFDDGKVQR 181
QY 182 GLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLDLYLTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAGQGYSNLLRIYRDNKTINSENHLDIYLYTS 233

RESULT 41
US-08-882-431B-4
; Sequence 4, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-4

Query Match 80.5%; Score 996; DB 2; Length 233;
Best Local Similarity 80.6%; Pred. No. 1e-93;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGSPFTGH 61
DB 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGSPFTDH 61
QY 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLTE 121
DB 62 SWNDLLVDFDSKDIYDKYKGGKVDLYGAYAGYQCAGGTPNKTCACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR 181
DB 122 EKKVPINLWDGKQNTVPLETVKTKNKNVTQVQLDLQARRYLOEKYNLYNSDVFDDGKVQR 181
QY 182 GLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLDLYLTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAGQGYSNLLRIYRDNKTINSENHLDIYLYTS 233

RESULT 42
US-09-350-841A-1599
; Sequence 1599, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jeffs, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; FILE REFERENCE: 7872-086-999
; CURRENT APPLICATION NUMBER: US/09/350,841A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1599
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1599

Query Match 74.8%; Score 926.5; DB 2; Length 252;
Best Local Similarity 79.1%; Pred. No. 1.5e-86;
Matches 185; Conservative 16; Mismatches 26; Indels 7; Gaps 6;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGSPFTG 60
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGSPFTD 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSK--IVDKY--KKCD--YGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 140
QY 121 EKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 141 EKKVPINLWDGKQNTVPLETVKTKNKNVTQVQLDLQARRYLOEK--NLNYSNDSVDFGKVQ 198
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLDLYLTT 233
DB 199 RGLIVFHTSTEPSVNYDLFGAGQGYSNLLRIYRDNKTINSENHLDIYLYTS 252

RESULT 43
US-08-896-933-25
; Sequence 25, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978

;
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-25

Query Match 53.1%; Score 657; DB 2; Length 228;
Best Local Similarity 55.6%; Pred. No. 4.8e-59;
Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0;
QY 7 INEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYND 66
Db 2 VKEKELHKXSELSSALNNMKHSYADKNPIIGENKSTGDFLENTLLYKKFFTDLINFED 61
QY 67 LLVDLGSKDATNKKYKGGKVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLTEKKVP 126
Db 62 LLINFNSKEMAQHFKSKNDVVPYRISYNCYGGEIDRTACTYGGVTPHSGNKLKERKKIP 121
QY 127 INLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQRLIVF 186
Db 122 INLWINGVQKESLDKVTQDKKNVTVOELDAQARYLQKDLKLYNNDTLGGKIQRGKIEF 181
QY 187 HSSEGSTVSYDLFDAQGOVPTDLLRIYRDNKNTINSENHLIDLYL 231
Db 182 DSSDGSKVSYDLFDVKGDFFPEKQLRIYSDNKTLSLSTHHLHIDIYLY 226

RESULT 44
US-09-314-235-25
; Sequence 25, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-25

Query Match 53.1%; Score 657; DB 2; Length 228;
Best Local Similarity 55.6%; Pred. No. 4.8e-59;
Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0;
QY 7 INEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYND 66
Db 2 VKEKELHKXSELSSALNNMKHSYADKNPIIGENKSTGDFLENTLLYKKFFTDLINFED 61
QY 67 LLVDLGSKDATNKKYKGGKVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLTEKKVP 126
Db 62 LLINFNSKEMAQHFKSKNDVVPYRISYNCYGGEIDRTACTYGGVTPHSGNKLKERKKIP 121

QY 127 INLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQRLIVF 186
Db 122 INLWINGVQKESLDKVTQDKKNVTVOELDAQARYLQKDLKLYNNDTLGGKIQRGKIEF 181
QY 187 HSSEGSTVSYDLFDAQGOVPTDLLRIYRDNKNTINSENHLIDLYL 231
Db 182 DSSDGSKVSYDLFDVKGDFFPEKQLRIYSDNKTLSLSTHHLHIDIYLY 226
RESULT 45
US-09-708-008B-25
; Sequence 25, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-708-008B-25

Query Match 53.1%; Score 657; DB 2; Length 228;
Best Local Similarity 55.6%; Pred. No. 4.8e-59;
Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0;
QY 7 INEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYND 66
Db 2 VKEKELHKXSELSSALNNMKHSYADKNPIIGENKSTGDFLENTLLYKKFFTDLINFED 61
QY 67 LLVDLGSKDATNKKYKGGKVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLTEKKVP 126
Db 62 LLINFNSKEMAQHFKSKNDVVPYRISYNCYGGEIDRTACTYGGVTPHSGNKLKERKKIP 121
QY 127 INLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQRLIVF 186
Db 122 INLWINGVQKESLDKVTQDKKNVTVOELDAQARYLQKDLKLYNNDTLGGKIQRGKIEF 181
QY 187 HSSEGSTVSYDLFDAQGOVPTDLLRIYRDNKNTINSENHLIDLYL 231
Db 182 DSSDGSKVSYDLFDVKGDFFPEKQLRIYSDNKTLSLSTHHLHIDIYLY 226

RESULT 46
US-09-144-776B-19
; Sequence 19, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; CMRR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012

```

; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-19

Query Match 36.9%; Score 457; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 3.1e-39;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 SDDQFLENTLLPKGPTTGHPTWINDLLVDLGSKDATNKYKGKKVDLYGAYGYOCAGGTPN 102
Db 1 SDDQFLENTLLPKGPTTGHPTWINDLLVDLGSKDATNKYKGKKVDLYGAYGYOCAGGTPN 60

QY 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 48
US-09-144-776B-17
; Sequence 17, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavazi
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC-504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown

```

MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-144-7768-17

Query Match 32.2%; Score 399; DB 2; Length 82;
Best Local Similarity 86.6%; Pred. No. 2.7e-33;
Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 43 SDQFLENTLLPKGFTGHPWINDLLVLSKDATNKYKGGKVDLYGAYGYQCAGGTN 102
DB 1 SHDQFLQHTILPKGFTGHSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTN 60

QY 103 KTACMYGGVTLHDNNRLTEKK 124
DB 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 49
US-08-882-431B-17
Sequence 17, Application US/08882431B
Patent No. 6713284
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MMCM -504 Scott Street MCNR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 82
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431B-17

Query Match 32.2%; Score 399; DB 2; Length 82;
Best Local Similarity 86.6%; Pred. No. 2.7e-33;
Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 43 SDQFLENTLLPKGFTGHPWINDLLVLSKDATNKYKGGKVDLYGAYGYQCAGGTN 102
DB 1 SHDQFLQHTILPKGFTGHSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTN 60

QY 103 KTACMYGGVTLHDNNRLTEKK 124
DB 61 KTACMYGGVTLHDNNRLTEKK 82

Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 50
US-08-446-918A-2
Sequence 2, Application US/08446918A
Patent No. 5705151
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Emslie, Robyn E.
TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,918A
FILING DATE: 18-MAY-1995
CLASSIFICATION: 552
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-918A-2

Query Match 24.2%; Score 300; DB 1; Length 255;
Best Local Similarity 34.0%; Pred. No. 1.9e-22;
Matches 83; Conservative 46; Mismatches 97; Indels 18; Gaps 7;

QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNNEKAITENKESDDQFLENTLLPKGFFTG 60
DB 15 SMESQDPKPKDELHKSSKFTGLMENMKVLYDDNHVSAT-NVKSIDQFLYFDLYIYSIKDTK 73

QY 61 HPWYNDLLVLSKDATNKYKGGKVDLYGAYGYQC-----AGTTPNKTCMYGG 110
DB 74 LGNYDNVRVEFKNKDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGG 133

QY 111 VTLHDNNRLTEKKVPIINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLY 170
DB 134 VTEHNGNQLDKYRSITRVFEDGK-NLGSFD-VQTNKKKVTAEQLDYLTRHLYLVKNKKLY 191

QY 171 NSDSFGKVGQRLIVFHSSEGSTVSVDLFDAGQYPD--TLRLIYRDNKTINSENLIHDL 228
DB 192 EFNN--SPVETGYIKFIENENS-FWYDMMPAGDKFDQSKYLMWYNDNKNQVSKDVKIEV 248

QY 229 YLYT 232
DB 249 YLTT 252

RESULT 51
US-08-580-806-2
Sequence 2, Application US/08580806
Patent No. 5935568
GENERAL INFORMATION:

QY 1 SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFFTG 60
Db 27 ASQPPKPDDELHKSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQC-----AGGTPNKTCMYGG 110
Db 85 LGDYDNVRVEFKNKDLADKYKVDVFGANGYCYFYSKKTNDINSHQTDKRTCMYGG 144
QY 111 VTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHLYLHGKFLY 170
Db 145 VTEHNGNQLDKYRSITVRVFEDEK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202
QY 171 NDSFGGKVGQGLIVFHSSEGSTVSDLFDAQOQ--YPTDLLRIYRDNKTINSENHLIDL 228
Db 203 EFNW--SPYETGYIKFIENENS-FWYDMPAPGDKFAQSKYLMYNDNKNWDSKDVKIEV 259
QY 229 YLYT 232
Db 260 YLTT 263

RESULT 60
US-08-882-431B-6
; Sequence 6, Application US/0882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-6

Query Match 23.7%; Score 293.5; DB 2; Length 266;
Best Local Similarity 32.8%; Pred. No. 9.2e-22;
Matches 80; Conservative 45; Mismatches 100; Indels 19; Gaps 7;
QY 1 SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFFTG 60

Db 27 ASQPPKPDDELHKSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQC-----AGGTPNKTCMYGG 110
Db 85 LGDYDNVRVEFKNKDLADKYKVDVFGANGYCYFYSKKTNDINSHQTDKRTCMYGG 144
QY 111 VTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHLYLHGKFLY 170
Db 145 VTEHNGNQLDKYRSITVRVFEDEK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202
QY 171 NDSFGGKVGQGLIVFHSSEGSTVSDLFDAQOQ--YPTDLLRIYRDNKTINSENHLIDL 228
Db 203 EFNW--SPYETGYIKFIENENS-FWYDMPAPGDKFAQSKYLMYNDNKNWDSKDVKIEV 259
QY 229 YLYT 232
Db 260 YLTT 263

RESULT 61
US-08-896-933-26
; Sequence 26, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-26

Query Match 23.6%; Score 292.5; DB 2; Length 239;
Best Local Similarity 34.0%; Pred. No. 1e-21;
Matches 82; Conservative 44; Mismatches 96; Indels 19; Gaps 8;
QY 2 EKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFFTG 61
Db 1 ESQPPKPDDELHKSKF-TGLMENMKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQC-----AGGTPNKTCMYGGV 111
Db 59 GNYDNVRVEFKNKDLADKYKVDVFGANGYCYFYSKKTNDINSHQTDKRTCMYGGV 118
QY 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHLYLHGKFLYN 171
Db 119 TEHNGNQLDKYRSITVRVFEDEK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYE 176
QY 172 SDSFGGKVGQGLIVFHSSEGSTVSDLFDAQOQYD--TLLRIYRDNKTINSENHLIDL 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNWDSKDVKIEV 233
QY 230 L 230
Db 234 L 234

RESULT 62
US-09-314-235-26
; Sequence 26, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

;; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
;; FILE REFERENCE: 09629/005004
;; CURRENT APPLICATION NUMBER: US/09/314,235
;; CURRENT FILING DATE: 1999-05-18
;; EARLIER APPLICATION NUMBER: 08/896,933
;; EARLIER FILING DATE: 1997-07-18
;; EARLIER APPLICATION NUMBER: 08/252,978
;; EARLIER FILING DATE: 1994-06-02
;; EARLIER APPLICATION NUMBER: 07/891,718
;; EARLIER FILING DATE: 1992-06-01
;; EARLIER APPLICATION NUMBER: US91/00342
;; EARLIER FILING DATE: 1991-01-17
;; EARLIER APPLICATION NUMBER: 07/466,577
;; EARLIER FILING DATE: 1990-01-17
;; EARLIER APPLICATION NUMBER: 07/416,530
;; EARLIER FILING DATE: 1989-10-03
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 26
;; LENGTH: 239
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-09-314-235-26

Query Match 23.6%; Score 292.5; DB 2; Length 239;
Best Local Similarity 34.0%; Pred. No. 1e-21;
Matches 82; Conservative 44; Mismatches 96; Indels 19; Gaps 8;
Qy 2 EKSEINEKDLRKSELQNALSNLRQIYYINEKAITENKESDDQFLENTLLFKGFTGH 61
Db 1 ESQDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVGLSGDATNKYKGVLYGAYGYQC-----AGGTENKTACMYGV 111
Db 59 GNYDNRVFEKNDLADKYDKYDVFVGANYYYQCYFSKKTNDINSHQTDKRTKCMYGV 118
Qy 112 TLHNNRLTEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEQLDYLTRHYLVKNKKLYE 176
Qy 172 SDSFGGKQVQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLLRIYRDNKNTINSENHLIDL 229
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEQLDYLTRHYLVKNKKLYE 176
Qy 172 SDSFGGKQVQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLLRIYRDNKNTINSENHLIDL 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDLMPPAGDKFDQSKYLMYNDNKNVDSKDVKEIV 233
Qy 230 L 230
Db 234 L 234

RESULT 63
US-09-708-008B-26
; Sequence 26, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Tetman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-708-008B-26

Query Match 23.6%; Score 292.5; DB 2; Length 239;

Best Local Similarity 34.0%; Pred. No. 1e-21;
Matches 82; Conservative 44; Mismatches 96; Indels 19; Gaps 8;
Qy 2 EKSEINEKDLRKSELQNALSNLRQIYYINEKAITENKESDDQFLENTLLFKGFTGH 61
Db 1 ESQDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVGLSGDATNKYKGVLYGAYGYQC-----AGGTENKTACMYGV 111
Db 59 GNYDNRVFEKNDLADKYDKYDVFVGANYYYQCYFSKKTNDINSHQTDKRTKCMYGV 118
Qy 112 TLHNNRLTEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEQLDYLTRHYLVKNKKLYE 176
Qy 172 SDSFGGKQVQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLLRIYRDNKNTINSENHLIDL 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDLMPPAGDKFDQSKYLMYNDNKNVDSKDVKEIV 233
Qy 230 L 230
Db 234 L 234

RESULT 64
US-09-414-276-8
; Sequence 8, Application US/09414276
; Patent No. 6392121
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh
; APPLICANT: Palmer, Kenneth
; APPLICANT: Hefferon, Kathleen
; APPLICANT: Mor, Tsafirir
; APPLICANT: Arntzen, Charles
; TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
; FILE REFERENCE: 4869/84453
; CURRENT APPLICATION NUMBER: US/09/414,276
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 266
; TYPE: PRT
; ORGANISM: bean yellow dwarf virus
US-09-414-276-8

Query Match 23.6%; Score 292.5; DB 2; Length 266;
Best Local Similarity 33.2%; Pred. No. 1.2e-21;
Matches 81; Conservative 47; Mismatches 97; Indels 19; Gaps 8;
Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYINEKAITENKESDDQFLENTLLFKGFTGH 60
Db 27 AESQDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQSLYFDLIYSIKDTK 84
Qy 61 HPWYNDLLVGLSGDATNKYKGVLYGAYGYQC-----AGGTENKTACMYGV 110
Db 85 LGYDNRVFEKNDLADKYDKYDVFVGANYYYQCYFSKKTNDINSHQTDKRTKCMYGV 144
Qy 111 VTLDHNNRLTEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEQLDYLTRHYLVKNKKLY 202
Qy 171 NSDSFGGKQVQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLLRIYRDNKNTINSENHLIDL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPPAGDKFDQSKYLMYNDNKNVDSKDVKEIV 259
Qy 229 YLYT 232
Db 260 YLYT 263

RESULT 65
US-08-973-391C-14

```

; Sequence 14, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-14

Query Match      23.5%; Score 291.5; DB 2; Length 221;
Best Local Similarity 35.1%; Pred. No. 1.1e-21;
Matches 79; Conservative 42; Mismatches 85; Indels 19; Gaps 10;

QY      16 SELQRNAL-SNLROIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTGHPMYNLLVLDLG 72
Db      7 SQLRRSLVKNLQNIYFYEGDPVTHENVKSDVOLLSHLLYN---VSGPNYDKLKTCLK 63
QY      73 SKDATNKYKGGKVDLYGAYTYGYQC-AGGTPNKTAICYGGVTLHDNNRLTEBKYPINLWI 131
Db      64 NQEMATLFDKNDVIYGYVEYHLYCLENASERSACIYGGVTNHEGNHLEIPKIVVKVSI 123
QY      132 DGQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRCGLIYVPHSSEG 191
Db      124 DGIQ-SLSFD-IETNKKQWVAQELDYKVRKYLTDNKQLYNGP--SKYETGYIKFIPKPK 179
QY      192 STVSYDLFD---AQOGYPTDLRIYRDNKTINSNLHIDLXYLT 232
Db      180 ESFWDFPPEPTQSKY----LMYKDNETLDSQIEVLTYT 220

RESULT 66
US-10-625-221-14
; Sequence 14, Application US/10625221
; Patent No. 6870042
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/10/625,221
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US/08/973,391C
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-625-221-14

Query Match      23.5%; Score 291.5; DB 2; Length 221;
Best Local Similarity 35.1%; Pred. No. 1.1e-21;

```


STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 239
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-144-776B-10

Query Match 23.3%; Score 288.5; DB 2; Length 239;
Best Local Similarity 33.9%; Pred. No. 2.6e-21;
Matches 80; Conservative 45; Mismatches 88; Indels 23; Gaps 8;
US-09-144-776B-10

QY 14 KXSELQRNA-----LSNLRQIYYNEKAITENKESDDQFLENTLLFKGPFTHGHPWYNDLL 68
DB 7 KPDELHKSSKFTGLMENMKVLDHNSAI-NVKSIDQRYFDLIYSIKDTKLGNDVNR 65
QY 69 VDLGSKDATNKYKKVDLYGAYGYQCAGG-----TPNKTACMYGGVTLHDNNR 118
DB 66 VEFKNKDLADKYKVDVFGANAYVQCASFSSKKTNDINSHQTDKRKTCMYGGVTEHNGQ 125
QY 119 LTEKKVPINLWDGKQTVTPIDKVKTSKEVTVOELDLOARHYLHGKFLYNSDSFGGK 178
DB 126 LDKYRSITVRVFEDEGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYEFNN--SP 181

QY 179 VORGLIVFHSSSGSTVSYDLFDAQGOYPD--TLRIYRDNKNTINSNLHIDLVL 232
DB 182 YETGVIKFIENENS-FWIDMPPAGDKFDQSKYLMYNDNKNVDSKDVKIEVLTT 236

RESULT 71
US-08-882-431B-10
Sequence 10, Application US/08882431B
Patent No. 6713284
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DENRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 239
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431B-10

Query Match 23.3%; Score 288.5; DB 2; Length 239;
Best Local Similarity 33.9%; Pred. No. 2.6e-21;
Matches 80; Conservative 45; Mismatches 88; Indels 23; Gaps 8;
US-08-882-431B-10

QY 14 KXSELQRNA-----LSNLRQIYYNEKAITENKESDDQFLENTLLFKGPFTHGHPWYNDLL 68
DB 7 KPDELHKSSKFTGLMENMKVLDHNSAI-NVKSIDQRYFDLIYSIKDTKLGNDVNR 65
QY 69 VDLGSKDATNKYKKVDLYGAYGYQCAGG-----TPNKTACMYGGVTLHDNNR 118
DB 66 VEFKNKDLADKYKVDVFGANAYVQCASFSSKKTNDINSHQTDKRKTCMYGGVTEHNGQ 125
QY 119 LTEKKVPINLWDGKQTVTPIDKVKTSKEVTVOELDLOARHYLHGKFLYNSDSFGGK 178
DB 126 LDKYRSITVRVFEDEGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYEFNN--SP 181

QY 179 VORGLIVFHSSSGSTVSYDLFDAQGOYPD--TLRIYRDNKNTINSNLHIDLVL 232
DB 182 YETGVIKFIENENS-FWIDMPPAGDKFDQSKYLMYNDNKNVDSKDVKIEVLTT 236

RESULT 72
US-09-555-115A-3
Sequence 3, Application US/09555115A
Patent No. 6872394
GENERAL INFORMATION:
APPLICANT: Bohach, Gregory I.
TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REFERENCE: 12136.1USWO
CURRENT APPLICATION NUMBER: US/09/555,115A
CURRENT FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: PCT/US98/25107
PRIOR FILING DATE: 1998-12-01
PRIOR APPLICATION NUMBER: US 60/067,357
PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 240
TYPE: PRT
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (240)..(240)
OTHER INFORMATION: Xaa is unknown.
US-09-555-115A-3

Query Match 23.3%; Score 288.5; DB 2; Length 240;
Best Local Similarity 32.1%; Pred. No. 2.6e-21;
Matches 75; Conservative 49; Mismatches 91; Indels 19; Gaps 9;

QY 11 DLKKSSELRNLSLRQIYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV 69
DB 10 DLKKSSEF-TGTWGNMK--LYDDHYVSATKVKSVDFKFLAHDLIYINISDKLKNYDKVKT 66
QY 70 DLGSKDATNKYKGGKVDLYGAYGYQC-----AGTGNKTKACMYGGVTLHDNNRLTEE 122
DB 67 ELLNEDLAKKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITKHGHNFDNG 126
QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKVEYTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 127 NLQNLVLRVY-ENKRNITISPE-VQTDKKSVTQAELDIKARNFLINKKNLYEFNS--SPYE 182
QY 181 RGLIVHSSGSGTVSDYDLFAQQGYPD--TLRIYRDNKTINSENHLIDLTYLT 232
DB 183 TGYIKFIENNGNTFYQDMPAPGDKFQSKYLMYNDKNTVDSKVKIEVHLTT 236

RESULT 74
US-09-555-115A-6
; Sequence 6, Application US/09555115A
; Patent No. 6872394
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
US-09-555-115A-6

Query Match 23.2%; Score 287.5; DB 2; Length 240;
Best Local Similarity 32.1%; Pred. No. 3.3e-21;
Matches 75; Conservative 48; Mismatches 92; Indels 19; Gaps 9;

QY 11 DLKKSSELRNLSLRQIYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV 69
DB 10 DLKKSSEF-TGTWGNMK--LYDDHYVSATKVKSVDFKFLAHDLIYINISDKRLKNYDKVKT 66
QY 70 DLGSKDATNKYKGGKVDLYGAYGYQC-----AGTGNKTKACMYGGVTLHDNNRLTEE 122
DB 67 ELLNEDLAKKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITKHGHNFDNG 126
QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKVEYTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 127 NLQNLVLRVY-ENKRNITISPE-VQTDKKSVTQAELDIKARNFLINKKNLYEFNS--SPYE 182
QY 181 RGLIVHSSGSGTVSDYDLFAQQGYPD--TLRIYRDNKTINSENHLIDLTYLT 232
DB 183 TGYIKFIENNGNTFYQDMPAPGDKFQSKYLMYNDKNTVDSKVKIEVHLTT 236

RESULT 74
US-09-555-115A-5
; Sequence 5, Application US/09555115A
; Patent No. 6872394
; GENERAL INFORMATION:

APPLICANT: Bohach, Gregory I.
TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REFERENCE: 12136.1USWO
CURRENT APPLICATION NUMBER: US/09/555,115A
CURRENT FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: PCT/US98/25107
PRIOR FILING DATE: 1998-12-01
PRIOR APPLICATION NUMBER: US 60/067,357
PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 240
TYPE: PRT
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (240)..(240)
OTHER INFORMATION: Xaa is unknown.
US-09-555-115A-5

Query Match 23.1%; Score 285.5; DB 2; Length 240;
Best Local Similarity 31.3%; Pred. No. 5.2e-21;
Matches 76; Conservative 49; Mismatches 99; Indels 19; Gaps 9;

QY 2 EKSEIEINEXDLRKLSELRNLSLRQIYYNEKAITENK-ESDDQFLENTLLFKGFFTG 60
DB 1 ESQPDPTDELKHSSEF-TGTWGNMK--LYDDHYVSATKVKSVDFKFLAHDLIYINISDKK 57
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQC-----AGTGNKTKACMYGGVTL 113
DB 58 LKNYDKVKTLELLEDLAKKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITK 117
QY 114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKVEYTVQELDLQARHYLHGKFGLYN 171
DB 118 HEGNFDNGNLQNLVLRVY-ENKRNITISPE-VQTDKKSVTQAELDIKARNFLINKKNLYE 175
QY 172 SDSFGGKVGRLIVHSSGSGTVSDYDLFAQQGYPD--TLRIYRDNKTINSENHLIDLTY 229
DB 176 FNS--SPYETGYIKFIENNGNTFYQDMPAPGDKFQSKYLMYNDKNTVDSKVKIEVH 233
QY 230 LYT 232
DB 234 LTT 236

RESULT 75
US-09-555-115A-2
; Sequence 2, Application US/09555115A
; Patent No. 6872394
; GENERAL INFORMATION:
APPLICANT: Bohach, Gregory I.
TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REFERENCE: 12136.1USWO
CURRENT APPLICATION NUMBER: US/09/555,115A
CURRENT FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: PCT/US98/25107
PRIOR FILING DATE: 1998-12-01
PRIOR APPLICATION NUMBER: US 60/067,357
PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 240
TYPE: PRT
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (240)..(240)
OTHER INFORMATION: Xaa is unknown.
US-09-555-115A-2

Query Match 22.9%; Score 283.5; DB 2; Length 240;

Best Local Similarity 31.3%; Pred. No. 8.4e-21;
Matches 76; Conservative 49; Mismatches 99; Indels 19; Gaps 9;

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Db	1	ESQDPPTPDELHKSEF-TGTGNMK--YLYDDHYVSATKMSVDKFLAHDLIYNISDKK	57
Qy	61	HPWYNDLLVDLGSKDATNKYKGGVDLYGAYGYQC-----AGGTPNKTACMYGGVTL	113
Db	58	LKNYDKVKTELLNEDLAKKYKDEWVDVYGSNYVYVNCYFSSKDNVGVKTCGGKTCMYGGITK	117
Qy	114	HNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN	171
Db	118	HEGNHFDNGNLQNLIRVY-ENKNTISPE-VQTDKKSVTAGELDIKARNFLINKNLYE	175
Qy	172	SDSFGGKVORGLIVFHSSEGSTVSYDLFDAQQGYD--TLLRIYRDNKNTINSENHLIDLY	229
Db	176	FNS--SPYETGYIKFTIENNGNTFQYDMMPAGDKFDQSKYLMWYNDNKTVDKSVKIEVH	233
Qy	230	LYT	232
Db	234	LTT	236

Search completed: February 15, 2006, 20:20:17
Job time : 21.7646 secs

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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:34:11 ; Search time 58.958 Seconds
(without alignments)
1651.247 Million cell updates/sec

Title: us-09-900-766-7

Perfect score: 1238

Sequence: 1 SEKSEINEKRLKRSSELQR.....RDNKTINSENHIDLYLTYT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications AA_Main*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1238	100.0	257	4	US-10-267-682-112
4	1238	100.0	257	4	US-10-267-748-112
5	1238	100.0	257	4	US-10-428-817A-188
6	1210	97.7	233	3	US-09-900-766-3
7	1188	96.0	248	3	US-09-870-759-16
8	1188	96.0	248	3	US-09-751-708A-16
9	1188	96.0	248	5	US-10-428-817A-12
10	1188	96.0	248	5	US-10-937-758A-16
11	1107	89.4	233	3	US-09-900-766-2
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15	1023	82.6	257	4	US-10-267-682-113
16	1023	82.6	257	4	US-10-267-748-113
17	1023	82.6	257	5	US-10-951-225-5
18	1019	82.3	233	4	US-10-354-948-4
19	1013	81.8	257	3	US-09-870-759-8
20	1013	81.8	257	3	US-09-751-708A-8
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61	294.5	23.8	251	3	US-09-308-830-13
62	293.5	23.7	240	5	US-10-923-324-4
63	293.5	23.7	266	4	US-10-002-784A-6
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65	292.5	23.6	266	4	US-10-151-336-8
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67	289.5	23.4	251	4	US-10-002-784A-16
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97	256	20.7	233	5	US-10-997-690-2
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Sequence 173, App
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Sequence 174, App
Sequence 177, App
Sequence 178, App
Sequence 172, App
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105	216	17.5	234	5	US-10-997-690-4	Sequence 4, Appl	178	92.5	7.5	227	4	US-10-428-817A-193	Sequence 193, App
106	217	17.4	210	4	US-10-428-817A-166	Sequence 166, App	179	92	7.4	631	5	US-10-481-032A-634	Sequence 634, App
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111	197	15.9	236	5	US-10-474-792-414	Sequence 414, App	184	89	7.2	171	4	US-10-282-122A-71154	Sequence 71154, A
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113	193	15.6	232	4	US-10-428-817A-168	Sequence 168, App	186	89	7.2	516	4	US-10-032-585-7147	Sequence 7147, Ap
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117	183.5	14.8	235	5	US-10-914-417-2	Sequence 2, Appl	190	89	7.2	1634	5	US-10-734-563-96	Sequence 96, Appl
118	183.5	14.8	235	5	US-10-914-665-2	Sequence 2, Appl	191	89	7.2	1634	5	US-10-853-973A-23	Sequence 23, Appl
119	181.5	14.7	204	5	US-10-997-690-20	Sequence 20, Appl	192	88.5	7.1	308	5	US-10-470-048B-438	Sequence 438, App
120	170	13.7	137	5	US-10-997-690-8	Sequence 8, Appl	193	88.5	7.1	313	5	US-10-470-048B-155	Sequence 155, App
121	159.5	12.9	204	5	US-10-997-690-9	Sequence 9, Appl	194	88	7.1	241	4	US-10-282-122A-70300	Sequence 70300, A
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128	116	9.4	231	4	US-10-428-817A-191	Sequence 191, App	201	87.5	7.1	1637	4	US-10-437-963-180397	Sequence 180397, A
129	114	9.2	231	4	US-10-428-817A-190	Sequence 190, App	202	87	7.0	286	4	US-10-724-972A-5172	Sequence 5172, Ap
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137	107.5	8.7	234	3	US-09-870-759-18	Sequence 18, Appl	210	86.5	7.0	494	4	US-10-425-115-358193	Sequence 358193, A
138	107.5	8.7	234	3	US-08-751-708A-18	Sequence 18, Appl	211	86.5	7.0	650	5	US-10-481-032A-182	Sequence 182, App
139	107.5	8.7	234	4	US-10-267-682-111	Sequence 111, App	212	86	6.9	399	4	US-10-374-780A-1313	Sequence 1313, Ap
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142	107.5	8.7	234	4	US-10-428-817A-189	Sequence 189, App	215	85.5	6.9	228	4	US-10-425-115-248728	Sequence 248728, A
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146	105.5	8.5	194	3	US-09-465-714-3	Sequence 3, Appl	219	85.5	6.9	584	5	US-10-998-232-24	Sequence 24, Appl
147	105.5	8.5	194	4	US-10-354-948-6	Sequence 6, Appl	220	85.5	6.9	618	4	US-10-767-701-46249	Sequence 46249, A
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160	98.5	8.0	628	4	US-10-425-114-57792	Sequence 57792, A	233	84.5	6.8	403	4	US-10-284-400-14	Sequence 14, Appl
161	96	7.8	227	4	US-10-282-122A-70243	Sequence 70243, A	234	84.5	6.8	403	4	US-10-284-400-14	Sequence 14, Appl
162	95.5	7.7	616	4	US-10-431-273-59	Sequence 59, Appl	235	84.5	6.8	579	5	US-10-732-923-18712	Sequence 18712, A
163	94.5	7.6	402	4	US-10-724-972A-6144	Sequence 6144, Ap	236	84	6.8	227	4	US-10-282-122A-70244	Sequence 70244, A
164	94	7.6	226	4	US-10-282-122A-43957	Sequence 43957, A	237	84	6.8	357	5	US-10-470-048B-555	Sequence 555, App
165	94	7.6	622	4	US-10-425-114-39433	Sequence 39433, A	238	84	6.8	366	4	US-10-724-972A-4827	Sequence 4827, Ap
166	94	7.6	622	4	US-10-425-114-60523	Sequence 60523, A	239	84	6.8	492	4	US-10-369-493-31	Sequence 31, Appl
167	93.5	7.6	61	4	US-10-043-344-111	Sequence 111, App	240	84	6.8	546	4	US-10-437-963-201874	Sequence 201874, A
168	93	7.5	36	4	US-10-983-838-20	Sequence 20, Appl	241	84	6.8	663	4	US-10-282-122A-52415	Sequence 52415, A
169	93	7.5	306	4	US-10-425-114-54166	Sequence 54166, A	242	84	6.8	675	4	US-10-724-972A-6913	Sequence 6913, Ap
170	93	7.5	335	4	US-10-425-115-257338	Sequence 257338, A	243	84	6.8	1014	4	US-10-654-416-2	Sequence 2, Appl
171	93	7.5	616	4	US-10-431-273-60	Sequence 60, Appl	244	84	6.8	1341	5	US-10-732-923-6938	Sequence 6938, Ap
172	93	7.5	616	4	US-10-425-115-257343	Sequence 257343, A	245	83.5	6.7	249	4	US-10-282-122A-69524	Sequence 69524, A
173	93	7.5	618	4	US-10-425-115-257337	Sequence 257337, A	246	83.5	6.7	361	4	US-10-452-024-175	Sequence 175, App

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Sequence 483, App
Sequence 5829, Ap
Sequence 8897, Ap
Sequence 206, App
Sequence 1161, Ap
Sequence 135, App
Sequence 52603, A
Sequence 20166, A
Sequence 1, Appli
Sequence 43923, A
Sequence 54, Appl
Sequence 436, App
Sequence 72, Appl
Sequence 31, Appl
Sequence 95, Appl
Sequence 5237, Ap
Sequence 178791,
Sequence 44, Appl
Sequence 114110,
Sequence 3710, Ap
Sequence 78278, A
Sequence 72, Appl
Sequence 2, Appli
Sequence 50, Appl
Sequence 7556, Ap
Sequence 3, Appli
Sequence 2, Appli
Sequence 12, Appl
Sequence 2, Appli
Sequence 5, Appli
Sequence 24252, A
Sequence 192974,
Sequence 452, App
Sequence 452, App
Sequence 452, App
Sequence 2, Appli
Sequence 2786, Ap
Sequence 450, App
Sequence 454, App
Sequence 450, App
Sequence 450, App
Sequence 56879, A
Sequence 450, App
Sequence 454, App
Sequence 10936, A
Sequence 10, Appl
Sequence 13, Appl
Sequence 192, App
Sequence 32, Appl
Sequence 43963, A
Sequence 176, App
Sequence 2376, App
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ALIGNMENTS

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RESULT 1
US-09-900-766-7
; Sequence 7, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P0218US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900, 766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-7

Query Match      100.0%; Score 1238; DB 3; Length 233;
Best Local Similarity 100.0%; Pred. No. 7,1e-105;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQNALSNLROYYNEKAITENKESDDQFLENTLLFKGFFTG 60
   |||||
Db 1 SEKSEINEKDLRKSELOQNALSNLROYYNEKAITENKESDDQFLENTLLFKGFFTG 60
   |||||
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHNNRLT 120
   |||||
Db 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHNNRLT 120
   |||||
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
   |||||
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
   |||||
QY 181 RGLIVHSSEGSTVSVDLFDAGQYPTLLRIYRDKNKTINSENHLDLYLTT 233
   |||||
Db 181 RGLIVHSSEGSTVSVDLFDAGQYPTLLRIYRDKNKTINSENHLDLYLTT 233
   |||||

RESULT 2
US-10-283-838-8
; Sequence 8, Application US/10283838
; Publication No. US20030092894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlstén,
;              Johan Hansson, Terje Kalland, Lars
;              Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
;              AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,838
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692
; FILING DATE: August 12, 1996
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REFERENCE/DOCKET NUMBER: 25,886
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 41986/1
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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;
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-283-838-8

Query Match      100.0%; Score 1238; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 7.1e-105;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKKSSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60

QY 61 HPWYNDDLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 61 HPWYNDDLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120

QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVQ 180
DB 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVQ 180

QY 181 RGLIVFHSSEGTSVSYDLFDAQGYPDPTLLRIYRDNKTINSENHLHIDLTYTT 233
DB 181 RGLIVFHSSEGTSVSYDLFDAQGYPDPTLLRIYRDNKTINSENHLHIDLTYTT 233

RESULT 3
US-10-267-682-112
; Sequence 112, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
;               Matthews, Thomas J.
;               Wild, Carl T.
;               Barney, Shawn O.
;               Lambert, Dennis M.
;               Petteway, Stephen R.
;               Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
;
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
;

;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-267-682-112

Query Match      100.0%; Score 1238; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 8.1e-105;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNDDLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 85 HPWYNDDLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVQ 204

QY 181 RGLIVFHSSEGTSVSYDLFDAQGYPDPTLLRIYRDNKTINSENHLHIDLTYTT 233
DB 205 RGLIVFHSSEGTSVSYDLFDAQGYPDPTLLRIYRDNKTINSENHLHIDLTYTT 257

RESULT 4
US-10-267-748-112
; Sequence 112, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
;               Matthews, Thomas J.
;               Wild, Carl T.
;               Barney, Shawn O.
;               Lambert, Dennis M.
;               Petteway, Stephen R.
;               Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
;
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
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; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 112;
US-10-267-748-112

Query Match 100.0%; Score 1238; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 8.1e-105; Indels 0; Gaps 0;
Matches 233; Conservative 0; Mismatches 0;

QY 1 SEKSEINEKDLRKKSQLNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKKSQLNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 84

QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 181 RGLIVFHSSEGSTVSVDLFDACQYPTLLRIYRDKNKTINSENHLHIDLILYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDACQYPTLLRIYRDKNKTINSENHLHIDLILYTT 257

RESULT 5
US-10-428-817A-188
; Sequence 188, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 188
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-188

Query Match 100.0%; Score 1238; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 8.1e-105;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSQLNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKKSQLNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 84

QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 181 RGLIVFHSSEGSTVSVDLFDACQYPTLLRIYRDKNKTINSENHLHIDLILYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDACQYPTLLRIYRDKNKTINSENHLHIDLILYTT 257

RESULT 6
US-09-900-766-3
; Sequence 3, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US010104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(233)
; OTHER INFORMATION: Chimeric Protein
US-09-900-766-3

Query Match 97.7%; Score 1210; DB 3; Length 233;
Best Local Similarity 97.9%; Pred. No. 2.6e-102;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSQLNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKKSQLNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 60

QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180

QY 181 RGLIVFHSSEGSTVSVDLFDACQYPTLLRIYRDKNKTINSENHLHIDLILYTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDACQYPTLLRIYRDKNKTINSENHLHIDLILYTT 233

RESULT 7
US-09-870-759-16
; Sequence 16, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-16

Query Match 96.0%; Score 1188; DB 3; Length 248;

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Best Local Similarity 100.0%; Pred. No. 2.9e-100;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNKTINSENL 224
Db 205 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNKTINSENL 248

RESULT 8
US-09-751-708A-16
; Sequence 16, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-16

Query Match 96.0%; Score 1188; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.9e-100;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNKTINSENL 224
Db 205 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNKTINSENL 248

RESULT 9
US-10-428-817A-12
; Sequence 12, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
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; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-12

Query Match 96.0%; Score 1188; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.9e-100;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNKTINSENL 224
Db 205 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNKTINSENL 248

RESULT 10
US-10-937-758A-16
; Sequence 16, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-937-758A-16

Query Match 96.0%; Score 1188; DB 5; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.9e-100;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
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QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVHSSSGSTVSVDLFAQGOYPTLLRIYRDNKTINSENL 224
Db 205 RGLIVHSSSGSTVSVDLFAQGOYPTLLRIYRDNKTINSENL 248

RESULT 11

US-09-900-766-2
; Sequence 2, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 233
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(233)
; OTHER INFORMATION: Chimeric Protein
US-09-900-766-2

Query Match 89.4%; Score 1107; DB 3; Length 233;
Best Local Similarity 89.7%; Pred. No. 6.8e-93;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQNALSNLROIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKSELOQNALSNLROIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
QY 181 RGLIVHSSSGSTVSVDLFAQGOYPTLLRIYRDNKTINSENLHIDLILYTT 233
Db 181 RGLIVHSSSGSTVSVDLFAQGOYPTLLRIYRDNKTINSENLHIDLILYTT 233

RESULT 12

US-09-900-766-1
; Sequence 1, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 672
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1

Query Match 89.4%; Score 1107; DB 3; Length 672;
Best Local Similarity 89.7%; Pred. No. 2.7e-92;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQNALSNLROIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 226 SEKSEINEKDLRKSELOQNALSNLROIYYNEKAITENKESDDOFLNTLLFKGFFTG 285
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 286 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 405
QY 181 RGLIVHSSSGSTVSVDLFAQGOYPTLLRIYRDNKTINSENLHIDLILYTT 233
Db 406 RGLIVHSSSGSTVSVDLFAQGOYPTLLRIYRDNKTINSENLHIDLILYTT 458

RESULT 13

US-09-900-766-4
; Sequence 4, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; TYPE: PRT
; LENGTH: 233
; ORGANISM: Staphylococcus sp.
US-09-900-766-4

Query Match 82.6%; Score 1023; DB 3; Length 233;
Best Local Similarity 82.0%; Pred. No. 3.3e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQNALSNLROIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKSELOQNALSNLROIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 61 HSWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
QY 181 RGLIVHSSSGSTVSVDLFAQGOYPTLLRIYRDNKTINSENLHIDLILYTT 233
Db 181 RGLIVHSSSGSTVSVDLFAQGOYPTLLRIYRDNKTINSENLHIDLILYTT 233

RESULT 14

US-10-283-838-7
; Sequence 7, Application US/10283838

; Publication No. US20030092894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohltsten,
; Johan Hansson, Terje Kalland, Lars
; Abrahamson and Goran Foreberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,838
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692
; FILING DATE: August 12, 1996
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,896
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-283-838-7

Query Match 82.6%; Score 1023; DB 4; Length 233;
Best Local Similarity 82.0%; Pred. No. 3.3e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTD 60
QY 61 HPWYNLLVDLGSKATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 61 HSWYNLLVDFDSKIDVYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTPIDVKYTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 180
DB 121 EEKVPINLWIDGKQNTVPLETVKTKNKNVTQELDLQARRYLQEKYLNYSDFGKQV 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYSDTLRLRIYRDNKTINSENHLDLYLT 233
DB 181 RGLIVFHTSTEPSVNYDLFGAQGYSENTLLRIYRDNKTINSENHLDIYLYTS 233

RESULT 15
US-10-267-682-113
; Sequence 113, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.

; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-267-682-113

Query Match 82.6%; Score 1023; DB 4; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.7e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLQHTLLFKGFFTD 84
QY 61 HPWYNLLVDLGSKATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDFDSKIDVYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTPIDVKYTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 180
DB 145 EEKVPINLWIDGKQNTVPLETVKTKNKNVTQELDLQARRYLQEKYLNYSDFGKQV 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYSDTLRLRIYRDNKTINSENHLDLYLT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGYSENTLLRIYRDNKTINSENHLDIYLYTS 257

RESULT 16
US-10-267-748-113
; Sequence 113, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.


```
/ Matthews, Thomas J.
/ Wild, Carl T.
/ Barney, Shawn O.
/ Lambert, Dennis M.
/ Petteway, Stephen R.
/ Langlois, Alphonse J.
/ TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
/ MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
/ TRANSMISSION
/
/ NUMBER OF SEQUENCES: 239
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/267,748
/ FILING DATE: 08-Oct-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/484,223A
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-029
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 113:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 113:
/
/ US-10-267-748-113
/
/ Query Match 82.6%; Score 1023; DB 4; Length 257;
/ Best Local Similarity 82.0%; Pred. No. 3.7e-85;
/ Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
/
/ QY 1 SEKSEINEKDLRKKSSELQARNLSNLROIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
/ Db 25 SEKSEINEKDLRKKSSELQALGNLQIYYNEKAKTENKESHDPLOHTILFKGFFTD 84
/
/ QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
/ Db 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
/
/ QY 121 EEKVPINLWDGKQTTPIDVKYTSKKEVTVOELDLQARHYLHGKFGLSNSDFGKVK 180
/ Db 145 EEKVPINLWLDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYLNYSDFGKVK 204
/
/ QY 181 RGLIVPHSSGSGTVSYDLFDAQOQYPTLRIYRDNKTINSENHLDLYLTT 233
/ Db 205 RGLIVFHTSTPSVNYDLFQAQOQYNTLLRIYRDNKTINSENHLDIYLYTS 257
/
/ RESULT 17
/ US-10-951-225-5
/ Sequence 5, Application US/10951225
/ Publication No. US2005023345A1
/ GENERAL INFORMATION:
/
/ Matthews, Thomas J.
/ Wild, Carl T.
/ Barney, Shawn O.
/ Lambert, Dennis M.
/ Petteway, Stephen R.
/ Langlois, Alphonse J.
/ TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
/ MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
/ TRANSMISSION
/
/ NUMBER OF SEQUENCES: 239
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/267,748
/ FILING DATE: 08-Oct-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/484,223A
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-029
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 113:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 113:
/
/ US-10-267-748-113
/
/ Query Match 82.6%; Score 1023; DB 4; Length 257;
/ Best Local Similarity 82.0%; Pred. No. 3.7e-85;
/ Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
/
/ QY 1 SEKSEINEKDLRKKSSELQARNLSNLROIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
/ Db 25 SEKSEINEKDLRKKSSELQALGNLQIYYNEKAKTENKESHDPLOHTILFKGFFTD 84
/
/ QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
/ Db 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
/
/ QY 121 EEKVPINLWDGKQTTPIDVKYTSKKEVTVOELDLQARHYLHGKFGLSNSDFGKVK 180
/ Db 145 EEKVPINLWLDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYLNYSDFGKVK 204
/
/ QY 181 RGLIVPHSSGSGTVSYDLFDAQOQYPTLRIYRDNKTINSENHLDLYLTT 233
/ Db 205 RGLIVFHTSTPSVNYDLFQAQOQYNTLLRIYRDNKTINSENHLDIYLYTS 257
/
/ RESULT 18
/ US-10-354-948-4
/ Sequence 4, Application US/10354948
/ Publication No. US20030202962A1
/ GENERAL INFORMATION:
/ APPLICANT: Dow, Steve W.
/ Elmellie, Robyn E.
/ Poter, Terence A.
/ TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
/ NUMBER OF SEQUENCES: 13
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sheridan Ross & McIntosh
/ STREET: 1700 Lincoln Street, Suite 3500
/ CITY: Denver
/ STATE: Colorado
/ COUNTRY: U.S.A.
/ ZIP: 80203
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/354,948
/ FILING DATE: 29-Jan-2003
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/580,806
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Connell, Gary J.
/ REGISTRATION NUMBER: 32,020
/ REFERENCE/DOCKET NUMBER: 2879-29-C1
```

```
/ APPLICANT: PADMAPRIYA, BANDA PADMANABHA
/ APPLICANT: RAMESH, AIYAGARI
/ APPLICANT: CHANDRASHEKAR, ARUN
/ APPLICANT: CHAKRAVARTHY, MANDYAM
/ TITLE OF INVENTION: PRIMERS FOR DETECTING FOOD POISONING BACTERIA AND A USE
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: 501303-2002
/ CURRENT APPLICATION NUMBER: US/10/951,225
/ CURRENT FILING DATE: 2004-09-27
/ PRIOR APPLICATION NUMBER: PCT/IB02/01150
/ PRIOR FILING DATE: 2002-03-26
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 5
/ LENGTH: 257
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
/ US-10-951-225-5
/
/ Query Match 82.6%; Score 1023; DB 5; Length 257;
/ Best Local Similarity 82.0%; Pred. No. 3.7e-85;
/ Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
/
/ QY 1 SEKSEINEKDLRKKSSELQARNLSNLROIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
/ Db 25 SEKSEINEKDLRKKSSELQALGNLQIYYNEKAKTENKESHDPLOHTILFKGFFTD 84
/
/ QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
/ Db 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
/
/ QY 121 EEKVPINLWDGKQTTPIDVKYTSKKEVTVOELDLQARHYLHGKFGLSNSDFGKVK 180
/ Db 145 EEKVPINLWLDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYLNYSDFGKVK 204
/
/ QY 181 RGLIVPHSSGSGTVSYDLFDAQOQYPTLRIYRDNKTINSENHLDLYLTT 233
/ Db 205 RGLIVFHTSTPSVNYDLFQAQOQYNTLLRIYRDNKTINSENHLDIYLYTS 257
/
/ RESULT 18
/ US-10-354-948-4
/ Sequence 4, Application US/10354948
/ Publication No. US20030202962A1
/ GENERAL INFORMATION:
/ APPLICANT: Dow, Steve W.
/ Elmellie, Robyn E.
/ Poter, Terence A.
/ TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
/ NUMBER OF SEQUENCES: 13
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sheridan Ross & McIntosh
/ STREET: 1700 Lincoln Street, Suite 3500
/ CITY: Denver
/ STATE: Colorado
/ COUNTRY: U.S.A.
/ ZIP: 80203
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/354,948
/ FILING DATE: 29-Jan-2003
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/580,806
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Connell, Gary J.
/ REGISTRATION NUMBER: 32,020
/ REFERENCE/DOCKET NUMBER: 2879-29-C1
```

```

;
; TELSCOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-354-948-4

Query Match      82.3%; Score 1019; DB 4; Length 233;
Best Local Similarity 81.9%; Pred. No. 7.6e-85;
Matches 190; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY  2 EKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
DB  2 EKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESHQDQLQHTILFKGFFTDH 61

QY  62 PNYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB  62 SWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121

QY  122 EKKVPINLWDGKQTTPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGGKVOR 181
DB  122 EKKVPINLWDGKQNTVPLETVTKNKNVTVQELDQARHYLQEKYNLYNSDVFDGKVOR 181

QY  182 GLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLDLYLYTT 233
DB  182 GLIVFHTSTEPSVNYDLFQAQGSNTLLRIYRDNKTINSENHHDILYLYTS 233

RESULT 19
US-09-870-759-8
; Sequence 8, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-8

Query Match      81.8%; Score 1013; DB 3; Length 257;
Best Local Similarity 81.5%; Pred. No. 3.1e-84;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY  1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB  25 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESHQDQLQHTILFKGFFTN 84

QY  61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB  85 HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY  121 EKKVPINLWDGKQTTPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 180
DB  145 EKKVPINLWDGKQNTVPLETVTKNKNVTVQELDQARHYLQEKYNLYNSDVFDGKVQ 204

QY  181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLDLYLYTT 233
DB  205 RGLIVFHTSTEPSVNYDLFQAQGSNTLLRIYRDNKTINSENHHDILYLYTS 257

RESULT 20
US-09-751-708A-8
; Sequence 8, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-8

Query Match      81.8%; Score 1013; DB 3; Length 257;
Best Local Similarity 81.5%; Pred. No. 3.1e-84;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY  1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB  25 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESHQDQLQHTILFKGFFTN 84

QY  61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB  85 HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY  121 EKKVPINLWDGKQTTPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 180
DB  145 EKKVPINLWDGKQNTVPLETVTKNKNVTVQELDQARHYLQEKYNLYNSDVFDGKVQ 204

QY  181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLDLYLYTT 233
DB  205 RGLIVFHTSTEPSVNYDLFQAQGSNTLLRIYRDNKTINSENHHDILYLYTS 257

RESULT 21
US-10-428-817A-4
; Sequence 4, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-4
```

Query Match 81.8%; Score 1013; DB 4; Length 257;
Best Local Similarity 81.5%; Pred. No. 3.1e-84;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNQLKQIYYNEKAKTENKESDQPLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNQLKQIYYNEKAKTENKESDQPLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVHSSGSGTVSDVLDFAQOQYPTLLRIYRDKNKTINSENHLDLYLTT 233
DB 205 RGLIVHSTSTPSVNYDLFGAQOQNSNLTLLRIYRDKNKTINSENHLDLYLTS 257

RESULT 22
US-10-937-758A-8
; Sequence 8, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-937-758A-8

Query Match 81.8%; Score 1013; DB 5; Length 257;
Best Local Similarity 81.5%; Pred. No. 3.1e-84;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNQLKQIYYNEKAKTENKESDQPLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNQLKQIYYNEKAKTENKESDQPLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVHSSGSGTVSDVLDFAQOQYPTLLRIYRDKNKTINSENHLDLYLTT 233
DB 205 RGLIVHSTSTPSVNYDLFGAQOQNSNLTLLRIYRDKNKTINSENHLDLYLTS 257

RESULT 23
US-10-002-784A-2
; Sequence 2, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A

; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A periplasmic
US-10-002-784A-2

Query Match 80.8%; Score 1000; DB 4; Length 257;
Best Local Similarity 80.7%; Pred. No. 4.7e-83;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNQLKQIYYNEKAKTENKESDQPLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNQLKQIYYNEKAKTENKESDQPLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVHSSGSGTVSDVLDFAQOQYPTLLRIYRDKNKTINSENHLDLYLTT 233
DB 205 RGLIVHSTSTPSVNYDLFGAQOQNSNLTLLRIYRDKNKTINSENHLDLYLTS 257

RESULT 24
US-10-767-687-2
; Sequence 2, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

```

;
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-767-687-2

Query Match      80.8%; Score 1000; DB 5; Length 257;
Best Local Similarity 80.7%; Pred. No. 4.7e-83;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQPROHTILFKGFTH 84
Qy 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAQMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVRFDSKOIVDKYKGGKVDLYGAYAGYQCAGGTPNKTAQMYGGVTLHDNNRLT 144
Qy 121 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EKKVPINLWIDGKQNTVPLETKNKNVTVQELDLQARRYLQEKYKLYNSDVFQGVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLFDAQGYQPDTLRIYRDNKTINSENHLHIDLTYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFQAQGYQNTLLRIYRDNKTINSENHMDIYLYTS 257
```

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RESULT 25
US-10-002-784A-4
; Sequence 4, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A cytoplasmic
US-10-002-784A-4
```

```

Query Match      80.5%; Score 996; DB 4; Length 233;
Best Local Similarity 80.6%; Pred. No. 9.7e-83;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

Qy 2 EKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTGH 61
Db 2 EKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQPROHTILFKGFTH 61
Qy 62 PWNDDLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAQMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKOIVDKYKGGKVDLYGAYAGYQCAGGTPNKTAQMYGGVTLHDNNRLTE 121
Qy 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 181
Db 122 EKKVPINLWIDGKQNTVPLETKNKNVTVQELDLQARRYLQEKYKLYNSDVFQGVQ 181
Qy 182 GLIVFHSSEGSTVSYDLFDAQGYQPDTLRIYRDNKTINSENHLHIDLTYTT 233
Db 182 GLIVFHTSTEPSVNYDLFQAQGYQNTLLRIYRDNKTINSENHMDIYLYTS 233
```

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RESULT 26
US-10-767-687-4
; Sequence 4, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-767-687-4
```

```

Query Match      80.5%; Score 996; DB 5; Length 233;
Best Local Similarity 80.6%; Pred. No. 9.7e-83;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

Qy 2 EKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTGH 61
Db 2 EKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQPROHTILFKGFTH 61
Qy 62 PWNDDLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAQMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKOIVDKYKGGKVDLYGAYAGYQCAGGTPNKTAQMYGGVTLHDNNRLTE 121
Qy 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 181
Db 122 EKKVPINLWIDGKQNTVPLETKNKNVTVQELDLQARRYLQEKYKLYNSDVFQGVQ 181
Qy 182 GLIVFHSSEGSTVSYDLFDAQGYQPDTLRIYRDNKTINSENHLHIDLTYTT 233
Db 182 GLIVFHTSTEPSVNYDLFQAQGYQNTLLRIYRDNKTINSENHMDIYLYTS 233
```

```

RESULT 27
US-10-428-817A-182
; Sequence 182, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
```


NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-4

Query Match 79.0%; Score 978; DB 2; Length 233;
Best Local Similarity 79.3%; Pred. No. 4.3e-81;
Matches 184; Conservative 17; Mismatches 31; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTGH 61
DB 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTGH 61

QY 62 PWYNDLLVLDGSKDATNKYKGVKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVDFDSKDIYVDKYKGVKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121

QY 122 EKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVR 181
DB 122 EKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVR 181

QY 182 GLIVHSSSGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYLTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAQGSNTLLRIYRDNKTINSENHLDLYLTS 233

RESULT 30
US-10-997-690-11
Sequence 11, Application US/10997690
Publication No. US20050153376A1
GENERAL INFORMATION:
APPLICANT: FRASER, JOHN DAVID
APPLICANT: PROFIT, THOMAS
TITLE OF INVENTION: SUPERANTIGENS
FILE REFERENCE: 12669-004001
CURRENT APPLICATION NUMBER: US/10/997,690
PRIOR FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: 09/869,136
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: PCT/NZ99/00228
PRIOR FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: NZ 333589
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 227
TYPE: PRT
ORGANISM: Streptococcus aureus
US-10-997-690-11

Query Match 74.4%; Score 921; DB 5; Length 227;
Best Local Similarity 79.4%; Pred. No. 6.8e-76;
Matches 185; Conservative 17; Mismatches 25; Indels 6; Gaps 6;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTG 60
DB 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTG 59

QY 61 HPWYNDLLVLDGSKDATNKYKGVKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 60 HSWYNDLLVDFDSKDIYVDKYKGVKVDLYGAYGYQCAGGTPNKTACMY-GVTLHDNNRLT 118

QY 121 BEKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVR 180
DB 119 BEKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVR 175

QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYLTT 233
DB 176 RGLIVFHTSTEPSVNYDLFGAQGSNTLLRIYRDNKTINSENHLDLYLTS 227

RESULT 31
US-10-428-817A-175
Sequence 175, Application US/10428817A
Publication No. US20040214783A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 38373-189118
CURRENT APPLICATION NUMBER: US/10/428,817A
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US 60/378,988
PRIOR FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: US 60/389,366
PRIOR FILING DATE: 2002-06-15
PRIOR APPLICATION NUMBER: US 60/406,697
PRIOR FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: US 60/406,750
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/415,310
PRIOR FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 60/415,400
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US 60/438,686
PRIOR FILING DATE: 2003-01-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn version 3.2
SEQ ID NO 175
LENGTH: 268
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-428-817A-175

Query Match 67.0%; Score 830; DB 4; Length 268;
Best Local Similarity 64.9%; Pred. No. 1.8e-67;
Matches 150; Conservative 38; Mismatches 43; Indels 0; Gaps 0;

QY 3 KSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTGH 62
DB 27 KNETIKEKNLHKKSELSSITLNNLRHIYFPNEKIGSEKIMTEDQFLDYTLFLKSPFISH 86

QY 63 WYNDLLVLDGSKDATNKYKGVKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 122
DB 87 QYNDLLVDFDSKETVKNKFGKQVDLYGSYGFQCSGKGNKTACMYGGVTLHDNNRLTE 146

QY 123 KKVPIINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVR 182
DB 147 KKVPIINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVR 206

QY 183 LIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYLTT 233
DB 207 LIVFHTSKEPLSVYDLFNVIGQYDPKLLKIYQDNKIISENHLDLYLTS 257

RESULT 32
US-09-870-759-14
Sequence 14, Application US/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128

```

; SEQUENCE 10, APPLICATION US/10428817A
; PUBLICATION NO. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-10

Query Match      53.6%; Score 663; DB 4; Length 258;
Best Local Similarity 54.5%; Pred. No. 3.2e-52;
Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLKKSELQARNLSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 26 NENIDSVKEKELHKKSELSTALNNMKHSYADKNPIIGENKSTGDOFLENTLLYKKFFTD 85

Qy 61 HPWYNDLLVDLGSKDQATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 120
Db 86 LINFEDLLINFNSKEMAQHFPSKNVDVPIRYINCYGGIEDTACTYGGVTPHEGKNLK 145

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 146 ERKKIPINLWINGVQKESVLDKQVTDKKNVTVOELDAQARRYLQKDLKLYNNDTLGGKIQ 205

Qy 181 RGLIVFHSSEGSVSYDLFDAQGYQPTDLLRIYRDNKNTINSENHLHDIYLY 231
Db 206 RGKIEFDSSDGSVSYDLFDVKGDFPEKQLRIYSDNKTLSLSTLHLDIYLY 256

RESULT 35
US-10-428-817A-187
; Sequence 187, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-10

Query Match      53.6%; Score 663; DB 3; Length 258;
Best Local Similarity 54.5%; Pred. No. 3.2e-52;
Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLKKSELQARNLSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 26 NENIDSVKEKELHKKSELSTALNNMKHSYADKNPIIGENKSTGDOFLENTLLYKKFFTD 85

Qy 61 HPWYNDLLVDLGSKDQATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 120
Db 86 LINFEDLLINFNSKEMAQHFPSKNVDVPIRYINCYGGIEDTACTYGGVTPHEGKNLK 145

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 146 ERKKIPINLWINGVQKESVLDKQVTDKKNVTVOELDAQARRYLQKDLKLYNNDTLGGKIQ 205

Qy 181 RGLIVFHSSEGSVSYDLFDAQGYQPTDLLRIYRDNKNTINSENHLHDIYLY 231
Db 206 RGKIEFDSSDGSVSYDLFDVKGDFPEKQLRIYSDNKTLSLSTLHLDIYLY 256

RESULT 34
US-10-428-817A-10
; Sequence 14, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-14

Query Match      53.6%; Score 663; DB 3; Length 258;
Best Local Similarity 54.5%; Pred. No. 3.2e-52;
Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLKKSELQARNLSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 26 NENIDSVKEKELHKKSELSTALNNMKHSYADKNPIIGENKSTGDOFLENTLLYKKFFTD 85

Qy 61 HPWYNDLLVDLGSKDQATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 120
Db 86 LINFEDLLINFNSKEMAQHFPSKNVDVPIRYINCYGGIEDTACTYGGVTPHEGKNLK 145

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 146 ERKKIPINLWINGVQKESVLDKQVTDKKNVTVOELDAQARRYLQKDLKLYNNDTLGGKIQ 205

Qy 181 RGLIVFHSSEGSVSYDLFDAQGYQPTDLLRIYRDNKNTINSENHLHDIYLY 231
Db 206 RGKIEFDSSDGSVSYDLFDVKGDFPEKQLRIYSDNKTLSLSTLHLDIYLY 256

RESULT 34
US-10-428-817A-10
; Sequence 14, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-14

Query Match      53.6%; Score 663; DB 3; Length 258;
Best Local Similarity 54.5%; Pred. No. 3.2e-52;
Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLKKSELQARNLSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 26 NENIDSVKEKELHKKSELSTALNNMKHSYADKNPIIGENKSTGDOFLENTLLYKKFFTD 85

Qy 61 HPWYNDLLVDLGSKDQATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 120
Db 86 LINFEDLLINFNSKEMAQHFPSKNVDVPIRYINCYGGIEDTACTYGGVTPHEGKNLK 145

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 146 ERKKIPINLWINGVQKESVLDKQVTDKKNVTVOELDAQARRYLQKDLKLYNNDTLGGKIQ 205

Qy 181 RGLIVFHSSEGSVSYDLFDAQGYQPTDLLRIYRDNKNTINSENHLHDIYLY 231
Db 206 RGKIEFDSSDGSVSYDLFDVKGDFPEKQLRIYSDNKTLSLSTLHLDIYLY 256

RESULT 34
US-10-428-817A-10
; Sequence 14, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-14

Query Match      53.6%; Score 663; DB 3; Length 258;
Best Local Similarity 54.5%; Pred. No. 3.2e-52;
Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLKKSELQARNLSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 26 NENIDSVKEKELHKKSELSTALNNMKHSYADKNPIIGENKSTGDOFLENTLLYKKFFTD 85

Qy 61 HPWYNDLLVDLGSKDQATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 120
Db 86 LINFEDLLINFNSKEMAQHFPSKNVDVPIRYINCYGGIEDTACTYGGVTPHEGKNLK 145

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 146 ERKKIPINLWINGVQKESVLDKQVTDKKNVTVOELDAQARRYLQKDLKLYNNDTLGGKIQ 205

Qy 181 RGLIVFHSSEGSVSYDLFDAQGYQPTDLLRIYRDNKNTINSENHLHDIYLY 231
Db 206 RGKIEFDSSDGSVSYDLFDVKGDFPEKQLRIYSDNKTLSLSTLHLDIYLY 256

RESULT 34
US-10-428-817A-10
; Sequence 14, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent
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Db 61 KTACMYGGVTLHDNNRLTEKK 82
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CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 32
LENGTH: 82
TYPE: PRT
ORGANISM: staphylococcal enterotoxin A
FEATURE:
OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-32

Query Match 32.2%; Score 399; DB 5; Length 82;
Best Local Similarity 86.6%; Pred. No. 9.8e-29;
Matches 71; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 43 SDOQFLENTLLFKGFFTHGHPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPN 102
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 SHDQFLQHTLTLFKGFFTHGHPWYNDLLVLDLGSKDIDVKYKGGKVDLYGAYGYQCAGGTPN 60

Qy 103 KTACMYGGVTLHDNNRLTEKK 124
|||||
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 39
US-10-767-687-19
; Sequence 19, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-767-687-19

Query Match 36.9%; Score 457; DB 5; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.9e-34;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 SDOQFLENTLLFKGFFTHGHPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPN 102
|||||
Db 1 SDOQFLENTLLFKGFFTHGHPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPN 60

Qy 103 KTACMYGGVTLHDNNRLTEKK 124
|||||
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 40
US-10-002-784A-32
; Sequence 32, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
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; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 32
; LENGTH: 82
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin A
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-32

Query Match 32.2%; Score 399; DB 4; Length 82;
Best Local Similarity 86.6%; Pred. No. 9.8e-29;
Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 43 SDOQFLENTLLFKGFFTHGHPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPN 102
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 SHDQFLQHTLTLFKGFFTHGHPWYNDLLVLDLGSKDIDVKYKGGKVDLYGAYGYQCAGGTPN 60

Qy 103 KTACMYGGVTLHDNNRLTEKK 124
|||||
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 41
US-10-767-687-17
; Sequence 17, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-767-687-17
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; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 173
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-173

Query Match      29.6%; Score 366; DB 4; Length 217;
Best Local Similarity 37.9%; Pred. No. 3.7e-25;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY 10 KDLRKSELQNALSNLROIYYNEKAITENKESDDOFLNTLLFKGFTGHPWYNDLLV 69
Db 1 EDLHKSELTDLALAN--AYQYNHPFIKENIKSDEISGEKDLIFRN--QGDSG-NDLRV 55
QY 70 DLGSKDATNKYGGKVDLYGAYGYOCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINL 129
Db 56 KPATADLAQKFNKNVDIYGASFYKCEKISENSECLYGGTTL-NSEKLAQSERVIGANV 114
QY 130 WIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQORGLIYVHSS 189
Db 115 WVDGIQKETEL--IRTNKNVTQLQELDIKIRKILSDKYKIYYKDS---EISKGLIEFDMK 169
QY 190 EGSTVSYDLFDAQGVPTDLLRIYRDNKTINSNL-HIDLILYT 232
Db 170 TPRDYSFDIYDLKGENDYEIDKIYEDNKTILKSDDISHDVNLVT 213

RESULT 44
US-10-474-792-416
; Sequence 416, Application US/10474792
; Publication No. US20040236072A1
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Stephen
; APPLICANT: Zagursky, Robert
; APPLICANT: Nickbarg, Elliot
; APPLICANT: Winter, Lourie
; TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
; FILE REFERENCE: AM 100399
; CURRENT APPLICATION NUMBER: US/10/474,792
; CURRENT FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 416
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-474-792-416

Query Match      27.7%; Score 343.5; DB 5; Length 259;
Best Local Similarity 34.1%; Pred. No. 5.3e-23;
Matches 78; Conservative 44; Mismatches 84; Indels 23; Gaps 6;

QY 17 ELQNALSNLROIYYNEKAITENKESDDOFLNTLLFKGFTGHPWYN---DLLYDLGS 73
Db 34 EMSVGVINLRLNLYSTYDTEVKGKINEGPPFSGSLFYKNI-----PYGNSSIELKVELNS 89
QY 74 KDATNKYGGKVDLYGAYGYOCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWIDG 133
Db 90 VEKANFFSGKRVDFITLTPLEYSPPCNSNIKNKS---YGGITLSDGNRI-DKKNIPVNFIDG 145
QY 134 ---KQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLY-----NSDSFGGKVOR 181
Db 146 VOOKSYTDTISTVTDKKEVTVOELDLQARHYLHGKFGLY-----NSDSFGGKVOR 205
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; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 173
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-173

Query Match      29.6%; Score 366; DB 4; Length 217;
Best Local Similarity 37.9%; Pred. No. 3.7e-25;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY 10 KDLRKSELQNALSNLROIYYNEKAITENKESDDOFLNTLLFKGFTGHPWYNDLLV 69
Db 1 EDLHKSELTDLALAN--AYQYNHPFIKENIKSDEISGEKDLIFRN--QGDSG-NDLRV 55
QY 70 DLGSKDATNKYGGKVDLYGAYGYOCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINL 129
Db 56 KPATADLAQKFNKNVDIYGASFYKCEKISENSECLYGGTTL-NSEKLAQSERVIGANV 114
QY 130 WIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQORGLIYVHSS 189
Db 115 WVDGIQKETEL--IRTNKNVTQLQELDIKIRKILSDKYKIYYKDS---EISKGLIEFDMK 169
QY 190 EGSTVSYDLFDAQGVPTDLLRIYRDNKTINSNL-HIDLILYT 232
Db 170 TPRDYSFDIYDLKGENDYEIDKIYEDNKTILKSDDISHDVNLVT 213

RESULT 44
US-10-474-792-416
; Sequence 416, Application US/10474792
; Publication No. US20040236072A1
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Stephen
; APPLICANT: Zagursky, Robert
; APPLICANT: Nickbarg, Elliot
; APPLICANT: Winter, Lourie
; TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
; FILE REFERENCE: AM 100399
; CURRENT APPLICATION NUMBER: US/10/474,792
; CURRENT FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 416
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-474-792-416

Query Match      27.7%; Score 343.5; DB 5; Length 259;
Best Local Similarity 34.1%; Pred. No. 5.3e-23;
Matches 78; Conservative 44; Mismatches 84; Indels 23; Gaps 6;

QY 17 ELQNALSNLROIYYNEKAITENKESDDOFLNTLLFKGFTGHPWYN---DLLYDLGS 73
Db 34 EMSVGVINLRLNLYSTYDTEVKGKINEGPPFSGSLFYKNI-----PYGNSSIELKVELNS 89
QY 74 KDATNKYGGKVDLYGAYGYOCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWIDG 133
Db 90 VEKANFFSGKRVDFITLTPLEYSPPCNSNIKNKS---YGGITLSDGNRI-DKKNIPVNFIDG 145
QY 134 ---KQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLY-----NSDSFGGKVOR 181
Db 146 VOOKSYTDTISTVTDKKEVTVOELDLQARHYLHGKFGLY-----NSDSFGGKVOR 205
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QY 25 NLRQIYYNEKAITENK--ESDDQFLENTLLFKGFTGHPWYNDDLLVDLGSKDQATNKYKG 82
Db 28 NLRN---YGSYPTEDHQSPENPNHLSHQLVFS-----MDNSTVTAEFKNVDDVKKFKN 79
QY 83 KKVVDLYGAYYQACAGTGNKTAACMYGGVTLHDNNRLTEBKVPINLWIDGKQTTVPIDK 142
Db 80 HAVDVVGLSYGVCL-----KNKYIYGGVTL-AGDYLEKSRRIPIPINLWNGEHOITISTDK 133
QY 143 VTSKKEVTVOELDLQARHYLHGKFGLY-----NSDSFGKVQVQGLIVPHSSE 190
Db 134 VSTNKKLVTAQEIDTKLRRYLOBEVNIYGFNDTKGRNYGNKSKFSSGFNAGKILPHLD 193
QY 191 GSTVSVDLDAQGOYPTDLLRIYRDNKTINSENHLIDL 228
Db 194 GGSFSYDLFDGTGQAESFLKIYDNKNTVETEFHLDV 231

RESULT 48
US-10-428-817A-172
; Sequence 172, Application US/104288017A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US 10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 172
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-176

Query Match 25.8%; Score 319.5; DB 4; Length 242;
Best Local Similarity 33.8%; Pred. No. 7.6e-21;
Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;

QY 25 NLRQIY--YNEK--AATENKESDDQFLENTLLFKGFTGHPWYNDDLLVDLGSKDQATNKY 80
Db 32 NLRNFAVYQPEKQLQGVSSGNFSTSHLE---YIDGKTYLSQFH-----NEY 76
QY 81 KGK-----KVDLYGAYYQACAGTGNKTAACMYGGVTLHDNNRLTEBKVPINLWIDGKQ 135
Db 77 EAKRLKDHKVDFIPGISYGLC-----NTKMYGGITLANQN-LDKPRNIPINLWNGKQ 129
QY 136 TTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYN-----SDSFGKVQVQGL 183
Db 130 NVISTDKVTSQKKEVTAQEIDIKRLYQLQNEVNIYGFNFKTKGQEQGYGSKFNKGNK 189
QY 184 IVFHSSEGSTVSVDLDAQGOYPTDLLRIYRDNKTINSENHLIDL 228
Db 190 IIFHLNNEPSFYDLYFTGTGQAESFLKIYDNKNTVETEFHLDV 234

RESULT 49
US-10-428-817A-176
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; Sequence 176, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US 10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 176
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-176

Query Match 25.0%; Score 310; DB 4; Length 242;
Best Local Similarity 33.2%; Pred. No. 5.6e-20;
Matches 74; Conservative 39; Mismatches 76; Indels 34; Gaps 9;

QY 23 LSNLRQIY----YYNEKAITENKESDDQFLENTLLFKGFTGHPWYNDDLLVDLGSKDQATN 78
Db 29 IDNLNRFYTKDFINLKVVDN-----DTPIANQLQF-----SNESY-DLISESKDFNKFS 78
QY 79 KYGKGVLDLYGAYYQACAGTGNKTAACMYGGVTLHDNNRLTEBKVPINLWIDGKQTTV 138
Db 79 NFKGKKLDVFGISYNGQC-----NTKYIYGGITA-TNEYLDKPRNIPINIWINGNHKTI 131
QY 139 PIDKVTSSKEVTVOELDLQARHYLHGKFGLY-----NSDSFGGK-----VQVGLIVF 186
Db 132 STNKYSTNKKFVTAQEIDIKLRYLQEEVNIYGHNGTKKGEEYGHKSKFVSGFNIGKVT 191
QY 187 HSSEGSTVSVDLP-DAQGOYPTDLLRIYRDNKTINSENHLIDL 228
Db 192 HLNNNDTFSYDLYFTGDDGLPKSFLKIYEDNKTVESEKPHLDV 234

RESULT 50
US-09-870-759-10
; Sequence 10, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US 09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-10

Query Match 24.3%; Score 300.5; DB 3; Length 266;
Best Local Similarity 33.6%; Pred. No. 4.7e-19;
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Qy 230 LYT 232
Db 234 LTT 236

RESULT 56
US-09-947B-12
; Sequence 12, Application US/09150947B
; Patent No. US2002028211A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
; FILE OF INVENTION: ANTAGONISTS AND VACCINES
; FILE REFERENCE: A31967-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/150,947B
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-150-947B-12

Query Match 24.2%; Score 299.5; DB 3; Length 239;
Best Local Similarity 33.7%; Pred. No. 5e-19;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;

Qy 2 EKSEINEKDLRKKSQELQNALSNLROIYYNEKAITENKESDDQFLENTLLPKGPFTH 61
Db 1 ESQDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVLGSKDATNKYKGGKVDLYGAYGYQC-----AGTPNKTAACMYGGV 111
Db 59 GNYDNVRVEPKNKLADKYKDYVDFGANYYYQCYFSKKTNDINSHETDKRKTCTMYGGV 118
Qy 112 TLHDNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNOLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYE 176
Qy 172 SDSFGGKVORGLIVFHSSEGSTVSVDLFDAGQGYPD--TLLRIYRDNKTINSENHLDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMPAGDKFDQSKYLMYNDNKNVDSKDKVIEVY 233
Qy 230 LYT 232
Db 234 LTT 236

RESULT 57
US-10-525-113-1
; Sequence 1, Application US/10525113
; Publication No. US2005024009A1
; GENERAL INFORMATION:
; APPLICANT: MERCK PATENT GMBH
; APPLICANT: CARR, Francis J.
; APPLICANT: BAKER, Matthew
; APPLICANT: CARTER, Graham
; TITLE OF INVENTION: T-CELL EPITOPES IN STAPHYLOCOCCAL
; FILE OF INVENTION: ENTEROTOXIN B
; FILE REFERENCE: MER-138
; CURRENT APPLICATION NUMBER: US/10/525,113
; PRIOR FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/EP2003/009116
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: EP 02018229.1
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-525-113-1

Query Match 24.2%; Score 299.5; DB 5; Length 239;
Best Local Similarity 33.7%; Pred. No. 5e-19;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;

Qy 2 EKSEINEKDLRKKSQELQNALSNLROIYYNEKAITENKESDDQFLENTLLPKGPFTH 61
Db 1 ESQDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVLGSKDATNKYKGGKVDLYGAYGYQC-----AGTPNKTAACMYGGV 111
Db 59 GNYDNVRVEPKNKLADKYKDYVDFGANYYYQCYFSKKTNDINSHETDKRKTCTMYGGV 118
Qy 112 TLHDNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNOLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYE 176
Qy 172 SDSFGGKVORGLIVFHSSEGSTVSVDLFDAGQGYPD--TLLRIYRDNKTINSENHLDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMPAGDKFDQSKYLMYNDNKNVDSKDKVIEVY 233
Qy 230 LYT 232
Db 234 LTT 236

RESULT 58
US-10-525-113-1
; Sequence 1, Application US/10525113
; Publication No. US2005024009A1
; GENERAL INFORMATION:
; APPLICANT: MERCK PATENT GMBH
; APPLICANT: CARR, Francis J.
; APPLICANT: BAKER, Matthew
; APPLICANT: CARTER, Graham
; TITLE OF INVENTION: T-CELL EPITOPES IN STAPHYLOCOCCAL
; FILE OF INVENTION: ENTEROTOXIN B
; FILE REFERENCE: MER-138
; CURRENT APPLICATION NUMBER: US/10/525,113
; PRIOR FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/EP2003/009116
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: EP 02018229.1
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-525-113-1

Query Match 24.2%; Score 299.5; DB 5; Length 239;
Best Local Similarity 33.7%; Pred. No. 5e-19;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;

Qy 2 EKSEINEKDLRKKSQELQNALSNLROIYYNEKAITENKESDDQFLENTLLPKGPFTH 61
Db 1 ESQDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVLGSKDATNKYKGGKVDLYGAYGYQC-----AGTPNKTAACMYGGV 111
Db 59 GNYDNVRVEPKNKLADKYKDYVDFGANYYYQCYFSKKTNDINSHETDKRKTCTMYGGV 118
Qy 112 TLHDNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNOLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYE 176
Qy 172 SDSFGGKVORGLIVFHSSEGSTVSVDLFDAGQGYPD--TLLRIYRDNKTINSENHLDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMPAGDKFDQSKYLMYNDNKNVDSKDKVIEVY 233
Qy 230 LYT 232
Db 234 LTT 236
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QY 172 SDSFGKVGORGLIVFHSSEGSTVSYDLFDAQGYDP--TLRIYRDNKTINSNLHIDLVT 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMFAPGDKFDQSKYLMYNDKNWDSKDVKEIVT 233
QY 230 LYT 232
Db 234 LIT 236

RESULT 59

US-10-428-817A-163
; Sequence 163, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 163
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-428-817A-163

Query Match 23.9%; Score 295.5; DB 4; Length 251;
Best Local Similarity 34.2%; Pred. No. 1.2e-18;
Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;

QY 4 SEINEKOLRKKSELQNAL-SNLRIQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
Db 25 SQEVFAQQDPDPFSQLRSSLVKNLQNIYFLYEGDPVTHENVKSVDDLHSHLIYN--VS 81
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGYGYQC-AGGTPNKTKACMYGGVTLHDNNRL 119
Db 82 GPNYDKLKTENKQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACIYGGVTNHEGHL 141
QY 120 TEEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKV 179
Db 142 EIPKKIVKVSIDGIQ-SLSFD-IETNKNMVAQELDYKVRKYLTDNKKQLYTNGP--SKY 197
QY 180 QRGLIVFHSSEGSTVSYDLFD----AQGOYPTDLLRIYRDNKTINSNLHIDLVT 232
Db 198 ETGYIKFIPKNKESFWDFPFPEFTQSKY----LMIYKDNELTDSNTSQIEVLYLT 250

RESULT 60

US-08-973-391A-13
; Sequence 13, Application US/08973391A
; Publication No. US20020054897A1
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoeher, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE

FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391A
; CURRENT FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391A-13

Query Match 23.8%; Score 294.5; DB 2; Length 251;
Best Local Similarity 34.2%; Pred. No. 1.5e-18;
Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;

QY 4 SEINEKOLRKKSELQNAL-SNLRIQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
Db 25 SQEVFAQQDPDPFSQLRSSLVKNLQNIYFLYEGDPVTHENVKSVDDLHSHLIYN--VS 81
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGYGYQC-AGGTPNKTKACMYGGVTLHDNNRL 119
Db 82 GPNYDKLKTENKQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACIYGGVTNHEGHL 141
QY 120 TEEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKV 179
Db 142 EIPKKIVKVSIDGIQ-SLSFD-IETNKNMVAQELDYKVRKYLTDNKKQLYTNGP--SKY 197
QY 180 QRGLIVFHSSEGSTVSYDLFD----AQGOYPTDLLRIYRDNKTINSNLHIDLVT 232
Db 198 ETGYIKFIPKNKESFWDFPFPEFTQSKY----LMIYKDNELTDSNTSQIEVLYLT 250

RESULT 61

US-09-308-830-13
; Sequence 13, Application US/09308830
; Publication No. US20020086813A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould P.C.
; STREET: P.O. Box 2903
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402-0903
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/308,830
; FILING DATE: 04-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/22228
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: 60/032,930
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Skoog, Mark T
; REGISTRATION NUMBER: 40,178
; REFERENCE/DOCKET NUMBER: 600.346USWO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081


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; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-767-687-6

Query Match      23.7%; Score 293.5; DB 5; Length 266;
Best Local Similarity 32.8%; Pred. No. 2e-18; Indels 19; Gaps 7;
Matches 80; Conservative 45; Mismatches 100;

QY 1 SEKSEINEKDLRKSKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 27 AESQPPKPEDELHKSKF--TGLMKNKVLVDNHNVSAINVKSIDQFLYDFDLIYSIKDTK 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTKACMYGG 110
Db 85 LGDYDNVRVEFNKDLADKYKDYVDVFGANYYCYFVSKTKTNDINSHQTDKRKTCMYGG 144
QY 111 VTLDHNNRLTEEEKVPIINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFLY 170
Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEQELDYLTRHYLVKNKKLY 202
QY 171 NSDSPGKQVQGLIVFHSSEGSTSVSYDLFDPAQOQ--YPTDLLRIYRDNKTINSENHIDL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFAQSKYLMYNDNKNKWDSDVKVIEV 259
QY 229 YLYT 232
Db 260 YLTT 263

; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-767-687-6

Query Match      23.7%; Score 293.5; DB 5; Length 266;
Best Local Similarity 32.8%; Pred. No. 2e-18; Indels 19; Gaps 7;
Matches 80; Conservative 45; Mismatches 100;

QY 1 SEKSEINEKDLRKSKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 27 AESQPPKPEDELHKSKF--TGLMKNKVLVDNHNVSAINVKSIDQFLYDFDLIYSIKDTK 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTKACMYGG 110
Db 85 LGDYDNVRVEFNKDLADKYKDYVDVFGANYYCYFVSKTKTNDINSHQTDKRKTCMYGG 144
QY 111 VTLDHNNRLTEEEKVPIINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFLY 170
Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEQELDYLTRHYLVKNKKLY 202
QY 171 NSDSPGKQVQGLIVFHSSEGSTSVSYDLFDPAQOQ--YPTDLLRIYRDNKTINSENHIDL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFAQSKYLMYNDNKNKWDSDVKVIEV 259
QY 229 YLYT 232
Db 260 YLTT 263

; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-767-687-6

Query Match      23.6%; Score 292.5; DB 4; Length 266;
Best Local Similarity 33.2%; Pred. No. 2.5e-18; Indels 19; Gaps 8;
Matches 81; Conservative 47; Mismatches 97;

QY 1 SEKSEINEKDLRKSKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 27 AESQPPKPEDELHKSKF--TGLMKNKVLVDNHNVSAINVKSIDQFLYDFDLIYSIKDTK 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTKACMYGG 110
Db 85 LGDYDNVRVEFNKDLADKYKDYVDVFGANYYCYFVSKTKTNDINSHQTDKRKTCMYGG 144
QY 111 VTLDHNNRLTEEEKVPIINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFLY 170
Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEQELDYLTRHYLVKNKKLY 202
QY 171 NSDSPGKQVQGLIVFHSSEGSTSVSYDLFDPAQOQYPD--TLRLIYRDNKTINSENHIDL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMYNDNKNKWDSDVKVIEV 259
QY 229 YLYT 232
Db 260 YLTT 263

; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
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; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-16

Query Match      23.4%; Score 289.5; DB 2; Length 251;
Best Local Similarity 33.8%; Pred. No. 4.4e-18;
Matches 80; Conservative 45; Mismatches 93; Indels 19; Gaps 10;

Qy 4 SEINEKDLRKSELOARNL-SNLRIYY-YNEKAIT-ENKESDDQPLENTLLFKGFFTG 60
Db 25 SQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYN---VS 81
Qy 61 HPWYNDDLVDLGSKDATNKYKGVLDLYGAYGYQC-AGGTPNKTKACMYGGVTLHDNNRL 119
Db 82 GPNYDKLKTTELKQEMATLFDKKNVDIYGVYVYHLCYLCEAERSACIYGGVTNHEGNHL 141
Qy 120 TEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKV 179
Db 142 EIPKIVVKVSIDGIQ-SLSFD-IETNKMVTAQELDYKVKYLTDNKQLYTNGP--SKY 197
Qy 180 QRLIVFHSSEGSVSYDLFD----AQGYPTDLLRIYRDNKTINSNLHIDLVLTYT 232
Db 198 ETGVKIPKNSFWDFPFPEFTQSKY----LMIYKDNETLDSNTSQIEVLTT 250

RESULT 67
US-10-002-784A-16
; Sequence 16, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 16
; TYPE: PRT
; LENGTH: 251
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
US-10-002-784A-16

Query Match      23.4%; Score 289.5; DB 4; Length 251;
Best Local Similarity 33.8%; Pred. No. 4.4e-18;
Matches 80; Conservative 45; Mismatches 93; Indels 19; Gaps 10;

Qy 4 SEINEKDLRKSELOARNL-SNLRIYY-YNEKAIT-ENKESDDQPLENTLLFKGFFTG 60
Db 25 SQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYN---VS 81
Qy 61 HPWYNDDLVDLGSKDATNKYKGVLDLYGAYGYQC-AGGTPNKTKACMYGGVTLHDNNRL 119
Db 82 GPNYDKLKTTELKQEMATLFDKKNVDIYGVYVYHLCYLCEAERSACIYGGVTNHEGNHL 141
Qy 120 TEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKV 179
Db 142 EIPKIVVKVSIDGIQ-SLSFD-IETNKMVTAQELDYKVKYLTDNKQLYTNGP--SKY 197
Qy 180 QRLIVFHSSEGSVSYDLFD----AQGYPTDLLRIYRDNKTINSNLHIDLVLTYT 232
Db 198 ETGVKIPKNSFWDFPFPEFTQSKY----LMIYKDNETLDSNTSQIEVLTT 250

RESULT 68
US-10-767-687-16
; Sequence 16, Application US/10767687
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; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US ARMY MMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-767-687-16

Query Match      23.4%; Score 289.5; DB 5; Length 251;
Best Local Similarity 33.8%; Pred. No. 4.4e-18;
Matches 80; Conservative 45; Mismatches 93; Indels 19; Gaps 10;

Qy 4 SEINEKDLRKSELOARNL-SNLRIYY-YNEKAIT-ENKESDDQPLENTLLFKGFFTG 60
Db 25 SQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYN---VS 81
Qy 61 HPWYNDDLVDLGSKDATNKYKGVLDLYGAYGYQC-AGGTPNKTKACMYGGVTLHDNNRL 119
Db 82 GPNYDKLKTTELKQEMATLFDKKNVDIYGVYVYHLCYLCEAERSACIYGGVTNHEGNHL 141
Qy 120 TEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKV 179
Db 142 EIPKIVVKVSIDGIQ-SLSFD-IETNKMVTAQELDYKVKYLTDNKQLYTNGP--SKY 197
Qy 180 QRLIVFHSSEGSVSYDLFD----AQGYPTDLLRIYRDNKTINSNLHIDLVLTYT 232
Db 198 ETGVKIPKNSFWDFPFPEFTQSKY----LMIYKDNETLDSNTSQIEVLTT 250

RESULT 69
US-10-002-784A-10
; Sequence 10, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
```

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; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 10
; SEQ ID NO 11
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin B cytoplasmic
US-10-002-784A-10

Query Match 23.3%; Score 288.5; DB 4; Length 239;
Best Local Similarity 33.9%; Pred.No.5.le-18;
Matches 80; Conservative 45; Mismatches 88; Indels 23; Gaps 8;

Qy 14 KKEFLQRNA-----LSNLROIYYNEKAITENKESDDQPLENTLLPKGFPTGHPWYNDLL 68
Db 7 KPDELHKSSFTGLMKNKVLVDNHNVSAL-NVKSIDQFRYFLDIYSIKDTKLGNTDNVR 65
Qy 69 VDLGSKDATNKYKGGKVDLYLCAYGYQCAGG-----TPNKTCACMYGGVTLHDNNR 118
Db 66 VEPGNKDLADKYDKYVDVFGANAYYQCAFSKKTINDINSHQTDKRTKCMYGGVTEHNGQ 125
Qy 119 LTEKKVPINLWDGKQTTVPIDKVTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGK 178
Db 126 LDKYRSITVAVFEDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKNKKLYEFNN--SP 181
Qy 179 VORGLIVFHSEGSTVSYDILFDAQGQVPD--TLIRIYRDNKNTINSENHLIDLYLT 232
Db 182 YETGYIKFIEIENS-FWYDMWPAEGDFDQSKYLMWYNDKNQVDSKDVKEIVLTT 236

RESULT 70
US-10-767-687-10
; Sequence 10, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714

```

Db 127 NLQNLVRVY-ENKRNITSEF-VQTDKSVTAQELDIKARNFLINKKNLYEFNS--SPYE 182

Qy 181 RGLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIDLTYLT 232

Db 183 TGYIKFIENNGNTFYQDMMPPAGDKFQSKYLMYNDNKTVDKSKVKIEVHLTT 236

RESULT 72

US-08-882-431-10

Sequence 10, Application US/08882431

Publication No. US20030009015A1

GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,

APPLICANT: Mark A. Olson

APPLICANT: Sina Bavari

TITLE OF INVENTION: Bacterial Superantigen

TITLE OF INVENTION: Vaccines

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: John Moran

STREET: US Army MPMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)

CITY: FORT DETRICK

STATE: MARYLAND

COUNTRY: USA

ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.5

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/882,431

FILING DATE: June 25, 1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Moran, John

REGISTRATION NUMBER: 26,313

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 619-2065

TELEFAX: (301) 619-7714

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 239

TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

US-08-882-431-10

Query Match 23.2%; Score 287.5; DB 2; Length 239;

Best Local Similarity 33.9%; Pred. No. 6.3e-18;

Matches 80; Conservative 45; Mismatches 88; Indels 23; Gaps 8;

Qy 14 KXSELQNA-----LSNLROIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLL 68

Db 7 KPDELHSSKFTGKMNKMYLDNHNVSAL-NVKSIDQFRFYDLIYSIKDTKLGNDVNR 65

Qy 69 VDLGSKDATNKYKGGKVDLYGAYGYQCAGG-----TPNKTACMYGGVTLHDNNR 118

Db 66 VEFKNKDLADKYDKYVDVFGANAYQCAF-SKKTNDINSHTDKRKTOMYGGVTEHNGNQ 125

Qy 119 LTEKKVPINLWDGKQTTPIDKVTSKKEVTQVELDLQARHYLHGKFGLYNSDSFGGK 178

Db 126 LDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEQLDYLTRHYLVKDKKLYEFNN--SP 181

Qy 179 VQRLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIDLTYLT 232

Db 182 YETGYIKFIENENS-FWYDMMPPAGDKFQSKYLMYNDNKMVDSKDVKIEVHLTT 236

RESULT 73

US-10-923-324-6

Sequence 6, Application US/10923324

Publication No. US20050026272A1

GENERAL INFORMATION:

APPLICANT: Bohach, Gregory I.

TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS

FILE REFERENCE: 12136.1USWO

CURRENT APPLICATION NUMBER: US/10/923,324

CURRENT FILING DATE: 2004-08-20

PRIOR APPLICATION NUMBER: US/09/555,115

PRIOR FILING DATE: 2000-08-01

PRIOR APPLICATION NUMBER: PCT/US98/25107

PRIOR FILING DATE: 1998-12-01

PRIOR APPLICATION NUMBER: US 60/067,357

PRIOR FILING DATE: 1997-12-02

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Patent in version 3.1

SEQ ID NO 6

TYPE: PRT

LENGTH: 240

ORGANISM: Staphylococcus aureus

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (240)..(240)

OTHER INFORMATION: Xaa is unknown.

US-10-923-324-6

Query Match 23.2%; Score 287.5; DB 5; Length 240;

Best Local Similarity 32.1%; Pred. No. 6.3e-18;

Matches 75; Conservative 48; Mismatches 92; Indels 19; Gaps 9;

Qy 11 DLRKXSELQNALSNLRQIYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV 69

Db 10 DLHKSSEF-TGTWGNMK--YLDDHYVSATKVSVDKFLAHDLIYNSDKRLKNYKVKY 66

Qy 70 DLGSKDATNKYKGGKVDLYGAYGYQC-----AGTTPNKTACMYGGVTLHDNNRLEE 122

Db 67 ELLNEDLAKKYKDEVVDVYGSNYVNCYFSSKDNVCKVTGGKTCMYGGITKHEGHPDNG 126

Qy 123 --KKVPINLWIDGKQTTPIDKVTSKKEVTQVELDLQARHYLHGKFGLYNSDSFGGKVQ 180

Db 127 NLQNLVRVY-ENKRNITSEF-VQTDKSVTAQELDIKARNFLINKKNLYEFNS--SPYE 182

Qy 181 RGLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIDLTYLT 232

Db 183 TGYIKFIENNGNTFYQDMMPPAGDKFQSKYLMYNDNKTVDKSKVKIEVHLTT 236

RESULT 74

US-10-525-113-5

Sequence 5, Application US/10525113

Publication No. US20050240009A1

GENERAL INFORMATION:

APPLICANT: MERCK PATENT GMBH

APPLICANT: CARR, Francis J.

APPLICANT: BAKER, Matthew

APPLICANT: CARTER, Graham

TITLE OF INVENTION: T-CELL EPITOPES IN STAPHYLOCOCCAL

TITLE OF INVENTION: ENTEROTOXIN B

FILE REFERENCE: MER-138

CURRENT APPLICATION NUMBER: US/10/525,113

CURRENT FILING DATE: 2005-02-18

PRIOR APPLICATION NUMBER: PCT/EP2003/009116

PRIOR FILING DATE: 2003-08-18

PRIOR APPLICATION NUMBER: EP 02018229.1

PRIOR FILING DATE: 2002-08-21

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 239

TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified enterotoxin protein
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 21, 24, 28
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, or Met
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, or Met
; OTHER INFORMATION: Xaa=Thr, Ala, Asp, Glu, Gly, His, Lys, Asn, Pro,
; OTHER INFORMATION: Gln, Arg, Ser, or Tyr
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 53, 58
; OTHER INFORMATION: Xaa=Ala or Ile
; OTHER INFORMATION: Xaa=His or Leu
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 81
; OTHER INFORMATION: Xaa=Thr, Ala, Asp, Glu, Gly, His, Lys, Asn, Pro,
; OTHER INFORMATION: Gln, Arg, Ser, or Tyr
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 82, 84, 85
; OTHER INFORMATION: Xaa=His or Val
; OTHER INFORMATION: Xaa=Ala, Pro, Gly, or Val
; OTHER INFORMATION: Xaa=Thr, His, or Phe
; US-10-525-113-5

Query Match      23.1%; Score 285.5; DB 5; Length 239;
Best Local Similarity 33.5%; Pred. No. 9.6e-18;
Matches 80; Conservative 43; Mismatches 87; Indels 29; Gaps 9;

QY 14 KKSELORNA-LSNLRQIYYNEKAITE-----NKESDDQFLENTLLFKGFTGHPWYN 65
Db 7 KPDELHKSKFTGLXE---NKKVLXDDNHVSAINVKSIDQFLYDPLIYSXKDTKXGNYD 62

QY 66 DLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGGVTLHD 115
Db 63 NVRVEFNKDLADKYKDKXXDXGANYYYQCYPFSKKTNDINSHQTDKRTKTCMYGGVTEHN 122

QY 116 NNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQBELDQARHYLHGKFGLYNSDSF 175
Db 123 GNQLDKYRSITVRVPEDGK-NLLSFD-VQTNKKKVTQAQLDYLTRHYLVKNKKLYEFNN- 179

QY 176 GGVQVQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRLIYRDNKTINSENHLIDLTY 232
Db 180 -SPYETGYIKFTIENENS-FWYDMMPPAGDKFDQSKYLMYNDNMVDSKDVKIEVYLT 236
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RESULT 75
US-10-923-324-5
; Sequence 5, Application US/10923324
; Publication No. US20050026272A1
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.USWO
; CURRENT APPLICATION NUMBER: US/10/923,324
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/555,115
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
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; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
; US-10-923-324-5

Query Match      23.1%; Score 285.5; DB 5; Length 240;
Best Local Similarity 31.3%; Pred. No. 9.6e-18;
Matches 76; Conservative 49; Mismatches 99; Indels 19; Gaps 9;

QY 2 EKSEINEKDLRKKSELQORNALSRLQIYYNEKAITENK-BSDDOFLENTLLFKGFFTG 60
Db 1 ESQPDPTPDELHKSSEF-TGTWGNMK--LYLDDHYVVSATKVKSVDKFLAHDLLIYNSDKK 57

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGGVTL 113
Db 58 LKNYDKVKTELLNEDLAKYKDEVDVVGNSYVVCYFSSKDNVGVKVTGKTCMYGGITK 117

QY 114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKEVTVQBELDQARHYLHGKFGLYN 171
Db 118 HEGNHFDNGNLQNLVIRVY-ENKRNITISPE-VQTDKKSVTQAQLDQELDIKARNFLINKKNLYE 175

QY 172 SDSFGKQVQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRLIYRDNKTINSENHLIDLTY 229
Db 176 FNS--SPYETGYIKFTIENNGNTFYDMMPPAGDKFDQSKYLMYNDNMVDSKRVKIEVH 233

QY 230 LYT 232
Db 234 LYT 236
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Search completed: February 15, 2006, 20:38:35
Job time : 63.958 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:34:56 ; Search time 5.66409 Seconds
(without alignments)
584.618 Million cell updates/sec

Title: US-09-900-766-7

Perfect score: 1238

Sequence: 1 SEKSEINKEURKKSQELOR.....RDNKTINSENHLIDLYLTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 107799 seqs, 14211699 residues

Total number of hits satisfying chosen parameters: 107799

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA_New.*
1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pap.*
2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pap.*
3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pap.*
4: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pap.*
5: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pap.*
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7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pap.*
8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1019	82.3	233	7	US-11-022-562-226
2	111.5	9.0	443	6	US-10-793-626-1860
3	94.5	7.6	402	6	US-10-485-517-422
4	89	7.2	171	6	US-10-793-626-1074
5	84.5	6.8	228	6	US-10-793-626-1166
6	84.5	6.8	579	7	US-11-045-802-33
7	83.5	6.7	752	6	US-10-793-626-1138
8	82.5	6.7	361	6	US-10-485-517-125
9	82.5	6.7	361	6	US-10-485-517-295
10	82	6.6	584	7	US-11-045-802-31
11	81.5	6.6	313	6	US-10-485-517-123
12	81.5	6.6	313	6	US-10-485-517-293
13	81.5	6.6	579	7	US-11-045-802-32
14	81.5	6.6	1017	7	US-11-072-512-2312
15	81	6.5	1562	7	US-11-052-554A-211
16	80	6.5	573	7	US-11-196-475-112
17	79	6.4	1208	7	US-11-115-639-46
18	79	6.4	1208	7	US-11-115-639-47
19	79	6.4	1208	7	US-11-115-639-48
20	78	6.3	392	6	US-10-793-626-2494
21	78	6.3	585	6	US-10-510-386-20
22	78	6.3	594	6	US-10-510-386-38
23	77.5	6.3	581	7	US-11-045-802-30
24	76.5	6.2	1604	7	US-11-037-243-73
25	76	6.1	182	7	US-11-065-943-55
					Sequence 226, App
					Sequence 1860, App
					Sequence 422, App
					Sequence 1074, App
					Sequence 1166, App
					Sequence 33, Appl
					Sequence 1138, App
					Sequence 125, App
					Sequence 295, App
					Sequence 31, Appl
					Sequence 123, App
					Sequence 232, Appl
					Sequence 32, Appl
					Sequence 211, App
					Sequence 112, App
					Sequence 46, Appl
					Sequence 47, Appl
					Sequence 48, Appl
					Sequence 2494, App
					Sequence 20, Appl
					Sequence 38, Appl
					Sequence 30, Appl
					Sequence 73, Appl
					Sequence 55, Appl

Sequence 214, App
Sequence 198, App
Sequence 8400, App
Sequence 2, Appl
Sequence 797, App
Sequence 191, App
Sequence 676, App
Sequence 14, Appl
Sequence 27, Appl
Sequence 506, App
Sequence 4, Appl
Sequence 252, App
Sequence 3086, App
Sequence 64, Appl
Sequence 76, Appl
Sequence 20, Appl
Sequence 216, App
Sequence 72, Appl
Sequence 184, App
Sequence 126, App
Sequence 340, App
Sequence 9, Appl
Sequence 12, Appl
Sequence 68, Appl
Sequence 3, Appl
Sequence 13, Appl
Sequence 4, Appl
Sequence 7, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 1015, App
Sequence 1015, App
Sequence 1076, App
Sequence 880, App
Sequence 2368, App
Sequence 29, Appl
Sequence 4, Appl
Sequence 20, Appl
Sequence 10, Appl
Sequence 1288, App
Sequence 2, Appl
Sequence 1, Appl
Sequence 5, Appl
Sequence 4, Appl
Sequence 11240, A
Sequence 42, Appl
Sequence 40, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 95, Appl
Sequence 100, App
Sequence 452, App
Sequence 505, App
Sequence 436, App
Sequence 3080, App
Sequence 68, Appl
Sequence 316, App
Sequence 36, Appl
Sequence 324, App
Sequence 36, Appl
Sequence 2306, App
Sequence 170, App
Sequence 114, App
Sequence 148, App
Sequence 136, App
Sequence 142, App
Sequence 146, App
Sequence 150, App
Sequence 154, App
Sequence 168, App

99	69	5.6	2765	6	US-10-453-372-116	Sequence 116, App	172	65	5.3	177	6	US-10-467-657-882	Sequence 882, App
100	68.5	5.5	335	7	US-11-072-512-2943	Sequence 2943, Ap	173	65	5.3	214	6	US-10-793-626-896	Sequence 896, App
101	68.5	5.5	374	6	US-10-995-561-668	Sequence 668, App	174	65	5.3	365	6	US-10-453-372-560	Sequence 560, App
102	68.5	5.5	374	6	US-10-995-561-669	Sequence 669, App	175	65	5.3	399	6	US-10-517-939-124	Sequence 124, App
103	68.5	5.5	428	7	US-11-156-084-329	Sequence 329, App	176	65	5.3	433	6	US-10-131-826A-334	Sequence 334, App
104	68.5	5.5	491	6	US-10-793-626-2808	Sequence 2808, Ap	177	65	5.3	503	7	US-11-074-176-350	Sequence 350, App
105	68.5	5.5	533	7	US-11-072-512-3224	Sequence 3224, Ap	178	65	5.3	506	7	US-11-074-176-176	Sequence 176, App
106	68.5	5.5	2105	7	US-11-052-554A-173	Sequence 173, App	179	65	5.3	915	7	US-11-073-112-3	Sequence 3, Appli
107	68	5.5	178	6	US-10-453-372-56	Sequence 56, App	180	65	5.3	2871	7	US-11-124-367A-264	Sequence 264, App
108	68	5.5	321	6	US-10-467-657-216	Sequence 216, App	181	64.5	5.2	272	6	US-10-793-626-2290	Sequence 2290, Ap
109	68	5.5	321	6	US-10-467-657-7912	Sequence 7912, Ap	182	64.5	5.2	373	6	US-10-498-026-99	Sequence 99, Appl
110	68	5.5	404	6	US-10-793-626-1130	Sequence 1130, Ap	183	64.5	5.2	374	6	US-10-498-026-96	Sequence 96, Appl
111	68	5.5	522	7	US-11-072-512-2264	Sequence 2264, Ap	184	64.5	5.2	698	6	US-10-793-626-2388	Sequence 2388, Ap
112	68	5.5	535	6	US-10-793-626-1084	Sequence 1024, Ap	185	64.5	5.2	926	6	US-10-873-528-194	Sequence 194, App
113	68	5.5	551	6	US-10-793-626-1668	Sequence 1668, App	186	64.5	5.2	1022	7	US-11-186-284-163	Sequence 163, App
114	68	5.5	572	7	US-11-072-512-3907	Sequence 3907, Ap	187	64.5	5.2	1022	7	US-11-072-175-244	Sequence 244, App
115	68	5.5	1031	6	US-10-857-780-22	Sequence 22, Appl	188	64.5	5.2	1122	7	US-11-191-374-3	Sequence 3, Appli
116	68	5.5	1114	6	US-10-857-780-27	Sequence 27, Appl	189	64.5	5.2	1122	7	US-11-191-375-3	Sequence 3, Appli
117	68	5.5	1484	6	US-10-517-939-74	Sequence 74, Appl	190	64.5	5.2	1122	7	US-11-191-588-3	Sequence 3, Appli
118	68	5.5	8746	7	US-11-098-686-10232	Sequence 10232, A	191	64.5	5.2	1332	7	US-11-091-643-18	Sequence 18, Appl
119	67.5	5.5	170	6	US-10-793-626-2518	Sequence 2518, Ap	192	64.5	5.2	2015	7	US-11-052-554A-374	Sequence 374, App
120	67.5	5.5	189	6	US-10-793-626-1998	Sequence 1998, Ap	193	64	5.2	266	6	US-10-793-626-212	Sequence 212, App
121	67.5	5.5	370	6	US-10-793-626-1064	Sequence 1064, Ap	194	64	5.2	316	7	US-11-156-084-184	Sequence 184, App
122	67.5	5.5	456	6	US-10-793-626-1190	Sequence 1190, Ap	195	64	5.2	352	6	US-10-517-939-226	Sequence 226, App
123	67.5	5.5	711	6	US-10-510-386-10	Sequence 10, Appl	196	64	5.2	503	6	US-10-793-626-1810	Sequence 1810, Ap
124	67.5	5.5	897	6	US-10-517-939-258	Sequence 258, App	197	64	5.2	515	6	US-11-052-554A-255	Sequence 255, App
125	67.5	5.5	944	6	US-10-467-657-4290	Sequence 4290, Ap	198	64	5.2	1176	6	US-10-821-234-897	Sequence 897, App
126	67.5	5.5	1036	7	US-11-072-512-2812	Sequence 2812, Ap	199	64	5.2	1206	6	US-10-467-657-72	Sequence 72, Appl
127	67.5	5.5	1889	7	US-11-102-476-46	Sequence 46, Appl	200	63.5	5.1	167	6	US-10-467-657-79	Sequence 79, Appl
128	67	5.4	227	6	US-10-793-626-2396	Sequence 2396, Ap	201	63.5	5.1	211	6	US-10-493-864A-1	Sequence 1, Appli
129	67	5.4	302	6	US-10-510-386-94	Sequence 94, Appl	202	63.5	5.1	211	6	US-10-493-864A-2	Sequence 2, Appli
130	67	5.4	320	6	US-10-793-626-2988	Sequence 2988, Ap	203	63.5	5.1	218	7	US-11-060-920-2	Sequence 2, Appli
131	67	5.4	489	6	US-10-793-626-3068	Sequence 3068, Ap	204	63.5	5.1	296	7	US-11-196-475-22	Sequence 22, Appl
132	67	5.4	489	6	US-10-793-626-3178	Sequence 3178, Ap	205	63.5	5.1	380	7	US-11-196-475-118	Sequence 118, App
133	67	5.4	552	6	US-10-131-826A-332	Sequence 332, App	206	63.5	5.1	393	7	US-11-196-475-114	Sequence 114, App
134	67	5.4	655	7	US-11-045-802-29	Sequence 29, Appl	207	63.5	5.1	422	6	US-10-873-528-77	Sequence 77, Appl
135	67	5.4	710	7	US-11-045-802-2	Sequence 2, Appli	208	63.5	5.1	441	7	US-11-196-475-120	Sequence 120, App
136	67	5.4	710	7	US-11-045-802-19	Sequence 19, Appl	209	63.5	5.1	454	7	US-11-196-475-116	Sequence 116, App
137	67	5.4	710	7	US-11-045-802-20	Sequence 20, Appl	210	63.5	5.1	484	7	US-11-052-554A-177	Sequence 177, App
138	67	5.4	710	7	US-11-045-802-21	Sequence 21, Appl	211	63.5	5.1	547	7	US-11-052-554A-285	Sequence 285, App
139	67	5.4	710	7	US-11-045-802-22	Sequence 22, Appl	212	63.5	5.1	554	5	US-09-978-360A-410	Sequence 410, App
140	67	5.4	710	7	US-11-045-802-23	Sequence 23, Appl	213	63.5	5.1	588	7	US-11-196-475-122	Sequence 122, App
141	67	5.4	710	7	US-11-045-802-24	Sequence 24, Appl	214	63.5	5.1	664	6	US-10-793-626-1258	Sequence 1258, Ap
142	67	5.4	826	6	US-10-793-626-1066	Sequence 1066, Ap	215	63.5	5.1	685	7	US-11-089-553A-2	Sequence 2, Appli
143	67	5.4	1963	6	US-10-877-346-43	Sequence 43, Appl	216	63.5	5.1	696	6	US-10-131-826A-354	Sequence 354, App
144	67	5.4	5034	6	US-11-072-512-2365	Sequence 2365, Ap	217	63.5	5.1	696	6	US-10-511-538-231	Sequence 231, App
145	66.5	5.4	251	7	US-10-935-494-5	Sequence 5, Appli	219	63.5	5.1	775	6	US-10-795-201-1	Sequence 1, Appli
146	66.5	5.4	459	6	US-10-793-626-406	Sequence 406, App	220	63.5	5.1	955	7	US-11-052-554A-179	Sequence 179, App
147	66.5	5.4	491	6	US-10-793-626-2104	Sequence 2104, Ap	221	63.5	5.1	1194	7	US-11-098-686-10270	Sequence 10270, A
148	66.5	5.4	491	6	US-10-793-626-10896	Sequence 10696, A	222	63.5	5.1	1594	7	US-11-052-554A-83	Sequence 83, Appl
149	66.5	5.4	597	7	US-11-045-802-28	Sequence 28, Appl	223	63	5.1	310	6	US-10-527-500-55	Sequence 55, Appl
150	66.5	5.4	597	7	US-11-045-802-28	Sequence 28, Appl	224	63	5.1	339	7	US-11-072-512-2843	Sequence 2843, Ap
151	66.5	5.4	692	7	US-11-072-512-2574	Sequence 2574, Ap	225	63	5.1	360	6	US-10-517-939-218	Sequence 218, App
152	66.5	5.4	920	7	US-11-072-512-2574	Sequence 31, Appl	226	63	5.1	380	6	US-10-624-932-20	Sequence 20, Appl
153	66.5	5.4	1394	6	US-10-935-494-31	Sequence 79, Appl	227	63	5.1	438	7	US-11-074-176-152	Sequence 152, App
154	66	5.3	334	6	US-10-498-026-79	Sequence 10, Appl	228	63	5.1	438	7	US-11-024-959-342	Sequence 342, App
155	66	5.3	430	6	US-10-525-710-30	Sequence 10, Appl	229	63	5.1	540	7	US-11-072-512-3747	Sequence 3747, Ap
156	66	5.3	612	7	US-11-098-686-10390	Sequence 10390, A	230	63	5.1	623	6	US-10-878-556A-62	Sequence 62, Appl
157	66	5.3	657	6	US-10-873-528-57	Sequence 57, Appl	231	63	5.1	690	7	US-11-052-554A-232	Sequence 232, Appl
158	66	5.3	700	7	US-11-196-475-66	Sequence 66, Appl	232	63	5.1	1147	6	US-10-615-668-5	Sequence 5, Appli
159	66	5.3	700	7	US-11-196-475-74	Sequence 74, Appl	233	63	5.1	1515	7	US-11-124-367A-402	Sequence 402, App
160	66	5.3	1299	6	US-10-821-234-1145	Sequence 1145, Ap	234	63	5.1	1516	7	US-11-124-367A-401	Sequence 401, App
161	66	5.3	1767	7	US-11-052-554A-372	Sequence 372, App	235	63	5.1	1518	7	US-11-124-367A-406	Sequence 406, App
162	66	5.3	2902	7	US-11-052-554A-91	Sequence 91, Appl	236	63	5.1	1532	7	US-11-124-367A-403	Sequence 403, App
163	66	5.3	3333	6	US-10-766-317-4	Sequence 4, Appli	237	63	5.1	1532	7	US-11-124-367A-404	Sequence 404, App
164	65.5	5.3	252	6	US-10-793-626-1948	Sequence 1948, Ap	238	63	5.1	1532	7	US-11-124-367A-405	Sequence 405, App
165	65.5	5.3	297	6	US-10-793-626-66	Sequence 66, Appl	239	63	5.1	1532	7	US-11-124-367A-407	Sequence 407, App
166	65.5	5.3	297	6	US-10-793-626-746	Sequence 746, App	240	63	5.1	1535	7	US-11-124-367A-408	Sequence 408, App
167	65.5	5.3	333	6	US-10-878-556A-48	Sequence 48, Appl	241	63	5.1	1713	6	US-10-766-317-2	Sequence 2, Appli
168	65.5	5.3	443	7	US-11-196-475-166	Sequence 166, App	242	63	5.1	1724	6	US-10-766-317-6	Sequence 6, Appli
169	65.5	5.3	478	6	US-10-793-626-768	Sequence 768, App	243	63	5.1	1730	7	US-11-192-967-4	Sequence 4, Appli
170	65.5	5.3	1386	6	US-10-517-939-284	Sequence 284, App	244	63	5.1	1730	7	US-11-193-715-4	Sequence 4, Appli
171	65.5	5.3	1449	7	US-11-052-554A-237	Sequence 237, App							

GENERAL INFORMATION:
APPLICANT: Gordon-Kamm, William
APPLICANT: Helentjaris, Tim
APPLICANT: Lowe, Keith
APPLICANT: Shen, Bo
APPLICANT: Tarczynski, Mitchell
APPLICANT: Zheng, Peizhong
TITLE OF INVENTION: AP2 Domain Transcription Factor ODP2 (Ovule Development Protein 2)
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: 035718/286074
CURRENT APPLICATION NUMBER: US/11/045,802
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: 60/541,122
PRIOR FILING DATE: 2004-02-02
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 579
TYPE: PRT
ORGANISM: Brassica napus
US-11-045-802-33

Query Match 6.8%; Score 84.5; DB 7; Length 579;
Best Local Similarity 21.0%; Pred. No. 4.1;
Matches 46; Conservative 32; Mismatches 84; Indels 57; Gaps 8;

QY 14 KXSELQNALSNLRQIYYVNEKAITENKESDD-----QFLENTLLPKGFTTCHP 62
DB 160 KGLSLMNSTSCDNNYSSNVLVAQKTIIDDSVEATPKTTIESFGQRTSIYRG-VTRHR 218
QY 63 W---YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTTPNKTCMYGGVTLHDNNRL 119
DB 219 WTGRYEHLWDNSCKREGQTRKGRQVYL-GGYDKEEKAARAYDLAALKYWGTTTTTFPM 277
QY 120 TEKKVPIINLWIDGKQTTVPIDKVTSKKEVTVOELDLQAR 165
DB 278 SEYEK-----EIEEMKMTQEVYASLRKSSGFSRGASIYRGVTRHHQHG 323
QY 166 KGLY-----NSDSFGGKQVORGLIVFHSSEGSTVSVDL 198
DB 324 RQARIGRVAGNKDLYL-----TFGTQEEAAEAYDI 355

RESULT 7
US-10-793-626-1138
Sequence 1138, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1138
LENGTH: 752
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: amino acid sequence
US-10-793-626-1138

Query Match 6.7%; Score 83.5; DB 6; Length 752;
Best Local Similarity 23.1%; Pred. No. 7.1;
Matches 56; Conservative 33; Mismatches 88; Indels 65; Gaps 12;

QY 12 LRKXSELQNALSNLRQI-YYNEKAITEN-----KESDDQFL-----ENTLLF 54
DB 438 LRNKNLK-----ENIREANHFYINPVTQNNLNNVKTSPKHLVLTGTGAGSGKSTLVK 493

QY 55 KGFFTG-HPWYND-----LLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTTPN 102
DB 494 AGFENNDDHTIFIDQKAVQGSNRSNLLTYLGVFDSVRSYFSKETGLNKAMFSYNSKGCACPN 553
QY 103 -----KTACMYGGVTLHDNNRLTE-----EKKVPINLWIDG-----KQTTV 138
DB 554 CGGKGYIKTELAFMG----DFSQTCVCHCKRYKQEVLDATIDGYSIADVLNLTVDDEGII 609
QY 139 PIDKVTSSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQVORGLIVFHSSEGSTVSVDL 198
DB 610 FFDKNDIKSK--LQSVSKTGLNYM--SLGQPLSTLSGSGEIORVKLGQHLDEEIKNSIFI 665
QY 199 FD 200
DB 666 FD 667

RESULT 8
US-10-485-517-125
Sequence 125, Application US/10485517
Publication No. US20050256299A1
GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Foster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629WO
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: GB 0200349.9
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: PatentIn version 3.1
SEQ ID NO 125
LENGTH: 361
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-485-517-125

Query Match 6.7%; Score 82.5; DB 6; Length 361;
Best Local Similarity 20.7%; Pred. No. 3.4;
Matches 28; Conservative 30; Mismatches 48; Indels 29; Gaps 3;

QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTTPNKTCMYGGVTLHDNNRLTEEK 123
DB 230 YDNIDVFIULED--NKYQLKKYSV-----GGITKTNSSKKVNHKV 266
QY 124 KVPINLWIDGKQTTVPIDKVTSSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQVORGL 183
DB 267 ELSITKQNGQMSIRDVSEYMITKEISLKELDFKLKQLIEKHNLV-----GNMGSQT 320
QY 184 IVFHSSEGSTVSVDL 198
DB 321 IVIKMKNGGKYTFEL 335

RESULT 9
US-10-485-517-295
Sequence 295, Application US/10485517
Publication No. US20050256299A1
GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Foster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629WO
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02


```
Db 478 EDEQASIKAALEKHKNEGDLTPSAQNLVYDLEPNANLSLTDDGKFLKASAVDDAF 537
QY 58 --FTGHPWYNDLLVDSKDATNKYKGKV-----DLYGAYYVQCAGGT--PNKTACMYG 109
Db 538 SKSTSKAKYDQKILQLDLDITNLEQSNVASSMELYG-NFGDKAGWSTTVSNNSQVKGW 596
QY 110 GYTLHDNNRLTEBKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKF-- 167
Db 597 SVLLERGQATATYTNLQNSYNGKISKIVKYTVDPKS-----KFOGQKWLGIFTD 650
QY 168 ---GLYNSDSFGKVQGRGLIVFHSSEGSTVSYDLFDAQOQ---YPTLLRIYRDNKTINS 221
Db 651 PTLGVFAS-AYTQVEKNTSIFIKNE-----FTFYDEGDKPINFONALLSV----ASLNR 700
QY 222 ENLHIDL 228
Db 701 ENNSIEM 707

RESULT 16
US-11-196-475-112
; Sequence 112, Application US/11196475
; Publication No. US20050271682A1
; GENERAL INFORMATION:
; APPLICANT: Dattwyler, Raymond J.
; APPLICANT: Gomes Solecki, Maria J. C.
; APPLICANT: Luft, Benjamin J.
; TITLE OF INVENTION: Recombinant Constructs of Borrelia
; FILE REFERENCE: 2631.1001-011
; CURRENT APPLICATION NUMBER: US/11/196,475
; PRIOR FILING DATE: 2005-08-03
; PRIOR APPLICATION NUMBER: US 08/148,191
; PRIOR FILING DATE: 1993-11-01
; PRIOR APPLICATION NUMBER: US 08/235,836
; PRIOR FILING DATE: 1994-04-29
; PRIOR APPLICATION NUMBER: US 09/666,017
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/226,484
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: PCT/US01/24736
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 573
; TYPE: PRT
; FEATURE:
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Chimeric Protein
US-11-196-475-112

Query Match 6.5%; Score 80; DB 7; Length 573;
Best Local Similarity 22.4%; Pred. No. 10;
Matches 44; Conservative 27; Mismatches 71; Indels 54; Gaps 8;

QY 2 EKSEENKED---LRKKSLEQRNALSNL-----ROIYYNEKAIT-ENKESDDQFL 48
Db 179 EVSVELNDTSSAATKKAWSNGTSLTITVNSKKTDLVFTKENTITVQQVDSNGTKL 238
QY 49 ENTLL-----FKGFTGHPWYNDLLV---DLGSKD-----ATNKYKKG 83
Db 239 EGSVEITKLDEIKNALKGHPWDEKMLKSKDKKDGKALDLDRELNSKSKSKSKAK 298
QY 84 KVDLYGAYYGYQCAGGTGNKTCMYGGVTLHDNNRLTEBKKVPINLWIDGKQTTVPIDKV 143
Db 299 EBEI-----TKGSKSGLDLDNNDENLWMPEDQKLPVVKKLSKKEFPVSEV 346
QY 144 ----KTSKKEVTVQEL 155
Db 347 EKLDKIFKSNNVGEL 362
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```
RESULT 17
US-11-115-639-46
; Sequence 46, Application US/11115639
; Publication No. US20050282242A1
; GENERAL INFORMATION:
; APPLICANT: Rothstein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 1208
; TYPE: PRT
; ORGANISM: E. faecium
US-11-115-639-46

Query Match 6.4%; Score 79; DB 7; Length 1208;
Best Local Similarity 24.8%; Pred. No. 33;
Matches 33; Conservative 17; Mismatches 65; Indels 18; Gaps 3;

QY 111 VTLDHNNRLTEBKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLY 170
Db 97 VTLRLTNRETGEIKAEQVFFGDFPLMTEGQTIINGAERVIVSQLVRSQGVYFHGKVDKN 156
QY 171 NSDSFGKV--QRGLIVFHSSEGSTVSYDLFDAQOQY-----DTLLRIYRD 215
Db 157 GKEGFGSTVIPNRGAWLEMETSAKDISYVRIDTRKIPLTVLVRALGFGSDDTIFEIFGD 216
QY 216 NKTINS---ENLH 225
Db 217 SETLRNTVEKOLH 229

RESULT 18
US-11-115-639-47
; Sequence 47, Application US/11115639
; Publication No. US20050282242A1
; GENERAL INFORMATION:
; APPLICANT: Rothstein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 1208
; TYPE: PRT
; ORGANISM: E. faecium
US-11-115-639-47

Query Match 6.4%; Score 79; DB 7; Length 1208;
Best Local Similarity 24.8%; Pred. No. 33;
Matches 33; Conservative 17; Mismatches 65; Indels 18; Gaps 3;

QY 111 VTLDHNNRLTEBKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLY 170
```

```

Db      97 VTLLRLNRTGTGSIKAQEVFFGDFPLMTBQGTFIINGAERVIVSQLVRSPGVYFHGKVDKN 156
QY      171 NSDSFGGKV--QRGLIVFHSSEGSTVSVDLFDACQGY------DTLLRIYRD 215
Db      157 GKGGFGSTVIPNRCAGWLEMETSAKDISIVRIDRTKIPLTVLVRLALGFGSDDTIFEIFGD 216
QY      216 NKTINS---ENLH 225
Db      217 SETLRNTVEKDLH 229

RESULT 19
US-11-115-639-48
; Sequence 48, Application US/11115639
; Publication No. US20050282242A1
; GENERAL INFORMATION:
; APPLICANT: Rothstein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 1208
; TYPE: PRT
; ORGANISM: E. faecium
US-11-115-639-48

Query Match      6.4%; Score 79; DB 7; Length 1208;
Best Local Similarity 24.8%; Pred. No.33;
Matches 33; Conservative 17; Mismatches 65; Indels 18; Gaps 3

QY      111 VTLDHNNRLTEKKVPINLWDGQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY 170
Db      97 VTLLRLNRTGTGSIKAQEVFFGDFPLMTBQGTFIINGAERVIVSQLVRSPGVYFHGKVDKN 156
QY      171 NSDSFGGKV--QRGLIVFHSSEGSTVSVDLFDACQGY------DTLLRIYRD 215
Db      157 GKGGFGSTVIPNRCAGWLEMETSAKDISIVRIDRTKIPLTVLVRLALGFGSDDTIFEIFGD 216
QY      216 NKTINS---ENLH 225
Db      217 SETLRNTVEKDLH 229

RESULT 20
US-10-793-626-2494
; Sequence 2494, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2494
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```

APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REFERENCE: 10294.204-US
CURRENT APPLICATION NUMBER: US/10/510,386
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PatentIn version 3.3
SEQ ID NO 38
LENGTH: 594
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-510-386-38

Query Match 6.3%; Score 78; DB 6; Length 594;

Best Local Similarity 26.0%; Pred. No. 16; Matches 45; Conservative 27; Mismatches 73; Indels 28; Gaps 9;

QY 56 GFFTGHPWYNDLLVDLGSKDATNKYKGK-KVDLYGAYGYQCAGGT-----PNKTA 105
DB 426 GFHTADRWNDI---SGTKLTKKGTGALKLEGDNTY-----SGGTRIDQGTLEGGSETA 477
QY 106 CMYGGVTLHDNNRLTEBEKVPINLWDG--KQTTVPIDKVKTSKKEVTVQELDLQARHYL 163
DB 478 FGRGDVAL--NGGILKE-DAPGKLIIEGDYKQSAKGILELQLSGKK---DQLKIKGKARL 531
QY 164 HKKFGLYNSDSFGGKVGRLIVFHSSEGSTVSYDLFDAQGQYPTDLLRIYRDN 216
DB 532 KGTLRINFNTDNYVPADGSAIITFRKRHGSFSSVETSGLPSKYKVKI--IYKSN 582

RESULT 23

US-11-045-802-30

Sequence 30, Application US/11045802

Publication No. US20050257289A1

GENERAL INFORMATION:

APPLICANT: Gordon-Kamm, William

APPLICANT: Helentjaris, Tim

APPLICANT: Lowe, Keith

APPLICANT: Shen, Bo

APPLICANT: Tarczynski, Mitchell

APPLICANT: Zheng, Peizhong

TITLE OF INVENTION: AP2 Domain Transcription Factor ODP2 (Ovule Development Protein 2

TITLE OF INVENTION: and Methods of Use

FILE REFERENCE: 035718/286074

CURRENT APPLICATION NUMBER: US/11/045,802

PRIOR FILING DATE: 2005-01-28

PRIOR FILING DATE: 2004-02-02

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 30

LENGTH: 581

TYPE: PRT

ORGANISM: Arabidopsis thaliana

US-11-045-802-30

Query Match

Best Local Similarity 6.3%; Score 77.5; DB 7; Length 581;

Mismatches 43; Conservative 34; Mismatches 78; Indels 59; Gaps 8;

QY 18 LORNALSNLRQIYYNEKAITN-----KESDDQFLENTLLFKGFTGHPW---Y 64
DB 165 LSNWSTSDSNNNNDVVQKTIIVDVETTPKKTIESFGORTSIYRG-VTRHRWTGRY 223
QY 65 NDLLVDLGSKDATNKYKGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTEBEKK 124
DB 224 EAHLDWNSCKREQQTKGRQ---GGYDKEEKAARAYDLAALKYGTGTTTTTFPLSEYEK 279
QY 125 VPINLWDGKQTTVPIDKVKTSKKEVTVQELDLQA-----RHYLHGKFGLY 170
DB 280 -----EVEEMKMHTRQBYVASLRKSSGFSRGASIRGVGVTTRHHQHRQWAR 325
QY 171 -----NSDSFGGKVGRLIVFHSSEGSTVSYDL 198

DB 326 IGRVAGNKDLYLG-----TFGTQEEAAEAYDI 352

RESULT 24

US-11-037-243-73

Sequence 73, Application US/11037243

Publication No. US20050287546A1

GENERAL INFORMATION:

APPLICANT: PLOWMAN, GREGORY

APPLICANT: WHYTE, DAVID

APPLICANT: CAENEPEEL, SEAN

APPLICANT: CHARYDCZAK, GLEN

APPLICANT: MANNING, GERARD

APPLICANT: SUDARSANAM, SUCHA

TITLE OF INVENTION: NOVEL PROTEASES

FILE REFERENCE: 038602/1214

CURRENT APPLICATION NUMBER: US/11/037,243

CURRENT FILING DATE: 2005-05-26

PRIOR APPLICATION NUMBER: US/09/888,615

PRIOR FILING DATE: 2001-08-26

PRIOR APPLICATION NUMBER: 60/214,047

PRIOR FILING DATE: 2000-06-26

NUMBER OF SEQ ID NOS: 150

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 73

LENGTH: 1604

TYPE: PRT

ORGANISM: Homo sapiens

US-11-037-243-73

Query Match

Best Local Similarity 6.2%; Score 76.5; DB 7; Length 1604;

Mismatches 41; Conservative 18; Mismatches 53; Indels 57; Gaps 9;

QY 74 KDATNKYKGKVDLYGAYGYQC-----AGGTPNKTA---CMYGGVT--LHDNNRLTE 121

DB 29 KDAFKRTCG-----LSYYMGQHCFFIREVLGDGVPKVAEVIYCSFGGTSKGLHFNNLI-- 81

QY 122 EKKVPINLWDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKQVOR 181

DB 82 ---VGLVLLTRGK-----DEEKAKYI---FSLFSSS-GNYVIR 113

QY 182 GLIVFHSSEGSTVSYDLFDAQGQYPTDLLRIYRDNKNTINSENLHIDLVL 230

DB 114 -----EEMERMLHVVDGKVPDTLKCFSEGEKVNVEKFRNWLFL 152

RESULT 25

US-11-065-943-55

Sequence 55, Application US/11065943

Publication No. US20050250131A1

GENERAL INFORMATION:

APPLICANT: JESTIN, JEAN-LUC

APPLICANT: VICHIER-GUERRE, SOPHIE

APPLICANT: FERRIS, STEPHANE

TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I

TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,

TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

FILE REFERENCE: 266426US0XCIP

CURRENT APPLICATION NUMBER: US/11/065,943

CURRENT FILING DATE: 2005-02-25

PRIOR APPLICATION NUMBER: US 10/787,219

PRIOR FILING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 106

SOFTWARE: PatentIn version 3.3

SEQ ID NO 55

LENGTH: 182

TYPE: PRT

ORGANISM: Bacillus subtilis

US-11-065-943-55

Query Match

Best Local Similarity 6.1%; Score 76; DB 7; Length 182;


```
QY 74 -----KDATNKYKGVLDYGYGYQCAGGTPNKACMYGGVTLHDNNRLTEKKVPI 128
Db 241 DKTQIKDIT---QGTVDLGLTKPRIELSKGWKNRLDRFLG-----NWTLSDKGVSVN 292
QY 129 LWIDGKQTTVPIDK-----VKTSKKEVTQVELDLQARHYLHGKFGLYNSDFGGKVGQ 182
Db 293 LGLPQVKGACINKPNPNNTKAPSALTAPAL-----WFGPVQNG 333
QY 183 LIVFHSSEGSTVSYDLFDAQGYPD-TLLRIYRDNKTINSEN 223
Db 334 KVMYSASVST-----YPDSSSRIVLQNLKRKTES 364

RESULT 29
US-10-873-528-2
; Sequence 2, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-2

Query Match 6.1%; Score 76; DB 6; Length 2233;
Best Local Similarity 20.3%; Pred. No. 1.4e+02;
Matches 55; Conservative 35; Mismatches 77; Indels 104; Gaps 16;

QY 3 KSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDQFLENTLLPKGPFTH- 61
Db 216 KTFKLEKDLK-----NVLTF-----DGVYMDSQVYVNGQLVGHY 252
QY 62 -PWYDNLVLDGSKDATNKYKGVLDYGYGYQCAGGTPNKACMYGGVTLHDNNRLT 120
Db 253 PNGYNQFSYDI-----TKYLQK-----DGENV-----IAVHAVN--- 282
QY 121 BEKKVPINLWDG-----KQTTVPI-DKVKTSKEVTQVELDLQARHYLHGKF-----GL 169
Db 283 ---KQPSRWYSGGIYRDVTIQTVDKHVKNKGTITLPKLEBQ--HGKVEHTVTSKI 337
QY 170 YNSD-----SFGKVQVGLIVFHS-----SEGSTVSYD-----LFD 200
Db 338 VNTDDKDHVLAEQYIVERGHAVTGLVTRTSLKAHSTSLDAITAEVERPKLMTVLND 397
QY 201 AQOQYPTLRIYRDNKTINSENHLIDLVL 231
Db 398 KPALY-ELITRYRDQQLVDAKK---DLFGY 424

RESULT 30
US-10-995-561-797
; Sequence 797, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
```

```
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 797
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-797

Query Match 6.1%; Score 75.5; DB 6; Length 457;
Best Local Similarity 26.2%; Pred. No. 20;
Matches 27; Conservative 23; Mismatches 38; Indels 15; Gaps 5;

QY 116 NNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFGLYNSDSF 175
Db 209 NFRDTEEAKEQINNVYVEKRTGRKVVLDVVKHLKDKTSLALVDVIS---PHGKW----KDKF 261
QY 176 GGVQVGLIV-FHSSEGSTVSYDLFDAQGYPTLTLRIYRDNK 217
Db 262 --KAERIMVEGFHVDKTIIRVPMINHLGRFD-----IHRDRE 297

RESULT 31
US-10-873-528-191
; Sequence 191, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 191
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-191

Query Match 6.1%; Score 75.5; DB 6; Length 627;
Best Local Similarity 21.1%; Pred. No. 30;
Matches 42; Conservative 21; Mismatches 67; Indels 69; Gaps 8;

QY 51 TLLFGKFFTGHPWYNDLLVLDGSKDATNKYKGVLDYGYGYQCAGGTPNKACMYG 110
Db 7 SLALVAGFLGLSWYGNVQAQESS-----GNKTHFINVQEGGSA----- 45
QY 111 VTLDHNNRLT-----BEKKVPINLWDGKQTT---VPIDKVKTSKEVTVQE 154
Db 46 IILESNGHFAMVDTGDEDYDFPDGSDSRYP---WREGIETSYKHVLTDRVFRRLKELGVQK 102
QY 155 LDLOARHYLHGKFGLYNSDSFGKVGQVGLIVFHSSEGSTVSYDLFDAQGYPT---DTLLRI 212
Db 103 LDFILVTHTH-----SDHIG-----NVDELLSTYPVDRVYLKK 135
QY 213 YRDNKTINSENHLIDLVL 231
Db 136 YSDSRITNSERLWDNLGY 154

RESULT 32
US-10-793-626-676
```



```

; APPLICANT: Kaufman, Paul L
; APPLICANT: Geiger, Benjamin
; APPLICANT: Berishadsky, Alexander
; APPLICANT: Borras, Teresa
; TITLE OF INVENTION: Method for Treating Glaucoma
; FILE REFERENCE: 960296.00128
; CURRENT APPLICATION NUMBER: US/11/060,914
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: US 60/545,722
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US 60/545,723
; PRIOR FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-060-914-4

Query Match          6.0%; Score 74; DB 7; Length 531;
Best Local Similarity 23.5%; Pred.No 33;
Matches 48; Conservative 22; Mismatches 70; Indels 64; Gaps 9;

QY 3 KSEINEKDLRKSEIQRNALSRLRIYYNEKAITENK-----ESDDQF 47
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 333 KAREEBEK-RLLEEIERRAAEAAEKQKMPDGLSGEDKKPFCKFTPKGSSLKTEERAEP 391
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 48 LENTLLFKGFFTHCHPWYNLLVDLGSKDATNKYKGKV-----DL----- 87
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 392 LNKSVQKGVKSTHQAAVSVKIDSLRLEQYTNATGKASKPMKPAASDLPLVPAGVGRNIK 451
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 88 ----YGAYGYQCAGGTPNK-TACMTGGVTLHDNNRLTEE---KKVPI----- 127
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 452 SMWEKGSVFSSPSASGTPNKETAGLKVGYSRRINELWLTKSPDGNKSPAPKPSDLRPGDVS 511
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 128 ----NLWIDGKQTTVPIDKVKTSKK 148
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 512 GKRNLM--BKQS---VDKVTSPTK 530
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 38
US-10-467-657-252
; Sequence 252, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 252
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-252

Query Match          5.9%; Score 73.5; DB 6; Length 345;
Best Local Similarity 24.9%; Pred.No 21;
Matches 45; Conservative 31; Mismatches 62; Indels 43; Gaps 11;

QY 18 LQRNALSRLRQI-----YYNEKAITENKESDDQL-ENTLLFKGFFTHCHPWYN-DLLV 69
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 VQKIAPEIRQLFAQTSEYHFSIPAKTEKSNLNVFFGEGRDKRGVFKRPWPVEVLIV 246

```


[illegible]

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RESULT 42
US-10-909-769-20
; Sequence 20, Application US/10909769
; Publication No. US2006024331A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Lin, Wei-Jen
; APPLICANT: Aoki, Kei Roger
; APPLICANT: Sachs, George
; TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characteristic
; FILE REFERENCE: ALLE010-100 (ROI2003-146)
; CURRENT APPLICATION NUMBER: US/10/909,769
; CURRENT FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 900
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of HC
; US-10-909-769-20

```

```

RESULT 43
US-10-793-626-216
; Sequence 216, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 216
; LENGTH: 352

```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-216

Query Match          59%;   Score 73;   DB 6;   Length 352;
Best Local Similarity 24.1%;   Pred. No. 24;
Matches 27;   Conservative 13;   Mismatches 34;   Indels 38;   Gaps 3

Qy      71  LGSKDATNKYKKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNRLTTEKKVPINLW 130
Db      202  IGRDKTKVPQSSKVKHIGN-----TKTDKTVKTNQK----- 233

Qy      131  IDGKQTTPVTDKVKTSKKEVTVOELDLQARH-----YLHGKFGLYNSDSF 175
Db      234  ---KQTSLTSPRVVKSQTKHINOLTAAOYENQYPPVFGHGFVGLVGDESF 282

```

```

RESULT 44
US-11-196-475-72
; Sequence 72, Application US/11196475
; Publication No. US20050271682A1
; GENERAL INFORMATION:
; APPLICANT: Dattwyler, Raymond J.
; APPLICANT: Gomes Solecki, Maria J. C.
; APPLICANT: Luft, Benjamin J.
; APPLICANT: Dunn, John J.
; TITLE OF INVENTION: Recombinant Constructs of Borrelia
; FILE REFERENCE: 2631.1001-011
; CURRENT APPLICATION NUMBER: US/11/196,475
; CURRENT FILING DATE: 2005-08-03
; PRIOR APPLICATION NUMBER: US 08/148,191
; PRIOR FILING DATE: 1993-11-01
; PRIOR APPLICATION NUMBER: US 08/235,836
; PRIOR FILING DATE: 1994-04-29
; PRIOR APPLICATION NUMBER: US 09/666,017
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/226,484
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: PCT/US01/24736
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 693
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-11-196-475-72

```

QY 31 YNEKAIT-ENKESDDQFLENTLLFKGFFTGHPWYNDDLVDLGSKDATNKYKG--KKVDL 87

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-11-013-759-9

Query Match
Best Local Similarity 5.9%; Score 72.5; DB 7; Length 2053;
Matches 45; Conservative 20; Mismatches 78; Indels 63; Gaps 7;

QY 68 LVDLGSKDATNKYKGGKVDLYGAYGYQCAGGPNKTCACMYGGVTLHDNNRLTEKKVPI 127
DB 1273 IVDVLGSAFNLQNGEAVDFVSITVNFANG--NTTAK---VTYDDTSKTS---KVY 1324

QY 128 NLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLGYNLSDSGFGKVGQGLIVPH 187
DB 1325 DVNVD--DTTIEVKDKKLGKVTTLTSTGTGA-----NKFALSNQATGDALVKASDIVAH 1377

QY 188 -----SSEGSTVSYDLFD----- 200
DB 1378 LNTLSGDIQTAKGASQANNSAGYVDADGNKVIYDSTDNKYQAKNDGTVDKTKVEAKDKL 1437

QY 201 -AQGQYPTDLLRIYRDNKNTINSENH 225
DB 1438 VAQAQTPDGTGLAQMNVKSVINKEQVN 1463

RESULT 49
US-10-517-939-12
; Sequence 12, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghalalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; PRIOR FILING DATE: 2004-12-13
; PRIOR FILING DATE: 2003-06-16
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(28)
US-10-517-939-12

Query Match
Best Local Similarity 5.8%; Score 72; DB 6; Length 407;
Matches 37; Conservative 27; Mismatches 72; Indels 38; Gaps 7;

QY 7 INEKLRKSEQLRNALSRLQIYYNEKAITENKESDDQF---LENTLLFKGFFTGHPW 63
DB 145 VNEDPVEKQNKQLLLKLELET-----HIKTVRYKDDIKYDWNVEVVDGDKLNSPW 200

QY 64 YNDLLVDL--GSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 201 YQIAGIDYIKVAFQAARKYGGGNIKLY-----NNDVNTVEVE 236
```

```
QY 122 EKKVPI-NLWIDGKQTTVPIDKVKTSKKEVTV---QELDLQARHYLHGKFLGYN 171
DB 237 PKRTALYNLVKQLKEGVPIDGI-GHQSHIQIGWPSEAEIEKTTINMPAAGLDN 289

RESULT 50
US-11-196-475-68
; Sequence 68, Application US/11196475
; Publication No. US20050271682A1
; GENERAL INFORMATION:
; APPLICANT: Dattwyler, Raymond J.
; APPLICANT: Gomez Solecki, Maria J. C.
; APPLICANT: Luft, Benjamin J.
; APPLICANT: Dunn, John J.
; TITLE OF INVENTION: Recombinant Constructs of Borrelia
; FILE REFERENCE: 2631.1001-011
; CURRENT APPLICATION NUMBER: US/11/196,475
; CURRENT FILING DATE: 2005-08-03
; PRIOR APPLICATION NUMBER: US 08/148,191
; PRIOR FILING DATE: 1993-11-01
; PRIOR APPLICATION NUMBER: US 08/235,836
; PRIOR FILING DATE: 1994-04-29
; PRIOR APPLICATION NUMBER: US 09/666,017
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/226,484
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: PCT/US01/24736
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 693
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-11-196-475-68

Query Match
Best Local Similarity 5.8%; Score 71.5; DB 7; Length 693;
Matches 45; Conservative 37; Mismatches 63; Indels 61; Gaps 11;

QY 2 EKSEIN-EKDLRKKSLEQ-----RNALSNL-----RQIYYVNEKAI 37
DB 329 EDIDEINKEKLPKPGDVSSPKVDQLQIKESLEDLQEQLKETSDENQKEI---EKQI 384

QY 38 TENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSK-DATNKYKGGKVDLYGAYGYQC 96
DB 385 -BIKKSDELLKSK-----DPKALDLNGDLNSKVSKEKIKGKEGI----- 425

QY 97 AGGTPNKTACMYGGVTLHDNNRLTEKKVPIINLWIDGKQTTVPIDKV-----KTSKKE 149
DB 426 ---VKEESKASLADLNNDENLRPEDQKLSDKSLNLPVSEIERVNEISKSNNE 482

QY 150 VTQVELDLQARHY--LHGKFLGYN 173
DB 483 IS-ESSPLYKPSYSDMSKEGIDNKD 507

RESULT 51
US-11-013-759-3
; Sequence 3, Application US/11013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Sasaki, Ken
; APPLICANT: Yang, Yan Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; FILE REFERENCE: 1038-921MIS:jb
; CURRENT APPLICATION NUMBER: US/11/013,759
; CURRENT FILING DATE: 2004-12-16
```


Best Local Similarity 21.8%; Pred. No. 3.1e+02;
Matches 45; Conservative 20; Mismatches 78; Indels 63; Gaps 7;
QY 68 LVDLGSKDATNKKYKKVLDYGYGYCAGGTPNKTACMYGGVTLHDNNRLTEKKVPI 127
Db 1264 IVDLSAGFNLOQNGBAVDFSVYDTVNFADG--NATTAK---VTYDDTSTKTS---KVYV 1315
QY 128 NLWIDGKQTTPVDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQVQGLIVPH 187
Db 1316 DVNVD--DTTIEVKDKLGVKTTLTSTGTGA-----NKFALSNQATGALVKASDIVAH 1368
QY 188 -----SSEGSTVSVDLFD----- 200
Db 1369 LNTLSGDIQTAKGASQANNSAGVVDADGNKVIYDSTDNKYVQAKNDGTVDTKTEVAKDKL 1428
QY 201 -AQGYPPDLLRIYRNKNTINSENH 225
Db 1429 VAQAQTPDGTGLAQMNVKSVINKEQVN 1454

RESULT 55
US-10-632-150-28
; Sequence 28, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chiaux, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; PRIOR FILING DATE: 2003-07-30
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-28

Query Match 5.7%; Score 71; DB 6; Length 621;
Best Local Similarity 20.6%; Pred. No. 75;
Matches 55; Conservative 39; Mismatches 75; Indels 98; Gaps 17;
QY 27 RQIYY-----NEKAITENKESDDQPLENTL----- 52
Db 167 KKILYLRQOKILNNLKAFLOQPDYSEYLEGAVIDQYCNPLDSLKDIAQAIDSIVE 226
QY 53 ----LPGGFTGHP-----WYNDLL--VDLGSK--DATN-----KYGKKVDLYGA- 90
Db 227 LVCKTLRGINSRHPSLAFKAGESSMIELOQSVLDAMNYVLYDQLKFKGNRMDYINAL 286
QY 91 -YGYQC---AGTPTNKTACMYGGVTLHDNNRLTEKKV-----PINL-----WIDGK 134
Db 287 NLYMHQVLIIRRTGIPISMSLLY-----LTIARQLGVPLEPVNFPFHFLLRWCOGA 336
QY 135 Q-TTVPI-DKVKTSK----KEVTVOELD-LQARHYLHGKFGLYNSDSFGGKVQVQGLIVPH 187
Db 337 EGATLDIFDIYIDAFGKGKQLTVKECEYLIGHVTAALYGVVNVKKVLQRMVGNLLSLG 396
QY 188 SSEGSTVS-----DLFDAQQQYPD 207
Db 397 KREGIDQSQLLRDSLDLYLA--MYPD 421

RESULT 56
US-11-073-457-28
; Sequence 28, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-28

Query Match 5.7%; Score 71; DB 7; Length 621;
Best Local Similarity 20.6%; Pred. No. 75;
Matches 55; Conservative 39; Mismatches 75; Indels 98; Gaps 17;
QY 27 RQIYY-----NEKAITENKESDDQPLENTL----- 52
Db 167 KKILYLRQOKILNNLKAFLOQPDYSEYLEGAVIDQYCNPLDSLKDIAQAIDSIVE 226
QY 53 ----LPGGFTGHP-----WYNDLL--VDLGSK--DATN-----KYGKKVDLYGA- 90
Db 227 LVCKTLRGINSRHPSLAFKAGESSMIELOQSVLDAMNYVLYDQLKFKGNRMDYINAL 286
QY 91 -YGYQC---AGTPTNKTACMYGGVTLHDNNRLTEKKV-----PINL-----WIDGK 134
Db 287 NLYMHQVLIIRRTGIPISMSLLY-----LTIARQLGVPLEPVNFPFHFLLRWCOGA 336
QY 135 Q-TTVPI-DKVKTSK----KEVTVOELD-LQARHYLHGKFGLYNSDSFGGKVQVQGLIVPH 187
Db 337 EGATLDIFDIYIDAFGKGKQLTVKECEYLIGHVTAALYGVVNVKKVLQRMVGNLLSLG 396
QY 188 SSEGSTVS-----DLFDAQQQYPD 207
Db 397 KREGIDQSQLLRDSLDLYLA--MYPD 421

RESULT 57
US-11-073-460-28
; Sequence 28, Application US/11073460
; Publication No. US20050272066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-28

Query Match 5.7%; Score 71; DB 7; Length 621;
Best Local Similarity 20.6%; Pred. No. 75;

```
Matches 55; Conservative 39; Mismatches 75; Indels 98; Gaps 17;
QY 27 RQIYVY-----NEKAITENKESDDQFLENTL----- 52
Db 167 KKILYLRQKILNNLKAFLQPPDDYSYLEGAVYIDQYCNPLSDISLKDIQAQDSIVE 226
QY 53 -----LFKGFTGHP-----WYNDLL--VDLGSK--DATN-----KYGKKVLDLYGA- 90
Db 227 LVCKTLRGINSRHPSLAFKAGESMIMEIELQSQVLDAMNYVLYDQLKFKGNRMYYNAL 286
QY 91 -YGYGQC---AGGTENKACMYGGVTLHDNNRLTEKKV-----PINL-----WIDGK 134
Db 287 NLYHQVLIIRRTGIPISMSLYL-----LTIAQLGVPLEPNPFPFLRWCOGA 336
QY 135 Q-TTVPI-DKVTSK-----KEVTVQELD-LQARHYLHGKFLGYNDSFGGKVQVGLIVFH 187
Db 337 EGATLDFDIYIDAFGKGQLTVKECEYLIGHVHTAALYGVNVKVLQRMVGNLLSIG 396
QY 188 SSEGSTVSY-----DLFDAQGOYPD 207
Db 397 KREGIDQSYQLLRDSLDTLALA--MYPD 421

RESULT 58
US-10-995-561-1016
; Sequence 1016, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1016
; LENGTH: 3690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1016

Query Match 5.7%; Score 71; DB 6; Length 3690;
Best Local Similarity 28.8%; Pred. No. 7.4e+02;
Matches 55; Conservative 23; Mismatches 69; Indels 44; Gaps 13;
QY 56 GFTGHPWYNDLLVDLGSKDATNKYKGV-----DLYGAYYGYOCAGTGNKT- 104
Db 41 GGFSLHPPYPNLAEE--GARIAASATCGEEAPARGSPRPRTEDLYCKLVGGPVAGGDPNQTI 98
QY 105 ACMYGGVTLHDNNRLTEKKVPINLWIDGKQ---TTVPIDK-VKTSKKEVTVQELDL-QA 159
Db 99 RGQYCDICTAANS-----NKAHPASNAIDGTERWQSPPLSRGLEYNVNT---LDLGQV 151
QY 160 RH--YLHGKFG-----LYNSDSFGGKVQVGLIVFHSSEGSTVSYDLFDAQGOYPD 208
Db 152 FHVAYVLIKFANSPRDLWLERSMDFGRTYQPMQF--FASSK-----RDCLERFG--PQT 203
QY 209 LLRIYRDNNTI 219
Db 204 LERITRDAAI 214

RESULT 59
US-10-995-561-1015
; Sequence 1015, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1015
; LENGTH: 3714
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1015

Query Match 5.7%; Score 71; DB 6; Length 3714;
Best Local Similarity 28.8%; Pred. No. 7.5e+02;
Matches 55; Conservative 23; Mismatches 69; Indels 44; Gaps 13;
QY 56 GFTGHPWYNDLLVDLGSKDATNKYKGV-----DLYGAYYGYOCAGTGNKT- 104
Db 63 GGFSLHPPYPNLAEE--GARIAASATCGEEAPARGSPRPRTEDLYCKLVGGPVAGGDPNQTI 120
QY 105 ACMYGGVTLHDNNRLTEKKVPINLWIDGKQ---TTVPIDK-VKTSKKEVTVQELDL-QA 159
Db 121 RGQYCDICTAANS-----NKAHPASNAIDGTERWQSPPLSRGLEYNVNT---LDLGQV 173
QY 160 RH--YLHGKFG-----LYNSDSFGGKVQVGLIVFHSSEGSTVSYDLFDAQGOYPD 208
Db 174 FHVAYVLIKFANSPRDLWLERSMDFGRTYQPMQF--FASSK-----RDCLERFG--PQT 225
QY 209 LLRIYRDNNTI 219
Db 204 LERITRDAAI 214
```

```
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1015
; LENGTH: 3714
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1015

Query Match 5.7%; Score 71; DB 6; Length 3714;
Best Local Similarity 28.8%; Pred. No. 7.5e+02;
Matches 55; Conservative 23; Mismatches 69; Indels 44; Gaps 13;
QY 56 GFTGHPWYNDLLVDLGSKDATNKYKGV-----DLYGAYYGYOCAGTGNKT- 104
Db 41 GGFSLHPPYPNLAEE--GARIAASATCGEEAPARGSPRPRTEDLYCKLVGGPVAGGDPNQTI 98
QY 105 ACMYGGVTLHDNNRLTEKKVPINLWIDGKQ---TTVPIDK-VKTSKKEVTVQELDL-QA 159
Db 99 RGQYCDICTAANS-----NKAHPASNAIDGTERWQSPPLSRGLEYNVNT---LDLGQV 151
QY 160 RH--YLHGKFG-----LYNSDSFGGKVQVGLIVFHSSEGSTVSYDLFDAQGOYPD 208
Db 152 FHVAYVLIKFANSPRDLWLERSMDFGRTYQPMQF--FASSK-----RDCLERFG--PQT 203
QY 209 LLRIYRDNNTI 219
Db 204 LERITRDAAI 214

RESULT 60
US-10-821-234-1076
; Sequence 1076, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1076
; LENGTH: 3717
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1076

Query Match 5.7%; Score 71; DB 6; Length 3717;
Best Local Similarity 28.8%; Pred. No. 7.5e+02;
Matches 55; Conservative 23; Mismatches 69; Indels 44; Gaps 13;
QY 56 GFTGHPWYNDLLVDLGSKDATNKYKGV-----DLYGAYYGYOCAGTGNKT- 104
Db 63 GGFSLHPPYPNLAEE--GARIAASATCGEEAPARGSPRPRTEDLYCKLVGGPVAGGDPNQTI 120
QY 105 ACMYGGVTLHDNNRLTEKKVPINLWIDGKQ---TTVPIDK-VKTSKKEVTVQELDL-QA 159
Db 121 RGQYCDICTAANS-----NKAHPASNAIDGTERWQSPPLSRGLEYNVNT---LDLGQV 173
QY 160 RH--YLHGKFG-----LYNSDSFGGKVQVGLIVFHSSEGSTVSYDLFDAQGOYPD 208
Db 174 FHVAYVLIKFANSPRDLWLERSMDFGRTYQPMQF--FASSK-----RDCLERFG--PQT 225
QY 209 LLRIYRDNNTI 219
Db 204 LERITRDAAI 214
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Db 226 LERITRDAAI 236

RESULT 61

US-10-793-626-880

; Sequence 880, Application US/10793626

; Publication No. US20050255478A1

; GENERAL INFORMATION:

; APPLICANT: KIMMERLY, WILLIAM JOHN

; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

; FILE REFERENCE: PU3480US

; CURRENT APPLICATION NUMBER: US/10/793,626

; CURRENT FILING DATE: 2004-03-04

; PRIOR APPLICATION NUMBER: 60/164,258

; PRIOR FILING DATE: 1999-11-09

; NUMBER OF SEQ ID NOS: 4472

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 880

; LENGTH: 269

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: amino acid sequence

US-10-793-626-880

Query Match 5.7%; Score 70.5; DB 6; Length 269;

Best Local Similarity 19.0%; Pred. No. 28;

Matches 33; Conservative 34; Mismatches 52; Indels 55; Gaps 7;

QY 7 INEKDLRKSELOARNLSNLQIYYNKAITEN-----KESDQFLENTLLPKGFT 59

Db 123 ISDRDQGGSTIQQVVKV---YYDNERSFTKKIKELFVARKVEKQYKKNQIL--SFTW 177

QY 60 GHPWYNLLVDLGSKDATNKYKGVLDLYGAYYQCAGTGNKTKACMYGGVTLHDNNRL 119

Db 178 NNIIYGD-----NQY-----TVEGAANHVFVTVDKNNGN 207

QY 120 TEKKVPINLWIDCKTTPV-----IDKVKTSKEVTVELDQARH 161

Db 208 MSQISV-LQSAILASKVNAFVYVDVNDMSNNYINRVKTNLEKMKQNFISEQY 260

RESULT 62

US-10-467-657-2368

; Sequence 2368, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON SPA

; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 2368

; LENGTH: 459

; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-2368

Query Match 5.7%; Score 70.5; DB 6; Length 459;

Best Local Similarity 21.0%; Pred. No. 56;

Matches 44; Conservative 38; Mismatches 81; Indels 47; Gaps 9;

QY 2 EKSEENKDLRKSEL-----QRNLSNLQIYYNKAITENKESDDQFLEN-T 51

Db 251 ERPEEVTEMSRSGVEVWSSTFDEPAQRHV--QVAEMVLEKAKRMVHEHKDVVILLDSIT 308

QY 52 LLFKGFFTGHPWYNLLVDLGSKDATNKYKGVLDLYGAYYQCAGG-TPNKTACM--- 107

Db 309 RLARAYNTVVPASGKILT--GGVDANALHRPKR--FFGAARNVEEGSLTIIATLVETG 364

QY 108 -----YGGVTLHDNNRLTEKKVPINLWIDGKQTTPIDKVKTSKKEVTVQE 154

Db 365 SRMDDVIYEEFGKTGNMELHDLRRMAEKRLFP-----AININKSGTRREELLVPN 414

QY 155 LDLQ-----ARHYLHGKFGLYNSDSFGKQV 180

Db 415 DQQRMWLLRKFLHPMDEIATEEFLNGKIK 444

RESULT 63

US-11-088-686-29

; Sequence 29, Application US/11088686

; Publication No. US20050260637A1

; GENERAL INFORMATION:

; APPLICANT: Yen, Yun

; TITLE OF INVENTION: DRUG SCREENING

; FILE REFERENCE: 14037-004001

; CURRENT APPLICATION NUMBER: US/11/088,686

; CURRENT FILING DATE: 2005-03-23

; PRIOR APPLICATION NUMBER: US 60/556,836

; PRIOR FILING DATE: 2004-03-25

; NUMBER OF SEQ ID NOS: 59

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 29

; LENGTH: 792

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-088-686-29

Query Match 5.7%; Score 70.5; DB 7; Length 792;

Best Local Similarity 19.1%; Pred. No. 11e+02;

Matches 55; Conservative 38; Mismatches 86; Indels 109; Gaps 14;

QY 11 DLRKSELOARNLSNLQI-----YYNKAITENK-----ES 43

Db 462 DFKKLAETVKVVRNLIIDINYPVPEACLSNKRHRPIGIGVQGLADAFILMRYPFES 521

QY 44 DQFLENTLLFKGFFTGHPWYNLLVDLGSKDATNKYKGVLDLYGAYYQCAGGTPNK 103

Db 522 AEAQLNKQIFETIYG---ALEASCDLAKEQ-----GPETEY---GSP-- 560

QY 104 TACMYGGVTLHDNNRLTEKKVPINLW-----PTDLWDKVLKEKIYKIRNSLLIAPMPTASTAQILG 612

Db 561 ---VSKGILQYDMWNVY---PTDLWDKVLKEKIYKIRNSLLIAPMPTASTAQILG 612

QY 148 ---KEVTVQELDQARHYLHGKFGLYNSDSFGKQVORGLIVFH-----SSEGSTVSYD 197

Db 613 NNESEIPTYTSNIYTRVLSEGFQIVNPHLLKOLTERGL--WHEEMKNQIIACNGSIQISIP 670

QY 198 LFDAGQGYDPTLLRIYR-----DNKTI-----NSENLHI 226

Db 671 -----EIPDDLKQLYKTWEISQIKVLKMAAERGAFFIDQSQSLNIHI 712

RESULT 64

US/11/062

; Sequence 4, Application US/11062471A

; Publication No. US20050255093A1

; GENERAL INFORMATION:

; APPLICANT: SHONE, Clifford Charles

; APPLICANT: SUTTON, John Mark

; APPLICANT: HALLIS, Basam

; APPLICANT: SILMAN, Nigel

; TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells

; FILE REFERENCE: 1581.0800001

; CURRENT APPLICATION NUMBER: US/11/062,471A

; CURRENT FILING DATE: 2005-02-22


```
US-11-082-544-10
; Sequence 10, Application US/11082544
; Publication No. US20050249706A1
; GENERAL INFORMATION:
; APPLICANT: Bermudes, G.
; APPLICANT: King, I.
; APPLICANT: Clairmont, C.
; APPLICANT: Lin, S.
; APPLICANT: Belcourt, M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
; FILE REFERENCE: 8002-059
; CURRENT APPLICATION NUMBER: US/11/082,544
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US/09/645,415
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/157,581
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/157,637
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion construct
US-11-082-544-10

Query Match          5.7%; Score 70; DB 7; Length 266;
Best Local Similarity 25.5%; Pred. No. 31;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

QY 8 NEKDLRKK-----SELQNALSNLR-----QIYYNEKAITENKES 43
DB 128 NEKALGRKINSWESSRSGHSFLSNLHRLNGELVHKGFFYYISQTYFRFQBEIKENTKN 187
QY 44 DQOFLNTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGVVDLYGAYGYQCAGGTPNK 103
DB 188 DKQMVQ--YIYK--YTSYP--DPILL---MKSARNCSWSKDAE-YGLYSIQ----- 229
QY 104 TACMGVGV-TLHDNNRL 119
DB 230 -----GGIFELKENDRI 241

RESULT 68
US-10-821-234-1288
; Sequence 1288, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1288
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1288

Query Match          5.7%; Score 70; DB 6; Length 281;
Best Local Similarity 25.5%; Pred. No. 33;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

US-11-082-544-10
; Sequence 10, Application US/11082544
; Publication No. US20050249706A1
; GENERAL INFORMATION:
; APPLICANT: Bermudes, G.
; APPLICANT: King, I.
; APPLICANT: Clairmont, C.
; APPLICANT: Lin, S.
; APPLICANT: Belcourt, M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
; FILE REFERENCE: 8002-059
; CURRENT APPLICATION NUMBER: US/11/082,544
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US/09/645,415
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/157,581
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/157,637
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion construct
US-11-082-544-10

Query Match          5.7%; Score 70; DB 7; Length 266;
Best Local Similarity 25.5%; Pred. No. 31;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

QY 8 NEKDLRKK-----SELQNALSNLR-----QIYYNEKAITENKES 43
DB 128 NEKALGRKINSWESSRSGHSFLSNLHRLNGELVHKGFFYYISQTYFRFQBEIKENTKN 187
QY 44 DQOFLNTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGVVDLYGAYGYQCAGGTPNK 103
DB 188 DKQMVQ--YIYK--YTSYP--DPILL---MKSARNCSWSKDAE-YGLYSIQ----- 229
QY 104 TACMGVGV-TLHDNNRL 119
DB 230 -----GGIFELKENDRI 241

RESULT 68
US-10-821-234-1288
; Sequence 1288, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1288
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1288

Query Match          5.7%; Score 70; DB 6; Length 281;
Best Local Similarity 25.5%; Pred. No. 33;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

US-11-077-272-2
; Sequence 2, Application US/11077272
; Publication No. US20050244927A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, MOON-LAM SUSAN
; APPLICANT: SWARTZ, JAMES R.
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDES
; FILE REFERENCE: P2019R1
; CURRENT APPLICATION NUMBER: US/11/077,272
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/552,678
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-077-272-2

Query Match          5.7%; Score 70; DB 7; Length 281;
Best Local Similarity 25.5%; Pred. No. 33;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

QY 8 NEKDLRKK-----SELQNALSNLR-----QIYYNEKAITENKES 43
DB 143 NEKALGRKINSWESSRSGHSFLSNLHRLNGELVHKGFFYYISQTYFRFQBEIKENTKN 202
QY 44 DQOFLNTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGVVDLYGAYGYQCAGGTPNK 103
DB 203 DKQMVQ--YIYK--YTSYP--DPILL---MKSARNCSWSKDAE-YGLYSIQ----- 244
QY 104 TACMGVGV-TLHDNNRL 119
DB 245 -----GGIFELKENDRI 256

RESULT 69
US-11-077-272-2
; Sequence 2, Application US/11077272
; Publication No. US20050244927A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, MOON-LAM SUSAN
; APPLICANT: SWARTZ, JAMES R.
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDES
; FILE REFERENCE: P2019R1
; CURRENT APPLICATION NUMBER: US/11/077,272
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/552,678
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-077-272-2

Query Match          5.7%; Score 70; DB 7; Length 281;
Best Local Similarity 25.5%; Pred. No. 33;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

QY 8 NEKDLRKK-----SELQNALSNLR-----QIYYNEKAITENKES 43
DB 143 NEKALGRKINSWESSRSGHSFLSNLHRLNGELVHKGFFYYISQTYFRFQBEIKENTKN 202
QY 44 DQOFLNTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGVVDLYGAYGYQCAGGTPNK 103
DB 203 DKQMVQ--YIYK--YTSYP--DPILL---MKSARNCSWSKDAE-YGLYSIQ----- 244
QY 104 TACMGVGV-TLHDNNRL 119
DB 245 -----GGIFELKENDRI 256

RESULT 70
US-11-136-842-1
; Sequence 1, Application US/11136842
; Publication No. US20060009387A1
; GENERAL INFORMATION:
; APPLICANT: Flores, Heather
; APPLICANT: Lin, Tanya P.
; APPLICANT: Matthews, Timothy C.
; APPLICANT: Pai, Roger
; APPLICANT: Shahrokh, Zahra
; TITLE OF INVENTION: APO-2 LIGAND/TRAIL FORMULATIONS
; FILE REFERENCE: 39766-0174A
; CURRENT APPLICATION NUMBER: US/11/136,842
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US 10/771,254
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/US02/36251
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 281
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-136-842-1

Query Match      5.7%; Score 70; DB 7; Length 281;
Best Local Similarity 25.5%; Pred. No. 33;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

QY      8 NEKDLRKK-----SELQRNALSRL-----QIYYNEKAITENKES 43
DB      143 NEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEI KENTKN 202
QY      44 DQOFLNTLLFKGFFTHGHPWYNLDLVLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNK 103
DB      203 DKQMVG--YIYK--YTSYP--DPILL---MKSARNCSWCKDAE-YGLYSIQ----- 244
QY      104 TACMYGGV-TLHDNNRL 119
DB      245 -----GGIFELKENDRI 256

RESULT 71
US-11-136-079-5
; Sequence 5, Application US/11136079
; Publication No. US20060014248A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Moore, Gregory L.
; APPLICANT: Chirino, Arthur J.
; APPLICANT: Desjarlais, John R.
; TITLE OF INVENTION: TNF SUPER FAMILY MEMBERS WITH ALTERED IMMUNOGENICITY
; FILE REFERENCE: A-72175-4
; CURRENT APPLICATION NUMBER: US/11/136,079
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: US 60/573,206
; PRIOR FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: US 60/573,301
; PRIOR FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: US 60/573,395
; PRIOR FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: US 60/588,314
; PRIOR FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/607,396
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/607,397
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 10/794,751
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 60/452,707
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/482,081
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US 10/338,785
; PRIOR FILING DATE: 2003-01-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 772
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-136-079-5

Query Match      5.7%; Score 70; DB 7; Length 281;
Best Local Similarity 25.5%; Pred. No. 33;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

QY      8 NEKDLRKK-----SELQRNALSRL-----QIYYNEKAITENKES 43
DB      143 NEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEI KENTKN 202
QY      44 DQOFLNTLLFKGFFTHGHPWYNLDLVLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNK 103
DB      203 DKQMVG--YIYK--YTSYP--DPILL---MKSARNCSWCKDAE-YGLYSIQ----- 244
QY      104 TACMYGGV-TLHDNNRL 119
DB      245 -----GGIFELKENDRI 256

RESULT 72
US-11-105-172-4
; Sequence 4, Application US/11105172
; Publication No. US20050244370A1
; GENERAL INFORMATION:
; APPLICANT: Pfizenmaier, Klaus
; APPLICANT: Wajant, Harald
; TITLE OF INVENTION: Selective local activation of members of the TNF
; TITLE OF INVENTION: receptor family by systemically inactive
; TITLE OF INVENTION: non-antibody TNF ligand fusion proteins
; FILE REFERENCE: 2910-1-001
; CURRENT APPLICATION NUMBER: US/11/105,172
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: DE 102 47 755.8
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: Coding
; OTHER INFORMATION: sequence and/or translated amino acid sequence
; OTHER INFORMATION: of the fusion protein CD40ex-Flag-TRAIL
; OTHER INFORMATION: (construct B) according to the invention.
US-11-105-172-4

Query Match      5.7%; Score 70; DB 7; Length 391;
Best Local Similarity 25.5%; Pred. No. 51;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

QY      8 NEKDLRKK-----SELQRNALSRL-----QIYYNEKAITENKES 43
DB      253 NEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEI KENTKN 312
QY      44 DQOFLNTLLFKGFFTHGHPWYNLDLVLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNK 103
DB      313 DKQMVG--YIYK--YTSYP--DPILL---MKSARNCSWCKDAE-YGLYSIQ----- 354
QY      104 TACMYGGV-TLHDNNRL 119
DB      355 -----GGIFELKENDRI 366

RESULT 73
US-11-098-686-11240
; Sequence 11240, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11240
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
```

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Db      203 DKQMVG--YIYK--YTSYP--DPILL---MKSARNCSWCKDAE-YGLYSIQ----- 244
QY      104 TACMYGGV-TLHDNNRL 119
DB      245 -----GGIFELKENDRI 256

RESULT 72
US-11-105-172-4
; Sequence 4, Application US/11105172
; Publication No. US20050244370A1
; GENERAL INFORMATION:
; APPLICANT: Pfizenmaier, Klaus
; APPLICANT: Wajant, Harald
; TITLE OF INVENTION: Selective local activation of members of the TNF
; TITLE OF INVENTION: receptor family by systemically inactive
; TITLE OF INVENTION: non-antibody TNF ligand fusion proteins
; FILE REFERENCE: 2910-1-001
; CURRENT APPLICATION NUMBER: US/11/105,172
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: DE 102 47 755.8
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: Coding
; OTHER INFORMATION: sequence and/or translated amino acid sequence
; OTHER INFORMATION: of the fusion protein CD40ex-Flag-TRAIL
; OTHER INFORMATION: (construct B) according to the invention.
US-11-105-172-4

Query Match      5.7%; Score 70; DB 7; Length 391;
Best Local Similarity 25.5%; Pred. No. 51;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

QY      8 NEKDLRKK-----SELQRNALSRL-----QIYYNEKAITENKES 43
DB      253 NEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEI KENTKN 312
QY      44 DQOFLNTLLFKGFFTHGHPWYNLDLVLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNK 103
DB      313 DKQMVG--YIYK--YTSYP--DPILL---MKSARNCSWCKDAE-YGLYSIQ----- 354
QY      104 TACMYGGV-TLHDNNRL 119
DB      355 -----GGIFELKENDRI 366

RESULT 73
US-11-098-686-11240
; Sequence 11240, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11240
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
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US-11-098-686-11240

Query Match 5.7%; Score 70; DB 7; Length 459;
Best Local Similarity 21.1%; Pred. No. 62;
Matches 56; Conservative 39; Mismatches 74; Indels 96; Gaps 15;

QY 7 INEKDL-RKXSELO--RNALSRLRQIYYNEKAITENKES-----DDQFLENTLLFK 55
Db 204 INKLDLTRAKEVETARTAL-----YQKRIAQENAEATLSVLLGRSPRLIMDTAER 255

QY 56 GFFTGHPWYNDLLVDLGSKDAT-----NKYKGKVDLYGAY-----GYQC 96
Db 256 G-----VSMKOLSCIPVPGQIPSELLERRPDIRQAEBYTLKATSANIGVAR 301

QY 97 AGTPTN-KTACMYGGVTLHDNNRLTEKKVPINLWIDGQTTVPIDIKVTSKKEVTVQEL 155
Db 302 AAWLPISISLTGLFGVISPH-----LSDLLKNPLKTSYGETGVPI-----L 343

QY 156 DLQARHYLHGKFG--LYNSDSFGGKVQORGLIVPHSSEGSTVSVDLPDAQGQYPTLLRIY 213
Db 344 D-----FGQVYVNEAAQAQKREALANYEKTVDQNAFK-DIHDA-----LIRY 385

QY 214 RDNKTINS-----ENLHIDLXYLT 233
Db 386 ESKNIVNSLERNVWYKELRIAVHLART 410

RESULT 74
US-10-453-372-42
; Sequence 42, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 42
; LENGTH: 3130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-42

Query Match 5.7%; Score 70; DB 6; Length 3130;
Best Local Similarity 25.6%; Pred. No. 7.4e+02;
Matches 30; Conservative 14; Mismatches 49; Indels 24; Gaps 3;

QY 25 NLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGK 84
Db 2894 NGRPINTAREPPLTQALIPGDVFAKNS-LWKGAY-----EYQGGK 2932

QY 85 VDLYGAYGYQCAGGTPNKTACMYGSGVTLLHDNNRLTEKKVPINLWIDGKQTTVPID 141
Db 2933 QPAMLRVTGFGQVANSKVNATMIDHSGVELH---LAGTYKKDFHLLLVQVYITGPVE 2986

RESULT 75
US-10-453-372-40
; Sequence 40, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 40
; LENGTH: 3483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-40

Query Match 5.7%; Score 70; DB 6; Length 3483;
Best Local Similarity 25.6%; Pred. No. 8.4e+02;
Matches 30; Conservative 14; Mismatches 49; Indels 24; Gaps 3;

QY 25 NLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGK 84
Db 3247 NGRPINTAREPPLTQALIPGDVFAKNS-LWKGAY-----EYQGGK 3285

QY 85 VDLYGAYGYQCAGGTPNKTACMYGSGVTLLHDNNRLTEKKVPINLWIDGKQTTVPID 141
Db 3286 QPAMLRVTGFGQVANSKVNATMIDHSGVELH---LAGTYKKDFHLLLVQVYITGPVE 3339

Search completed: February 15, 2006, 20:39:08
Job time : 9.66409 secs